

FILE 'REGISTRY' ENTERED AT 14:23:21 ON 01 MAR 2004  
L1 18 SEA ABB=ON PLU=ON AGACAATCACAGTCTCTGCGGA | ATCCTTGTCCTC  
CACGGGTT | CTCATTTGGAATTTTGCC | CGAGTGAAGATCCCCTT/SQSN  
AND SQL=<60

L1 ANSWER 1 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 644078-30-8 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 143: PN: WO2004003140 SEQID: 144 unclaimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 140:92602

L1 ANSWER 2 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 644078-29-5 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 142: PN: WO2004003140 SEQID: 143 unclaimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 140:92602

L1 ANSWER 3 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 566959-46-4 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 127: PN: WO03060090 SEQID: 129 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:132464

L1 ANSWER 4 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 566959-45-3 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 126: PN: WO03060090 SEQID: 128 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:132464

L1 ANSWER 5 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 515226-13-8 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 21

SEQ 1 cgagtgaaga tccccttttt a  
=====

HITS AT: 1-17

REFERENCE 1: 138:332416

L1 ANSWER 6 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 515226-12-7 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:332416

L1 ANSWER 7 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-55-2 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 17

SEQ 1 cgagtgaaga tcccctt  
=====

HITS AT: 1-17

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 8 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-54-1 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 18

SEQ 1 ctcatttgga attttgcc  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 9 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-53-0 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atcccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 10 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-52-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 11 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 475604-53-6 REGISTRY  
CN DNA, d(A-T-C-C-T-T-G-T-C-C-T-C-C-A-C-G-G-G-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 20

SEQ 1 atccttggtcc tccacgggtt  
=====

HITS AT: 1-20

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 475604-52-5 REGISTRY  
CN DNA, d(A-G-A-C-A-A-T-C-A-C-A-G-T-C-T-C-T-G-C-G-G-A) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 22

SEQ 1 agacaatcac agtctctgcg ga  
=====

HITS AT: 1-22

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-56-0 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 17: PN: WO02070751 SEQID: 17 claimed DNA  
CI MAN  
SQL 17

SEQ 1 cgagtgaaga tcccctt  
=====

HITS AT: 1-17

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-55-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 16: PN: WO02070751 SEQID: 16 claimed DNA  
CI MAN  
SQL 18

SEQ 1 ctcatattgga attttgcc  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-50-4 REGISTRY  
CN DNA, d(A-T-C-C-T-T-G-T-C-C-T-C-C-A-C-G-G-G-T-T) (9CI) (CA INDEX



NAME)  
OTHER NAMES:  
CN 7: PN: WO02070751 SEQID: 7 claimed DNA  
CI MAN  
SQL 20

SEQ 1 atccttggtc tccacgggtt  
=====

HITS AT: 1-20

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-49-1 REGISTRY  
CN DNA, d(A-G-A-C-A-A-T-C-A-C-A-G-T-C-T-C-T-G-C-G-G-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 6: PN: WO02070751 SEQID: 6 claimed DNA  
CI MAN  
SQL 22

SEQ 1 agacaatcac agtctctgcg ga  
=====

HITS AT: 1-22

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-48-0 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 4: PN: WO02070751 SEQID: 4 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-47-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 3: PN: WO02070751 SEQID: 3 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

FILE 'HCAPLUS' ENTERED AT 14:27:10 ON 01 MAR 2004  
L2 5 S L1

L2 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
ED Entered STN: 11 Jan 2004

ACCESSION NUMBER: 2004:20803 HCAPLUS

DOCUMENT NUMBER: 140:92602

TITLE: Cytokine receptor zcytor17 multimers, encoding  
polynucleotides and antibodies for diagnosis and  
treatment of inflammatory diseases

INVENTOR(S): Sprecher, Cindy A.; Gao, Zeren; Kuijper, Joseph  
L.; Dasovich, Maria M.; Grant, Francis J.;  
Presnell, Scott R.; Whitmore, Theodore E.;  
Hammond, Angela K.; Novak, Julia E.; Gross, Jane  
A.; Dillon, Stacey R.

PATENT ASSIGNEE(S): Zymogenetics, Inc., USA

SOURCE: PCT Int. Appl., 372 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004003140	A2	20040108	WO 2003-US1983	20030121
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003215838	A1	20031120	US 2003-351157	20030121
PRIORITY APPLN. INFO.:			US 2002-350325P	P 20020118
			US 2002-389108P	P 20020614
			US 2002-435361P	P 20021219

AB Novel polypeptide combinations, polynucleotides encoding the polypeptides, and related compns. and methods are disclosed for zcytor17-containing multimeric or heterodimer cytokine receptors that may be used as novel cytokine antagonists, and within methods for detecting ligands that stimulate the proliferation and/or development of hematopoietic, lymphoid and myeloid cells in vitro

and in vivo. The present invention also includes methods for producing the multimeric or heterodimeric cytokine receptor, uses therefor and antibodies thereto.

IT 644078-29-5 644078-30-8

RL: PRP (Properties)

(unclaimed nucleotide sequence; cytokine receptor zcytor17 multimers, encoding polynucleotides and antibodies for diagnosis and treatment of inflammatory diseases)

L2 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN

ED Entered STN: 25 Jul 2003

ACCESSION NUMBER: 2003:571117 HCAPLUS

DOCUMENT NUMBER: 139:132464

TITLE: Cytokine zcytor17 ligand, polynucleotides and antibodies for diagnosis and treatment of acute inflammatory diseases

INVENTOR(S): Sprecher, Cindy A.; Kuijper, Joseph L.; Dasovich, Maria M.; Grant, Francis J.; Hammond, Angela K.; Novak, Julia E.; Gross, Jane A.; Dillon, Stacey R.

PATENT ASSIGNEE(S): Zymogenetics, Inc., USA

SOURCE: PCT Int. Appl., 372 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003060090	A2	20030724	WO 2003-US1984	20030121
W:			AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM	
RW:			GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG	
US 2003224487	A1	20031204	US 2003-352554	20030121
PRIORITY APPLN. INFO.:			US 2002-350325P	P 20020118
			US 2002-375323P	P 20020425
			US 2002-435315P	P 20021219

AB The present invention relates to zcytor17lig polynucleotide, polypeptide and anti-zcytor17 antibody mols. The zcytor17lig is a novel cytokine. The polypeptides may be used within methods for stimulating the immune system, and proliferation and/or development of hematopoietic cells or hematopoietic cell progenitors in vitro and in vivo. The present invention also includes methods for producing the protein, polynucleotides and antibodies for diagnosis and treatment of acute inflammatory diseases such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia, toxic shock

syndrome, and infectious disease.

IT 566959-45-3 566959-46-4  
RL: ARU (Analytical role, unclassified); DGN (Diagnostic use); PRP  
(Properties); ANST (Analytical study); BIOL (Biological study); USES  
(Uses)  
(cytokine zcytor17 ligand for hematopoietic cell expansion and  
for diagnosis and treatment of acute inflammatory diseases)

L2 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN

ED Entered STN: 04 Mar 2003

ACCESSION NUMBER: 2003:161443 HCAPLUS

DOCUMENT NUMBER: 138:332416

TITLE: Quantitative intra-individual monitoring of  
BCR-ABL transcript levels in archival bone  
marrow trephines of patients with chronic  
myeloid leukemia

AUTHOR(S): Bock, Oliver; Lehmann, Ulrich; Kreipe, Hans  
CORPORATE SOURCE: Institute of Pathology, Medizinische Hochschule  
Hannover, Hannover, Germany

SOURCE: Journal of Molecular Diagnostics (2003), 5(1),  
54-60

CODEN: JMDIFP; ISSN: 1525-1578

PUBLISHER: Association for Molecular Pathology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We established a quant. real-time RT-PCR assay for the detection of  
chimeric BCR-ABL transcripts in archival formalin-fixed bone marrow  
trephines, both acrylate-embedded and paraffin-embedded. This new  
methodol. enables determination of transcript levels in direct comparison to  
histopathol. findings and therapeutic interventions during the time  
course of the disease in a retrospective and a prospective manner.  
We found an excellent correlation between the quant. mol. data and  
the morphol. evaluation as well as the clin. outcome for a cohort of  
chronic myeloid leukemia patients (n = 10). To the best of our  
knowledge, this is the first study demonstrating the feasibility of  
large-scale quant. expression anal. in archival bone marrow  
trephines for monitoring mol. markers over several years or even  
decades.

IT 515226-12-7 515226-13-8

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP  
(Properties); ANST (Analytical study); BIOL (Biological study); USES  
(Uses)

(PCR primer for BCR-ABL transcript in chronic myeloid leukemia;  
quant. intra-individual monitoring of BCR-ABL transcript levels  
in archival bone marrow trephines of patients with chronic  
myeloid leukemia)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

L2 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN

ED Entered STN: 13 Sep 2002

ACCESSION NUMBER: 2002:696171 HCAPLUS

DOCUMENT NUMBER: 137:227595

TITLE: Methods for quantitative multiplex reverse  
transcriptase-polymerase chain reaction for

esophageal adenocarcinoma diagnosis by detection  
of carcinoembryonic antigen gene expression in  
sentinel lymph nodes

INVENTOR(S): Godfrey, Tony E.; Luketich, James D.; Raja,  
Siva; Kelly, Lori A.; Finkelstein, Sydney D.  
PATENT ASSIGNEE(S): University of Pittsburgh of the Commonwealth  
System of Higher Education, USA  
SOURCE: PCT Int. Appl., 141 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002070751	A1	20020912	WO 2002-US6504	20020304
W:				
				AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW:				GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2003017482	A1	20030123	US 2002-90326	20020304
EP 1373569	A1	20040102	EP 2002-715027	20020304
R:				AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.:			US 2001-273277P	P 20010302
			WO 2002-US6504	W 20020304

AB A method for balancing multiplexed PCR methods is provided. In the method, two or more sequential temporal PCR stages are used to effectively sep. two or more PCR reactions in a single tube as an alternative to primer limiting to modulate the relative rate of production of a first amplicon by a first primer set and a second amplicon by a second primer set during the first and second amplification stages. Also provided are rapid RT-PCR methods that find particular use in intraoperative diagnoses and prognoses, for instance in diagnosing malignant esophageal adenocarcinoma by determining expression levels of carcinoembryonic antigen (CEA) in sentinel lymph nodes.

IT 458572-47-9 458572-48-0 458572-49-1  
458572-50-4 458572-55-9 458572-56-0

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(primer sequence; methods for multiplex quant. RT-PCR for esophageal adenocarcinoma diagnosis by detection of carcinoembryonic antigen gene expression in sentinel lymph nodes)

L2 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
RD Entered STN: 04 Aug 2002

*Advances*

ACCESSION NUMBER: 2002:576750 HCAPLUS  
DOCUMENT NUMBER: 137:380556  
TITLE: Temperature-controlled primer limit for  
multiplexing of rapid, quantitative reverse  
transcription-PCR assays: application to  
intraoperative cancer diagnostics  
AUTHOR(S): Raja, Siva; El-Hefnawy, Talal; Kelly, Lori A.;  
Chestney, Melissa L.; Luketich, James D.;  
Godfrey, Tony E.  
CORPORATE SOURCE: Division of Thoracic Surgery, University of  
Pittsburgh Medical Center, Pittsburgh, PA,  
15213, USA  
SOURCE: Clinical Chemistry (Washington, DC, United  
States) (2002), 48(8), 1329-1337  
CODEN: CLCHAU; ISSN: 0009-9147  
PUBLISHER: American Association for Clinical Chemistry  
DOCUMENT TYPE: Journal  
LANGUAGE: English

*peptides' work*

AB Rapid-cycling, real-time PCR instruments bring the opportunity for improved intraoperative detection of metastasis to sentinel lymph nodes. Rapid, standardized, and internally controlled assays need to be developed that are sensitive and accurate. The authors describe rapid, multiplexed, internally controlled, quant. reverse transcription-PCR (QRT-PCR) assays for tyrosinase and carcinoembryonic antigen mRNAs on the SmartCycler (Cepheid). A temperature-controlled primer-limiting approach was used to eliminate amplification of the endogenous control gene as soon as its signal had reached threshold. Pos.-control oligonucleotide mimics were incorporated into all reactions to differentiate failed reactions from true neg. samples. The optimized assays for rapid QRT-PCR yielded results with threshold cycle values that were only 1-2 cycles higher than slower, more conventional protocols. In rapid PCR, the temperature-controlled multiplex assay was quant. over a dynamic range of at least 15 cycles, compared with only 6 cycles for conventional multiplexing methods. All histol. pos. lymph nodes examined were also QRT-PCR pos. for the appropriate marker, and the exogenous, internal pos.-control mimics produced signals in all neg. samples. Internally controlled, rapid QRT-PCR assays can be performed in an intraoperative time frame and with sufficient sensitivity to detect histol. identified metastases to lymph nodes.

*August 2002*

IT 475604-52-5 475604-53-6 479323-52-9  
479323-53-0 479323-54-1 479323-55-2

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(primer; temperature-controlled primer limit for multiplexing of rapid, quant. reverse transcription-PCR assays and application to intraoperative cancer diagnostics)

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

=> fil hom  
FILE 'HOME' ENTERED AT 14:28:07 ON 01 MAR 2004

09:38:24 2004

us-10-090-326-6.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model  
February 29, 2004, 08:42:24 : Search time 686.857 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

S-10-090-326-6  
2  
agacaatcacagtctctcgga 22  
DENTIFY\_NUC  
apop 10.0 , Gapext 1.0  
470272 seqs, 21671516995 residues  
its satisfying chosen parameters: 1685580

ngth: 0  
ngth: 60  
Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl: \*  
: gb.ba.\*  
: gb.htg.\*  
: gb.in.\*  
: gb.om.\*  
: gb.ov.\*  
: gb.pat.\*  
: gb.ph.\*  
: gb.pl.\*  
: gb.pr.\*  
: gb.ro.\*  
: gb.sts.\*  
: gb.sy.\*  
: gb.un.\*  
: gb.vi.\*  
: gb.ba.\*  
: em.fun.\*  
: em.hum.\*  
: em.in.\*  
: em.mu.\*  
: em.om.\*  
: em.or.\*  
: em.ov.\*  
: em.pat.\*  
: em.ph.\*  
: em.pl.\*  
: em.ro.\*  
: em.sts.\*  
: em.un.\*  
: em.vi.\*  
: em.htg.hum.\*  
: em.htg.inv.\*  
: em.htg.other.\*  
: em.htg.mus.\*  
: em.htg.pln.\*  
: em.htg.pln.\*  
: em.htg.rod.\*  
: em.htg.mam.\*  
: em.htg.vrt.\*  
: em.sy.\*  
: em.go.hum.\*  
: em.go.mus.\*  
: em.go.other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being pr  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Descriptio
1	15.8	71.8	46	6	A39901	A39901 Seq
2	15.8	71.8	46	6	A39902	A39902 Seq
3	15.8	71.8	46	6	I67749	I67749 Seq
4	15.8	71.8	46	6	I67750	I67750 Seq
5	15.6	70.9	30	6	AR073249	AR073249 S
6	14.2	64.5	20	12	AB069564	AB069564
7	14	63.6	25	6	AX688871	AX688871 S
8	14	63.6	25	6	AX688872	AX688872 S
9	14	63.6	25	6	AX688873	AX688873 S
10	14	63.6	25	6	AX688874	AX688874 S
11	14	63.6	58	11	BX322287	BX322287
12	13.6	61.8	21	6	AX154379	AX154379 S
13	13.6	61.8	37	6	AR268993	AR268993 S
14	13.6	61.8	50	6	AX794202	AX794202 S
15	13.6	61.8	50	14	APHCNOV5E	MI0505 FC
16	13.6	61.8	53	6	AX794228	AX794228 S
17	13.2	60.0	22	6	AR252308	AR252308 S
18	13.2	60.0	22	6	BD133429	BD133429 S
19	13.2	60.0	35	6	I20757	I20757 Seq
20	13.2	60.0	35	6	AR381829	AR381829 S
21	13.2	60.0	35	6	BD107806	BD107806 S
22	13.2	60.0	47	6	AR289738	AR289738 S
23	13.2	60.0	51	6	AX199173	AX199173 S
24	13.2	60.0	51	6	AX199174	AX199174 S
25	13	59.1	22	6	AR072233	AR072233 S
26	13	59.1	22	6	I26344	I26344 Seq
27	13	59.1	25	6	AX688870	AX688870 S
28	13	59.1	25	6	AX688875	AX688875 S
29	13	59.1	28	6	AR090992	AR090992 S
30	13	59.1	28	6	AR198027	AR198027 S
31	13	59.1	28	6	AR260181	AR260181 S
32	13	59.1	28	6	AX794235	AX794235 S
33	13	59.1	34	6	I92361	I92361 Seq
34	13	59.1	40	6	AX538476	AX538476 S
35	13	59.1	47	6	AX195024	AX195024 S
36	13	59.1	50	6	AX234381	AX234381 S
37	13	59.1	51	6	AX158793	AX158793 S
38	13	59.1	51	6	AX158794	AX158794 S
39	13	59.1	51	6	AX158795	AX158795 S
40	13	59.1	60	6	AX234390	AX234390 S
41	12.8	58.2	20	6	AX285267	AX285267 S
42	12.8	58.2	20	6	AX302070	AX302070 S
43	12.8	58.2	24	6	AX117974	AX117974 S
44	12.8	58.2	47	6	AR289827	AR289827 S
45	12.8	58.2	51	6	AX190056	AX190056 S
46	12.8	58.2	53	6	A38622	A38622 Se
47	12.6	57.3	20	6	BD000414	BD000414
48	12.6	57.3	24	6	AX444764	AX444764 S
49	12.6	57.3	25	6	AX487737	AX487737 S
50	12.6	57.3	25	6	AX688876	AX688876 S
51	12.6	57.3	25	6	AX688877	AX688877 S
52	12.6	57.3	28	6	BD012173	BD012173 S
53	12.6	57.3	29	6	BD007101	BD007101 S
54	12.6	57.3	30	6	AX611183	AX611183 S
55	12.6	57.3	35	6	EL1201	EL1201 Pr
56	12.6	57.3	35	6	AR381830	AR381830 S
57	12.6	57.3	35	6	BD107807	BD107807 S
58	12.6	57.3	45	6	E41224	E41224 Me
59	12.6	57.3	47	6	AR291461	AR291461 S
60	12.6	57.3	48	6	AR038999	AR038999 S
61	12.6	57.3	48	6	AR107391	AR107391 S
62	12.6	57.3	48	6	AR179353	AR179353 S
63	12.6	57.3	48	6	BD191616	BD191616 S
64	12.6	57.3	49	6	I88612	I88612 Se
65	12.6	57.3	50	6	BD021860	BD021860 S

57.3	51	6	AX156752	AX156752 Sequence	139	12.2	55.5	43	6	AR066433	AR066433
57.3	59	6	AR117938	AR117938 Sequence	140	12.2	55.5	48	6	AR032396	AR032396
57.3	59	6	AX702420	AX702420 Sequence	141	12.2	55.5	48	6	I29136	I29136 Se
57.3	60	6	AX601604	AX601604 Sequence	142	12.2	55.5	48	6	I90810	I90810 Se
57.3	60	9	HUMSAU3A18	D49602 Homo sapien	143	12.2	55.5	49	6	AR0209060	AR0209060
57.3	60	14	POLDIPE	M30215 Poliovirus	144	12.2	55.5	49	6	AR032467	AR032467
56.4	17	6	AR264874	AR264874 Sequence	145	12.2	55.5	49	6	I29207	I29207 Se
56.4	17	6	AX672976	AX672976 Sequence	146	12.2	55.5	49	6	I90881	I90881 Se
56.4	21	6	AX096905	AX096905 Sequence	147	12.2	55.5	49	6	AR209131	AR209131
56.4	23	6	AX609017	AX609017 Sequence	148	12.2	55.5	50	6	AR282107	AR282107
56.4	24	6	BD123414	BD123414 SREBP-2 g	149	12.2	55.5	50	6	AR282183	AR282183
56.4	27	6	AX115218	AX115218 Sequence	151	12.2	55.5	51	6	AX155780	AX155780
56.4	29	6	AR275150	AR275150 Sequence	152	12.2	55.5	52	6	AX203927	AX203927
56.4	29	6	AR275152	AR275152 Sequence	153	12.2	55.5	52	6	AX358962	AX358962
56.4	29	6	AR275656	AR275656 Sequence	154	12.2	54.5	20	6	AX823877	AX823877
56.4	29	6	AR275658	AR275658 Sequence	155	12.2	54.5	21	6	BD142669	BD142669
56.4	29	6	AR302383	AR302383 Sequence	156	12.2	54.5	21	6	AX546754	AX546754
56.4	29	6	AR302385	AR302385 Sequence	157	12.2	54.5	21	6	BD076524	BD076524
56.4	30	6	AR201030	AR201030 Sequence	158	12.2	54.5	22	6	AR173645	AR173645
56.4	30	6	AR202721	AR202721 Sequence	159	12.2	54.5	22	6	BD057079	BD057079
56.4	30	6	BD009773	BD009773 Humanized	160	12.2	54.5	23	6	AR252592	AR252592
56.4	30	6	BD103748	BD103748 A method	161	12.2	54.5	23	6	AX055761	AX055761
56.4	33	6	AX166487	AX166487 Sequence	162	12.2	54.5	23	6	AX403436	AX403436
56.4	34	6	AR073271	AR073271 Sequence	163	12.2	54.5	23	6	AX742290	AX742290
56.4	34	6	AR073272	AR073272 Sequence	164	12.2	54.5	23	6	AX742689	AX742689
56.4	35	6	AR261794	AR261794 Sequence	165	12.2	54.5	23	6	BD184114	BD184114
56.4	40	6	A22794	A22794 NS3/NS4 HCV	166	12.2	54.5	23	6	BD184542	BD184542
56.4	40	6	AR031221	AR031221 Sequence	167	12.2	54.5	24	6	AR124725	AR124725
56.4	40	6	AR145037	AR145037 Sequence	168	12.2	54.5	24	6	E44013 NC	E44013 NC
56.4	47	6	AR291053	AR291053 Sequence	169	12.2	54.5	25	6	AX688869	AX688869
56.4	48	6	AX538900	AX538900 Sequence	170	12.2	54.5	26	6	AX181875	AX181875
56.4	48	6	AX538901	AX538901 Sequence	171	12.2	54.5	26	6	BD077275	BD077275
56.4	48	6	AX777222	AX777222 Sequence	172	12.2	54.5	29	6	E44009 NC	E44009 NC
56.4	50	10	MMU41939	U41939 Mus musculus	173	12.2	54.5	29	6	AX923503	AX923503
56.4	51	6	AX158733	AX158733 Sequence	174	12.2	54.5	30	6	AR092575	AR092575
56.4	51	6	AX158734	AX158734 Sequence	175	12.2	54.5	30	6	AR161734	AR161734
56.4	51	6	AX161895	AX161895 Sequence	176	12.2	54.5	30	6	BD076521	BD076521
56.4	51	6	AX189854	AX189854 Sequence	177	12.2	54.5	32	6	BD228400	BD228400
56.4	51	6	AX189855	AX189855 Sequence	178	12.2	54.5	32	6	AX021034	AX021034
55.5	21	6	AX189853	AX189853 Sequence	179	12.2	54.5	32	6	AX742153	AX742153
55.5	22	6	AR164381	AR164381 Sequence	180	12.2	54.5	33	6	AR216133	AR216133
55.5	22	6	AR205924	AR205924 Sequence	181	12.2	54.5	34	6	BD091493	BD091493
55.5	22	6	AX613801	AX613801 Sequence	182	12.2	54.5	34	6	BD091522	BD091522
55.5	22	6	BD204896	BD204896 Compositi	183	12.2	54.5	35	6	I86946	I86946 S
55.5	24	6	AR164359	AR164359 Sequence	184	12.2	54.5	39	6	AR075226	AR075226
55.5	24	6	AR205902	AR205902 Sequence	185	12.2	54.5	39	6	AR110756	AR110756
55.5	24	6	BD204874	BD204874 Compositi	186	12.2	54.5	39	6	AR152638	AR152638
55.5	25	6	AX487081	AX487081 Sequence	187	12.2	54.5	39	6	I61250 S	I61250 S
55.5	27	6	AX298450	AX298450 Sequence	188	12.2	54.5	39	6	AR238478	AR238478
55.5	27	6	AX804126	AX804126 Sequence	189	12.2	54.5	39	6	AX323317	AX323317
55.5	29	6	A94089	A94089 Sequence 70	190	12.2	54.5	39	6	AX453615	AX453615
55.5	29	6	BD234835	BD234835 FAP-alpha	191	12.2	54.5	40	6	AR088238	AR088238
55.5	29	6	AR232611	AR232611 Sequence	192	12.2	54.5	41	6	AR031370	AR031370
55.5	29	6	AX011174	AX011174 Sequence	193	12.2	54.5	41	6	AR428932	AR428932
55.5	29	6	AX115675	AX115675 Sequence	194	12.2	54.5	41	6	BD009738	BD009738
55.5	30	6	E09320	E09320 Primer. 9/1	195	12.2	54.5	41	6	BD134372	BD134372
55.5	30	6	AX397876	AX397876 Sequence	196	12.2	54.5	42	6	AR087150	AR087150
55.5	32	6	AX397876	AX397876 Sequence	197	12.2	54.5	42	6	AR087567	AR087567
55.5	33	6	AR138388	AR138388 Sequence	198	12.2	54.5	42	6	I23964	I23964 S
55.5	36	6	A94088	A94088 Sequence 69	199	12.2	54.5	42	6	AX538891	AX538891
55.5	36	6	BD234834	BD234834 FAP-alpha	200	12.2	54.5	48	6	AR239863	AR239863
55.5	36	6	AR232610	AR232610 Sequence	201	12.2	54.5	48	6	AX279665	AX279665
55.5	36	6	AX011173	AX011173 Sequence	202	12.2	54.5	49	6	AX098901	AX098901
55.5	37	6	AX351243	AX351243 Sequence	203	12.2	54.5	49	6	AX099321	AX099321
55.5	38	6	AX351227	AX351227 Sequence	204	12.2	54.5	51	6	AX203930	AX203930
55.5	38	6	AX351241	AX351241 Sequence	205	12.2	54.5	51	6	AX204088	AX204088
55.5	38	6	AX351242	AX351242 Sequence	206	12.2	54.5	52	6	AX098924	AX098924
55.5	38	6	AX351244	AX351244 Sequence	207	12.2	54.5	52	6	AX099344	AX099344
55.5	38	6	AX351245	AX351245 Sequence	208	12.2	54.5	52	6	AX616677	AX616677
55.5	38	6	AX351249	AX351249 Sequence	209	12.2	54.5	52	6	AF22410	AF22410
55.5	42	6	AX33012	AX33012 Synthetic P	210	12.2	54.5	57	6	A20235	A20235 C
55.5	42	6	AX357182	AX357182 Sequence	211	12.2	54.5	57	6	A21530	A21530 C



54.5	57	6	I43788	I43788 Sequence 6	C 285	11.8	53.6	36	6	E15602	E15602 PCR
54.5	60	6	AX365982	AX365982 Sequence	C 286	11.8	53.6	36	6	AR241669	AR241669 S
54.5	60	6	BD102027	BD102027 Agonist a	C 287	11.8	53.6	36	6	AR255385	AR255385 S
54.5	60	6	BD102181	BD102181 Apoptosis	C 288	11.8	53.6	36	6	BD131670	BD131670 V
54.5	60	6	BD169241	BD169241 Degraded	C 289	11.8	53.6	37	6	A73059	A73059 Sec
54.5	60	6	BD169352	BD169352 Small rem	C 290	11.8	53.6	37	6	A73151	A73151 Sec
54.5	60	6	AX731931	AX731931 Sequence	C 291	11.8	53.6	37	6	AR091834	AR091834 S
53.6	17	6	AX733647	AX733647 Sequence	C 292	11.8	53.6	37	6	AR093116	AR093116 S
53.6	17	6	AR015985	AR015985 Sequence	C 293	11.8	53.6	37	6	AR126955	AR126955 S
53.6	20	6	AR082026	AR082026 Sequence	C 294	11.8	53.6	37	6	AR157742	AR157742 S
53.6	20	6	AR137290	AR137290 Sequence	C 295	11.8	53.6	37	6	AX329127	AX329127 S
53.6	20	6	BD231273	BD231273 Genes for	C 296	11.8	53.6	37	6	AX351239	AX351239 S
53.6	20	6	AR311725	AR311725 Sequence	C 297	11.8	53.6	38	6	E17023	E17023 Pr
53.6	20	6	AR311728	AR311728 Sequence	C 298	11.8	53.6	38	6	AX351230	AX351230 S
53.6	20	6	AR337230	AR337230 Sequence	C 299	11.8	53.6	38	6	AX351240	AX351240 S
53.6	20	6	AR337231	AR337231 Sequence	C 300	11.8	53.6	39	6	BD101752	BD101752 C
53.6	20	6	AX037412	AX037412 Sequence	C 301	11.8	53.6	40	6	A62104	A62104 Sec
53.6	20	6	BD075164	BD075164 Methods f	C 302	11.8	53.6	40	6	AR077632	AR077632 S
53.6	22	6	AX804127	AX804127 Sequence	C 303	11.8	53.6	41	6	BD271465	BD271465 S
53.6	22	6	BD130428	BD130428 DNAs and	C 304	11.8	53.6	41	6	AR265695	AR265695 S
53.6	24	6	A07553	A07553 Synthetic O	C 305	11.8	53.6	41	6	BD092132	BD092132 I
53.6	25	6	AX614257	AX614257 Sequence	C 306	11.8	53.6	42	6	AX351180	AX351180 S
53.6	27	6	AR088840	AR088840 Sequence	C 307	11.8	53.6	43	6	E54984	E54984 Pei
53.6	27	6	AR167314	AR167314 Sequence	C 308	11.8	53.6	43	6	I08287	I08287 Sec
53.6	27	6	I36697	I36697 Sequence 6	C 309	11.8	53.6	43	6	AX601780	AX601780 S
53.6	27	6	AX467533	AX467533 Sequence	C 310	11.8	53.6	43	6	BD092131	BD092131 I
53.6	28	6	AR091064	AR091064 Sequence	C 311	11.8	53.6	46	6	A25742	A25742 Mo
53.6	28	6	AR158099	AR158099 Sequence	C 312	11.8	53.6	46	6	AR051359	AR051359 S
53.6	28	6	AR260253	AR260253 Sequence	C 313	11.8	53.6	47	6	AR362003	AR362003 S
53.6	28	6	AX006984	AX006984 Sequence	C 314	11.8	53.6	47	6	AX194953	AX194953 S
53.6	30	6	AR089389	AR089389 Sequence	C 315	11.8	53.6	48	6	AR078401	AR078401 S
53.6	30	6	AR093589	AR093589 Sequence	C 316	11.8	53.6	48	6	I05893	I05893 Sec
53.6	30	6	E23305	E23305 Antibody ag	C 317	11.8	53.6	48	6	I05937	I05937 Sec
53.6	30	6	E27074	E27074 Remedy for	C 318	11.8	53.6	48	6	I09170	I09170 Sec
53.6	30	6	AX793129	AX793129 Sequence	C 319	11.8	53.6	48	6	AR431342	AR431342 S
53.6	30	6	BD011905	BD011905 Ameliorat	C 320	11.8	53.6	50	6	A25699	A25699 MO
53.6	30	6	BD011961	BD011961 Therapeut	C 321	11.8	53.6	50	6	AR051358	AR051358 S
53.6	30	6	BD012022	BD012022 Therapeut	C 322	11.8	53.6	50	6	AX156824	AX156824 S
53.6	30	6	BD012909	BD012909 Inhibitin	C 323	11.8	53.6	51	6	AR251898	AR251898 S
53.6	30	6	BD095479	BD095479 Remedies	C 324	11.8	53.6	51	6	AR356682	AR356682 S
53.6	30	6	BD095640	BD095640 Stable an	C 325	11.8	53.6	51	6	AX118085	AX118085 S
53.6	30	6	BD140965	BD140965 An agent	C 326	11.8	53.6	51	6	AX156823	AX156823 S
53.6	30	6	BD182377	BD182377 An agent	C 327	11.8	53.6	51	6	AX160633	AX160633 S
53.6	31	6	A07573	A07573 p11197 DNA	C 328	11.8	53.6	53	6	BD057275	BD057275 S
53.6	31	6	A07575	A07575 p11197 DNA	C 329	11.8	53.6	53	6	BD174596	BD174596 S
53.6	31	6	AR7722	AR7722 Sequence 16	C 330	11.8	53.6	53	6	BD174885	BD174885 S
53.6	31	6	E07915	E07915 Synthetic D	C 331	11.8	53.6	56	6	E30639	E30639 An
53.6	31	6	E30637	E30637 Antibody an	C 332	11.8	53.6	56	6	E31248	E31248 De
53.6	31	6	E31246	E31246 Device for	C 333	11.8	53.6	57	10	AY205874	AY205874
53.6	31	6	AR219869	AR219869 Sequence	C 334	11.8	53.6	57	10	AY205896	AY205896
53.6	31	6	BD195818	BD195818 Method fo	C 335	11.8	53.6	57	10	AY205907	AY205907
53.6	31	6	BD195839	BD195839 Method fo	C 336	11.8	53.6	60	5	AF416916	AF416916
53.6	31	6	BD195851	BD195851 Method fo	C 337	11.8	53.6	60	6	AX100156	AX100156
53.6	31	6	BD195868	BD195868 Method fo	C 338	11.8	53.6	60	10	AY205721	AY205721
53.6	32	6	AR022569	AR022569 Sequence	C 339	11.8	53.6	60	10	AY205734	AY205734
53.6	32	6	AR037584	AR037584 Sequence	C 340	11.8	53.6	60	10	AY205894	AY205894
53.6	32	6	AR084675	AR084675 Sequence	C 341	11.8	53.6	60	10	AY205924	AY205924
53.6	32	6	AR096198	AR096198 Sequence	C 342	11.8	53.6	60	10	AY205945	AY205945
53.6	32	6	AR178042	AR178042 Sequence	C 343	11.6	52.7	18	6	AR292947	AR292947
53.6	32	6	E15598	E15598 PCR primer	C 344	11.6	52.7	20	6	AR136354	AR136354
53.6	32	6	AR210597	AR210597 Sequence	C 345	11.6	52.7	20	6	AR144293	AR144293
53.6	32	6	AR255381	AR255381 Sequence	C 346	11.6	52.7	20	6	BD247809	BD247809
53.6	32	6	BD131666	BD131666 Variable	C 347	11.6	52.7	20	6	AR298926	AR298926
53.6	32	6	AR152555	AR152555 Sequence	C 348	11.6	52.7	22	6	AR037111	AR037111
53.6	33	6	AX351179	AX351179 Sequence	C 349	11.6	52.7	22	6	AR070349	AR070349
53.6	33	6	A62593	A62593 Sequence 12	C 350	11.6	52.7	22	6	AR349320	AR349320
53.6	35	6	AR381831	AR381831 Sequence	C 351	11.6	52.7	23	6	E10558	E10558 PC
53.6	35	6	BD107808	BD107808 Opsonic a	C 352	11.6	52.7	23	6	AX445988	AX445988
53.6	36	6	A62102	A62102 Sequence 2	C 353	11.6	52.7	25	6	E17210	E17210 PC
53.6	36	6	A62105	A62105 Sequence 5	C 354	11.6	52.7	25	6	AX610204	AX610204
53.6	36	6	AR084679	AR084679 Sequence	C 355	11.6	52.7	25	6	AX688878	AX688878
53.6	36	6	AR174687	AR174687 Sequence	C 356	11.6	52.7	28	6	BD012169	BD012169
53.6	36	6			C 357	11.6	52.7	30	6	I71916	I71916 Se

52.7	30	6	AX611107	AX611107 Sequence	431	11.4	51.8	27	6	AR344251	AR344251
52.7	30	6	AX710177	AX710177 Sequence	C 432	11.4	51.8	27	6	AR363454	AR363454
52.7	30	6	AX710183	AX710183 Sequence	433	11.4	51.8	27	6	AX019224	AX019224
52.7	30	6	BD009722	BD009722 A small v	434	11.4	51.8	27	6	AX380913	AX380913
52.7	30	10	MMJ4BMAR	X60916 M.musculus	435	11.4	51.8	27	6	BD130451	BD130451
52.7	31	6	E26048	E26048 Peptide fra	C 436	11.4	51.8	28	6	AR090417	AR090417
52.7	31	6	BD175925	BD175925 Adenoviru	C 437	11.4	51.8	28	6	AR197452	AR197452
52.7	31	6	BD175926	BD175926 Adenoviru	C 438	11.4	51.8	28	6	AR259606	AR259606
52.7	36	6	I57363	I57363 Sequence 6	C 439	11.4	51.8	28	6	AX546587	AX546587
52.7	38	6	AR286994	AR286994 Sequence	440	11.4	51.8	28	6	BD062367	BD062367
52.7	38	6	AR398984	AR398984 Sequence	441	11.4	51.8	28	6	BD062528	BD062528
52.7	40	6	AR026948	AR026948 Sequence	442	11.4	51.8	28	6	BD123404	BD123404
52.7	40	6	E04719	E04719 Probe for d	443	11.4	51.8	30	6	A23417	A23417
52.7	40	6	E05927	E05927 DNA sequenc	444	11.4	51.8	30	6	AR162670	AR162670
52.7	40	6	AX538479	AX538479 Sequence	445	11.4	51.8	30	6	A23417	A23417
52.7	42	6	AR072943	AR072943 Sequence	C 446	11.4	51.8	30	6	AR162670	AR162670
52.7	42	6	AR072947	AR072947 Sequence	C 447	11.4	51.8	30	6	A23417	A23417
52.7	42	6	AR220076	AR220076 Sequence	448	11.4	51.8	30	6	AR162670	AR162670
52.7	42	6	AR220080	AR220080 Sequence	449	11.4	51.8	30	6	A23417	A23417
52.7	42	6	BD002269	BD002269 Cellulase	450	11.4	51.8	32	6	AR242441	AR242441
52.7	42	6	BD002273	BD002273 Cellulase	451	11.4	51.8	32	6	AR280209	AR280209
52.7	42	6	BD010873	BD010873 Cellulase	452	11.4	51.8	32	6	AR322424	AR322424
52.7	42	6	BD010877	BD010877 Cellulase	C 453	11.4	51.8	32	6	AX298092	AX298092
52.7	43	6	AR018916	AR018916 Sequence	C 454	11.4	51.8	32	6	BD000519	BD000519
52.7	43	6	AR061564	AR061564 Sequence	455	11.4	51.8	33	6	AR041116	AR041116
52.7	43	6	AR066544	AR066544 Sequence	456	11.4	51.8	33	6	AR066010	AR066010
52.7	43	6	AR108463	AR108463 Sequence	457	11.4	51.8	33	6	AR072752	AR072752
52.7	43	6	AR112082	AR112082 Sequence	C 458	11.4	51.8	34	6	A05385	A05385
52.7	43	6	I16420	I16420 Sequence 24	C 459	11.4	51.8	34	6	A09592	A09592
52.7	43	6	I66906	I66906 Sequence 24	C 460	11.4	51.8	34	6	AR052830	AR052830
52.7	43	6	I72261	I72261 Sequence 38	C 461	11.4	51.8	34	6	AR288142	AR288142
52.7	43	6	I76828	I76828 Sequence 38	C 462	11.4	51.8	34	6	AX027687	AX027687
52.7	43	6	I85000	I85000 Sequence 24	C 463	11.4	51.8	37	6	AX219934	AX219934
52.7	43	6	AR263424	AR263424 Sequence	C 464	11.4	51.8	38	6	AR365398	AR365398
52.7	45	6	AR042820	AR042820 Sequence	465	11.4	51.8	39	6	AR084390	AR084390
52.7	46	6	AX705163	AX705163 Sequence	466	11.4	51.8	39	6	AR403790	AR403790
52.7	47	6	AR212399	AR212399 Sequence	467	11.4	51.8	40	6	AR089791	AR089791
52.7	47	6	AR289748	AR289748 Sequence	468	11.4	51.8	40	6	BD232084	BD232084
52.7	47	6	AX194957	AX194957 Sequence	C 469	11.4	51.8	40	6	AX365219	AX365219
52.7	50	6	AX513771	AX513771 Sequence	C 470	11.4	51.8	41	6	AX514816	AX514816
52.7	50	6	AX697124	AX697124 Sequence	471	11.4	51.8	41	6	AX517174	AX517174
52.7	51	6	A25124	A25124 Synthetic F	472	11.4	51.8	41	6	A87720	A87720
52.7	51	6	AX204427	AX204427 Sequence	473	11.4	51.8	42	6	AR086060	AR086060
52.7	51	6	MM086736	U86736 Mus musculu	474	11.4	51.8	42	6	AR140414	AR140414
52.7	51	10	MM086740	U86740 Mus musculu	475	11.4	51.8	42	6	AR146895	AR146895
51.8	16	6	A39006	A39006 Sequence 93	C 476	11.4	51.8	42	6	AX179394	AX179394
51.8	16	6	AR054397	AR054397 Sequence	478	11.4	51.8	42	6	AX259868	AX259868
51.8	16	6	AR265147	AR265147 Sequence	479	11.4	51.8	42	6	BD195803	BD195803
51.8	17	6	BD241733	BD241733 Methods a	480	11.4	51.8	43	6	AX601639	AX601639
51.8	17	6	AX760444	AX760444 Sequence	481	11.4	51.8	45	6	A33049	A33049
51.8	17	6	BD200699	BD200699 Method an	482	11.4	51.8	45	6	AR062253	AR062253
51.8	17	6	BD203129	BD203129 Method an	483	11.4	51.8	45	6	AX304972	AX304972
51.8	17	6	BD203130	BD203130 Method an	484	11.4	51.8	45	6	AX306501	AX306501
51.8	19	6	A65726	A65726 Sequence 7	C 485	11.4	51.8	45	6	BD015548	BD015548
51.8	19	6	A87715	A87715 Sequence 9	C 486	11.4	51.8	45	6	BD094926	BD094926
51.8	19	6	BD195812	BD195812 Method fo	C 487	11.4	51.8	46	12	BD131219	BD131219
51.8	19	6	BD195862	BD195862 Method fo	C 488	11.4	51.8	46	12	SYNPRWF	SYNPRWF
51.8	20	6	AR310983	AR310983 Sequence	C 489	11.4	51.8	47	6	I05912	I05912
51.8	20	6	AR310988	AR310988 Sequence	C 490	11.4	51.8	47	6	I05957	I05957
51.8	21	6	BD168673	BD168673 Novel G p	C 491	11.4	51.8	47	6	I09192	I09192
51.8	21	6	BD183781	BD183781 Novel G p	C 492	11.4	51.8	47	6	AR284836	AR284836
51.8	22	6	AR077182	AR077182 Sequence	C 493	11.4	51.8	47	6	AR290374	AR290374
51.8	22	6	AX642816	AX642816 Sequence	494	11.4	51.8	47	6	AR292006	AR292006
51.8	22	6	AX298966	AX298966 Sequence	495	11.4	51.8	47	6	AR292117	AR292117
51.8	23	6	I63118	I63118 Sequence 1	496	11.4	51.8	47	6	AR431365	AR431365
51.8	24	6	I63118	I63118 Sequence 3	497	11.4	51.8	47	6	AX214331	AX214331
51.8	24	6	I85497	I85497 Sequence 1	498	11.4	51.8	47	6		
51.8	25	6	AR157582	AR157582 Sequence	C 499	11.4	51.8	47	6		
51.8	25	6	AR212631	AR212631 Sequence	C 500	11.4	51.8	47	6		
51.8	25	6	AR430029	AR430029 Sequence	501	11.4	51.8	47	6		
51.8	25	6	AX115456	AX115456 Sequence	502	11.4	51.8	47	6		
51.8	25	6	AX201530	AX201530 Sequence	C 503	11.4	51.8	47	6		
51.8	25	6	AX675234	AX675234 Sequence	C 503	11.4	51.8	47	6		

51.8	48	6	BD135852	BD135852 Selective	c	577	11.2	50.9	23	6	AR345232	AR345232
51.8	50	6	AR040811	AR040811 Sequence	578	11.2	50.9	24	6	E37252	E37252 No	
51.8	50	9	S59168	S59168 TCR delta {	579	11.2	50.9	24	6	AR266294	AR266294	
51.8	51	6	AX115457	AX115457 Sequence	c	580	11.2	50.9	24	6	AX446937	AX446937
51.8	51	6	AX156991	AX156991 Sequence	c	581	11.2	50.9	24	6	AX447316	AX447316
51.8	51	6	AX156992	AX156992 Sequence	c	582	11.2	50.9	24	6	AX493448	AX493448
51.8	51	6	AX158796	AX158796 Sequence	583	11.2	50.9	24	6	AX776557	AX776557	
51.8	51	6	AX161602	AX161602 Sequence	584	11.2	50.9	24	12	ASE011719	AJ011719	
51.8	51	6	AX165013	AX165013 Sequence	585	11.2	50.9	25	6	AX688865	AX688865	
51.8	51	10	MUSMABBS	K00122 Mouse MHC c	586	11.2	50.9	25	6	AX688866	AX688866	
51.8	51	10	MUSMABBS	K00113 Mouse MHC c	587	11.2	50.9	25	6	AX688867	AX688867	
51.8	52	6	Al0854	Al0854 Oligonucleo	588	11.2	50.9	25	6	AX688868	AX688868	
51.8	54	6	Al0855	Al0855 Oligonucleo	589	11.2	50.9	25	6	AX688869	AX688869	
51.8	54	6	AX913960	AX913960 Sequence	590	11.2	50.9	25	6	AX688880	AX688880	
51.8	54	6	BD049493	BD049493 Sequence	c	591	11.2	50.9	25	6	AX691206	AX691206
51.8	57	6	AX594012	AX594012 Sequence	c	592	11.2	50.9	25	6	AX691207	AX691207
51.8	57	6	BD135845	BD135845 Selective	c	593	11.2	50.9	25	6	AX691208	AX691208
51.8	58	6	BD237364	BD237364 Improve	c	594	11.2	50.9	25	6	AX691209	AX691209
51.8	58	6	AX027031	AX027031 Sequence	c	595	11.2	50.9	25	6	AX691210	AX691210
51.8	59	6	BD135846	BD135846 Selective	c	596	11.2	50.9	25	6	AX691211	AX691211
51.8	59	6	AX011439	AX011439 Sequence	c	597	11.2	50.9	25	6	AX691212	AX691212
51.8	59	6	BD225730	BD225730 Screening	c	598	11.2	50.9	25	6	AX691213	AX691213
51.8	59	9	AX152457	AX152457 Homo sapi	c	599	11.2	50.9	25	6	AX691214	AX691214
51.8	60	6	A27400	A27400 cloning sit	c	600	11.2	50.9	25	6	AX691215	AX691215
51.8	60	6	A33042	A33042 Synthetic f	c	601	11.2	50.9	26	6	AR3750	AR3750 Se
51.8	60	6	A93057	A93057 Sequence 34	c	602	11.2	50.9	26	6	AR054696	AR054696
51.8	60	6	B65256	B65256 Mutant of E	c	603	11.2	50.9	26	6	AX300568	AX300568
51.8	60	6	AR227925	AR227925 Sequence	c	604	11.2	50.9	27	6	AX105555	AX105555
51.8	16	6	AR436222	AR436222 Sequence	c	605	11.2	50.9	27	6	AX350069	AX350069
50.9	17	6	BD241336	BD241336 Methods a	c	606	11.2	50.9	28	6	AX456997	AX456997
50.9	17	6	AX266671	AX266671 Sequence	c	607	11.2	50.9	28	6	AR083272	AR083272
50.9	17	6	AX266672	AX266672 Sequence	c	608	11.2	50.9	29	6	AR105934	AR105934
50.9	17	6	AX687368	AX687368 Sequence	c	609	11.2	50.9	29	6	AX002800	AX002800
50.9	17	6	AX687369	AX687369 Sequence	c	610	11.2	50.9	29	6	AX078805	AX078805
50.9	17	6	AX687374	AX687374 Sequence	c	611	11.2	50.9	29	6	AX149568	AX149568
50.9	17	6	AX687375	AX687375 Sequence	c	612	11.2	50.9	29	6	BD092214	BD092214
50.9	17	6	AX690745	AX690745 Sequence	c	613	11.2	50.9	29	6	BD136170	BD136170
50.9	17	6	AX690746	AX690746 Sequence	c	614	11.2	50.9	30	6	AR090106	AR090106
50.9	17	6	AX732199	AX732199 Sequence	c	615	11.2	50.9	30	6	AR141393	AR141393
50.9	17	6	AX734876	AX734876 Sequence	c	616	11.2	50.9	30	6	E32127	E32127 Se
50.9	17	6	AX738428	AX738428 Sequence	c	617	11.2	50.9	30	6	AR197141	AR197141
50.9	17	6	AX760170	AX760170 Sequence	c	618	11.2	50.9	30	6	AR259295	AR259295
50.9	17	6	AR302181	AR302181 Sequence	c	619	11.2	50.9	30	6	AX203796	AX203796
50.9	18	6	AX112174	AX112174 Sequence	c	620	11.2	50.9	31	6	AX59857	AX59857 Se
50.9	18	6	AX358732	AX358732 Sequence	c	621	11.2	50.9	31	6	A84815	A84815 Se
50.9	18	6	AX684999	AX684999 Sequence	c	622	11.2	50.9	31	6	AR075169	AR075169
50.9	18	6	AX815724	AX815724 Sequence	c	623	11.2	50.9	31	6	AR154131	AR154131
50.9	18	6	AX067175	AX067175 Sequence	c	624	11.2	50.9	31	6	AR339674	AR339674
50.9	20	6	AR100386	AR100386 Sequence	c	625	11.2	50.9	31	6	AX089633	AX089633
50.9	20	6	AR150041	AR150041 Sequence	c	626	11.2	50.9	31	6	AX248977	AX248977
50.9	20	6	BD227914	BD227914 Antisense	c	627	11.2	50.9	31	6	AX477522	AX477522
50.9	20	6	E08943	E08943 PCR primer	c	628	11.2	50.9	31	6	BD002360	BD002360
50.9	20	6	E15115	E15115 Primer 7/1	c	629	11.2	50.9	31	6	BD082263	BD082263
50.9	20	6	AR228974	AR228974 Sequence	c	630	11.2	50.9	32	6	AR090305	AR090305
50.9	20	6	AR311783	AR311783 Sequence	c	631	11.2	50.9	32	6	AR197340	AR197340
50.9	20	6	AR313956	AR313956 Sequence	c	632	11.2	50.9	32	6	AR259494	AR259494
50.9	20	6	AX080381	AX080381 Sequence	c	633	11.2	50.9	33	6	AX203794	AX203794
50.9	20	6	AX119655	AX119655 Sequence	c	634	11.2	50.9	34	6	BD263615	BD263615
50.9	20	6	AX348129	AX348129 Sequence	c	635	11.2	50.9	34	6	E59675	E59675 Me
50.9	20	6	AX418249	AX418249 Sequence	c	636	11.2	50.9	34	6	AX168006	AX168006
50.9	20	6	AX662849	AX662849 Sequence	c	637	11.2	50.9	34	6	AX343116	AX343116
50.9	20	6	AX785499	AX785499 Sequence	c	638	11.2	50.9	35	6	115205	115205 Se
50.9	20	6	AX785501	AX785501 Sequence	c	639	11.2	50.9	35	6	AR430578	AR430578
50.9	21	6	BD266155	BD266155 Universal	c	640	11.2	50.9	36	6	AR106146	AR106146
50.9	21	6	E58784	E58784 Novel human	c	641	11.2	50.9	36	6	E15059	E15059 Pr
50.9	21	6	AX203448	AX203448 Sequence	c	642	11.2	50.9	36	6	E15097	E15097 Pr
50.9	21	6	AX804691	AX804691 Sequence	c	643	11.2	50.9	36	6	AR436526	AR436526
50.9	21	6	BD056670	BD056670 Method to	c	644	11.2	50.9	37	6	AR034257	AR034257
50.9	22	6	AX040624	AX040624 Sequence	c	645	11.2	50.9	37	6	BD235638	BD235638
50.9	22	6	BD133433	BD133433 Method fo	c	646	11.2	50.9	37	6	AR287723	AR287723
50.9	23	6	AR112639	AR112639 Sequence	c	647	11.2	50.9	38	6	A84837	A84837 Se
50.9	23	6	BD272795	BD272795 Detection	c	648	11.2	50.9	38	6	AR063769	AR063769
50.9	23	6	AR279424	AR279424 Sequence	c	649	11.2	50.9	38	6	I30132	I30132 Se

50.9	38	6	AR339696	AR339696 Sequence	723	11	50.0	20	6	AX643826	AX643826
50.9	38	6	AX089644	AX089644 Sequence	C 724	11	50.0	20	6	BD128114	BD128114
50.9	38	6	AX425451	AX425451 Sequence	C 725	11	50.0	20	11	HUMPEX5B	DS0194
50.9	38	6	BD082285	BD082285 Modified	726	11	50.0	21	6	AX001238	AX001238
50.9	39	6	AR064069	AR064069 Sequence	727	11	50.0	21	6	AX133208	AX133208
50.9	39	6	AR366555	AR366555 Sequence	C 728	11	50.0	21	6	BD177808	BD177808
50.9	39	6	AR430709	AR430709 Sequence	C 729	11	50.0	21	6	BD177810	BD177810
50.9	39	6	AX055005	AX055005 Sequence	C 730	11	50.0	22	6	BD177810	BD177810
50.9	39	6	BD008468	BD008468 Targeting	C 731	11	50.0	22	6	I46723 S	I46723 S
50.9	40	6	AX496368	AX496368 Sequence	C 732	11	50.0	22	6	I46725	I46725
50.9	40	6	AX538299	AX538299 Sequence	C 733	11	50.0	23	6	AR084413	AR084413
50.9	40	6	BD013117	BD013117 Peptide 1	734	11	50.0	23	6	AX612644	AX612644
50.9	40	6	BD188770	BD188770 Peptide 1	735	11	50.0	23	6	BD140220	BD140220
50.9	41	6	BD260010	BD260010 Polynucle	C 736	11	50.0	23	6	BD142818	BD142818
50.9	41	6	I32610	I32610 Sequence 1	737	11	50.0	24	6	AX3153 S	AX3153 S
50.9	41	6	I32614	I32614 Sequence 5	C 738	11	50.0	24	6	A43154	A43154
50.9	41	6	AX045496	AX045496 Sequence	739	11	50.0	24	6	AR079543	AR079543
50.9	41	6	AX298062	AX298062 Sequence	C 740	11	50.0	24	6	AR079544	AR079544
50.9	41	6	AX411701	AX411701 Sequence	C 741	11	50.0	24	6	AR097511	AR097511
50.9	41	6	AX411705	AX411705 Sequence	C 742	11	50.0	24	6	AR103738	AR103738
50.9	41	6	AX516593	AX516593 Sequence	C 743	11	50.0	24	6	AR139825	AR139825
50.9	41	6	AX518766	AX518766 Sequence	C 744	11	50.0	24	6	AR140132	AR140132
50.9	41	6	AX520397	AX520397 Sequence	C 745	11	50.0	24	6	AR142849	AR142849
50.9	41	6	AX520397	AX520397 Sequence	C 746	11	50.0	24	6	I05926	I05926
50.9	42	6	AR200741	AR200741 Sequence	C 747	11	50.0	24	6	AR374664	AR374664
50.9	42	6	AX776725	AX776725 Sequence	748	11	50.0	24	6	AR431378	AR431378
50.9	42	6	AR238604	AR238604 Sequence	749	11	50.0	24	6	AX289899	AX289899
50.9	43	6	AX484449	AX484449 Sequence	750	11	50.0	24	6	AX291547	AX291547
50.9	43	6	E63267	E63267 Collagen-bi	751	11	50.0	24	6	AX292167	AX292167
50.9	44	6	BD142781	BD142781 Collagen	C 752	11	50.0	24	6	AX446993	AX446993
50.9	44	6	AR064068	AR064068 Sequence	C 753	11	50.0	24	6	AX487427	AX487427
50.9	45	6	AR366554	AR366554 Sequence	C 754	11	50.0	24	6	BD129968	BD129968
50.9	45	6	AR430708	AR430708 Sequence	C 755	11	50.0	24	6	BD183607	BD183607
50.9	45	6	BD008467	BD008467 Targeting	756	11	50.0	25	6	A00437	A00437
50.9	46	6	AX225236	AX225236 Sequence	C 757	11	50.0	25	6	AR090383	AR090383
50.9	47	6	AR284696	AR284696 Sequence	C 758	11	50.0	25	6	AR197418	AR197418
50.9	47	6	AR289080	AR289080 Sequence	C 759	11	50.0	25	6	AR259572	AR259572
50.9	47	6	AX195009	AX195009 Sequence	C 760	11	50.0	25	6	AX118148	AX118148
50.9	48	6	AR009864	AR009864 Sequence	761	11	50.0	25	6	AX378885	AX378885
50.9	50	6	AX159152	AX159152 Sequence	C 762	11	50.0	26	6	AX181783	AX181783
50.9	50	6	AX159154	AX159154 Sequence	C 763	11	50.0	26	6	BD077186	BD077186
50.9	50	6	AX159154	AX159154 Sequence	C 764	11	50.0	26	6	BD170718	BD170718
50.9	50	6	AX159154	AX159154 Sequence	C 765	11	50.0	27	6	A94073	A94073
50.9	51	6	AX118229	AX118229 Sequence	C 766	11	50.0	27	6	BD234826	BD234826
50.9	51	6	AX159151	AX159151 Sequence	C 767	11	50.0	27	6	AR232603	AR232603
50.9	51	6	AX159153	AX159153 Sequence	C 768	11	50.0	27	6	AX011158	AX011158
50.9	51	6	AX165288	AX165288 Sequence	C 769	11	50.0	27	6	BD102001	BD102001
50.9	53	14	S65446	S65446 {5, region,	C 770	11	50.0	27	6	BD169215	BD169215
50.9	53	14	S65447	S65447 {5, region,	C 771	11	50.0	27	6	BD169326	BD169326
50.9	55	14	S65449	S65449 {5, region,	C 772	11	50.0	27	6	BD169326	BD169326
50.9	60	6	A47881	A47881 Sequence 1	773	11	50.0	28	6	AR084382	AR084382
50.9	60	6	A59312	A59312 Sequence 1	774	11	50.0	28	6	AR236246	AR236246
50.9	60	6	A59878	A59878 Sequence 1	775	11	50.0	28	6	AR258702	AR258702
50.9	60	6	AR028665	AR028665 Sequence	776	11	50.0	28	6	BD169431	BD169431
50.9	60	6	AR092687	AR092687 Sequence	C 777	11	50.0	28	6	BD169432	BD169432
50.9	60	6	AR141392	AR141392 Sequence	C 778	11	50.0	28	6	BD169433	BD169433
50.9	60	6	E64748	E64748 Reagent for	C 779	11	50.0	28	6	BD169433	BD169433
50.9	60	6	E64749	E64749 Reagent for	779	11	50.0	28	6	BD169433	BD169433
50.9	60	6	BD102316	BD102316 Probe for	C 780	11	50.0	29	6	AR015968	AR015968
50.9	60	6	BD102317	BD102317 Probe for	781	11	50.0	29	6	AR159629	AR159629
50.9	60	6	MMVJ512X4	Z69806 M.musculus	C 782	11	50.0	29	6	AR211057	AR211057
50.9	18	6	AR110881	AR110881 Sequence 5	C 783	11	50.0	29	6	AX008185	AX008185
50.0	18	6	I23760	I23760 Sequence 5	C 784	11	50.0	29	6	BD004719	BD004719
50.0	18	6	I68688	I68688 Sequence 5	C 785	11	50.0	29	6	BD217253	BD217253
50.0	20	6	AR066932	AR066932 Sequence	C 786	11	50.0	30	6	A08335	A08335
50.0	20	6	AR226024	AR226024 Sequence	C 787	11	50.0	30	6	AR085771	AR085771
50.0	20	6	AR271117	AR271117 Sequence	C 788	11	50.0	30	6	AR089318	AR089318
50.0	20	6	AX294532	AX294532 Sequence	C 789	11	50.0	30	6	AR093518	AR093518
50.0	20	6	AX296800	AX296800 Sequence	C 790	11	50.0	30	6	AR097044	AR097044
50.0	20	6	AX477166	AX477166 Sequence	C 791	11	50.0	30	6	I73049	I73049
50.0	20	6	AX526542	AX526542 Sequence	C 792	11	50.0	30	6	AR279263	AR279263
50.0	20	6	AX608776	AX608776 Sequence	C 793	11	50.0	30	6	AR381839	AR381839
50.0	20	6	AX613440	AX613440 Sequence	C 794	11	50.0	30	6	AX611182	AX611182
50.0	20	6	AX615179	AX615179 Sequence	795	11	50.0	30	6	AX792676	AX792676

50.0	30	6	BD107816	BD107816 Opsonic a	c	869	11	50.0	45	6	AR304366	AR304366
50.0	31	6	AR301137	AR301137 Sequence	870	11	50.0	46	6	IO5891	IO5891 Se	
50.0	31	6	AX248120	AX248120 Sequence	871	11	50.0	46	6	IO5936	IO5936 Se	
50.0	31	6	AX248608	AX248608 Sequence	872	11	50.0	46	6	AR431341	AR431341	
50.0	31	6	AX375910	AX375910 Sequence	873	11	50.0	46	11	BX469976	BX469976	
50.0	32	6	AX122586	AX122586 Sequence	c	874	11	50.0	47	6	A94788	A94788 Se
50.0	32	6	AI19540	AI19540 Oligonucleo	875	11	50.0	47	6	AR289639	AR289639	
50.0	33	6	AX47286	AX47286 Sequence 10	c	876	11	50.0	47	6	AR290903	AR290903
50.0	33	6	AX349971	AX349971 Sequence	c	877	11	50.0	47	6	AR291280	AR291280
50.0	33	6	AX351181	AX351181 Sequence	c	878	11	50.0	47	6	AR291354	AR291354
50.0	33	6	AX351181	AX351181 Sequence	c	879	11	50.0	47	6	AR291718	AR291718
50.0	34	6	AR049884	AR049884 Sequence 37	c	880	11	50.0	47	6	AX114388	AX114388
50.0	34	6	I13434	I13434 Sequence 4	881	11	50.0	47	6	AX194666	AX194666	
50.0	34	6	I24524	I24524 Sequence 4	c	882	11	50.0	47	6	AX300062	AX300062
50.0	34	6	I33866	I33866 Sequence 20	883	11	50.0	48	6	AX538016	AX538016	
50.0	34	6	I83690	I83690 Sequence 20	884	11	50.0	48	11	BX664048	BX664048	
50.0	34	6	AR195153	AR195153 Sequence	885	11	50.0	49	6	AR123866	AR123866	
50.0	34	6	BD101999	BD101999 Agonist a	886	11	50.0	49	6	BD133116	BD133116	
50.0	34	6	BD102153	BD102153 Apoptosis	887	11	50.0	49	9	S49737S3	S50130 5-	
50.0	34	6	BD169213	BD169213 Degraded	c	888	11	50.0	51	6	A25693	A25693 BI
50.0	34	6	BD169324	BD169324 Small rem	c	889	11	50.0	51	6	AR051368	AR051368
50.0	35	6	AR050875	AR050875 Sequence	c	890	11	50.0	51	6	BD235907	BD235907
50.0	35	6	AR219886	AR219886 Sequence	c	891	11	50.0	51	6	BD235908	BD235908
50.0	35	6	AX190433	AX190433 Sequence	c	892	11	50.0	51	6	BD236998	BD236998
50.0	35	6	AX594127	AX594127 Sequence	c	893	11	50.0	51	6	BD202693	BD202693
50.0	35	6	AX658929	AX658929 Sequence	894	11	50.0	51	6	AR224113	AR224113	
50.0	36	6	E35332	E35332 Assay for m	c	895	11	50.0	51	6	AR224114	AR224114
50.0	36	6	IO5975	IO5975 Sequence 46	c	896	11	50.0	51	6	AR268571	AR268571
50.0	36	6	AR428484	AR428484 Sequence	897	11	50.0	51	6	AR269244	AR269244	
50.0	36	6	BD017747	BD017747 Test for	c	898	11	50.0	51	6	AR367580	AR367580
50.0	37	6	A22365	A22365 oligonucleo	c	899	11	50.0	51	6	AR379301	AR379301
50.0	37	6	AR076113	AR076113 Sequence	900	11	50.0	51	6	AR390916	AR390916	
50.0	37	6	AX080997	AX080997 Sequence	901	11	50.0	51	6	AR390916	AR390916	
50.0	37	6	AX658960	AX658960 Sequence	902	11	50.0	51	6	AR411474	AR411474	
50.0	38	6	A08333	A08333 Oligonucleo	903	11	50.0	51	6	AX105423	AX105423	
50.0	38	6	BD250818	BD250818 Glycosyla	c	904	11	50.0	51	6	AX105424	AX105424
50.0	38	6	AR373199	AR373199 Sequence	c	905	11	50.0	51	6	AX118149	AX118149
50.0	39	6	AX513773	AX513773 Sequence	906	11	50.0	51	6	AX134028	AX134028	
50.0	39	6	AR029687	AR029687 Sequence	c	907	11	50.0	51	6	AX156751	AX156751
50.0	39	6	BD235903	BD235903 Alzheimer	908	11	50.0	51	6	AX157646	AX157646	
50.0	39	6	BD235904	BD235904 Alzheimer	c	909	11	50.0	51	6	AX159869	AX159869
50.0	39	6	AR224109	AR224109 Sequence	c	910	11	50.0	51	6	AX159870	AX159870
50.0	39	6	AR224110	AR224110 Sequence	c	911	11	50.0	51	6	AX161499	AX161499
50.0	39	6	AR269240	AR269240 Sequence	c	912	11	50.0	51	6	AX286106	AX286106
50.0	39	6	AR269241	AR269241 Sequence	913	11	50.0	51	6	AX573861	AX573861	
50.0	39	6	AR301136	AR301136 Sequence	c	914	11	50.0	51	6	AX573862	AX573862
50.0	39	6	AX105419	AX105419 Sequence	c	915	11	50.0	51	10	AF005625	AF005625
50.0	39	6	AX105420	AX105420 Sequence	c	916	11	50.0	51	11	BX546411	BX546411
50.0	39	6	AX573857	AX573857 Sequence	c	917	11	50.0	52	11	BX469941	BX469941
50.0	39	6	AX573858	AX573858 Sequence	c	918	11	50.0	52	11	G67703	G67703
50.0	39	11	AL824208	AL824208 Arabidops	c	919	11	50.0	53	6	AI4708	AI4708 N
50.0	40	6	AR179461	AR179461 Sequence	c	920	11	50.0	53	6	AR020790	AR020790
50.0	40	6	IO8694	IO8694 Sequence 2	c	921	11	50.0	53	6	AR043083	AR043083
50.0	40	6	AX053201	AX053201 Sequence	c	922	11	50.0	53	6	AR161341	AR161341
50.0	40	6	AX059800	AX059800 Sequence	c	923	11	50.0	53	6	AR181292	AR181292
50.0	40	6	AX201963	AX201963 Sequence	c	924	11	50.0	53	6	AR363873	AR363873
50.0	40	11	BX465328	BX465328 Arabidops	c	925	11	50.0	53	6	AR369934	AR369934
50.0	41	6	AX514542	AX514542 Sequence	c	926	11	50.0	53	6	AX495159	AX495159
50.0	41	6	AX515100	AX515100 Sequence	c	927	11	50.0	53	6	BD096571	BD096571
50.0	41	6	AX520133	AX520133 Sequence	c	928	11	50.0	53	11	BX465351	BX465351
50.0	41	6	AX521357	AX521357 Sequence	c	929	11	50.0	54	6	A28014	A28014 p
50.0	42	6	AR043080	AR043080 Sequence	c	930	11	50.0	54	6	AX166287	AX166287
50.0	42	6	AR161338	AR161338 Sequence	c	931	11	50.0	54	9	AF254561	AF254561
50.0	42	6	AR369931	AR369931 Sequence	c	932	11	50.0	54	10	AY205717	AY205717
50.0	42	6	AX351182	AX351182 Sequence	c	933	11	50.0	55	6	A67485	A67485 S
50.0	42	6	BD096568	BD096568 Transgeni	c	934	11	50.0	55	6	A67486	A67486 S
50.0	43	6	AX601782	AX601782 Sequence	c	935	11	50.0	55	6	AR226384	AR226384
50.0	43	11	BX548225	BX548225 Arabidops	c	936	11	50.0	55	6	AR226385	AR226385
50.0	44	11	BX664052	BX664052 Arabidops	c	937	11	50.0	56	8	ATH528248	ATH528248
50.0	45	6	AR018915	AR018915 Sequence	c	938	11	50.0	57	6	AX611908	AX611908
50.0	45	6	AR066543	AR066543 Sequence	c	939	11	50.0	57	6	AX611909	AX611909
50.0	45	6	AR112081	AR112081 Sequence	c	940	11	50.0	57	6	AX614535	AX614535
50.0	45	6	I72260	I72260 Sequence 37	c	941	11	50.0	57	10	MWVA2AJ24	MWVA2AJ24
50.0	45	6	I76827	I76827 Sequence 37	c	941	11	50.0	57	10	MWVA2AJ24	MWVA2AJ24

50.0 58 6 AR096989 Sequence  
 50.0 58 6 BD265867 Schizophr  
 50.0 58 6 AR244397 Sequence  
 50.0 58 6 AR367326 Sequence  
 50.0 60 6 BD262210 Chimeric  
 50.0 60 6 AR355543 Sequence  
 50.0 60 6 AR3036743 Sequence  
 50.0 60 6 AX100155 Sequence  
 50.0 60 6 AX601374 Sequence  
 50.0 60 6 AX701058 Sequence  
 50.0 60 9 S75377 Smu-S gamma  
 50.0 60 10 AY205881 Mus muscu  
 49.1 16 6 BD235056 A method  
 49.1 16 6 AX009127 Sequence  
 49.1 17 6 BD254296 Regulatio  
 49.1 17 6 AR264875 Sequence  
 49.1 17 6 AR263748 Sequence  
 49.1 17 6 AX263749 Sequence  
 49.1 17 6 AX263752 Sequence  
 49.1 17 6 AX263753 Sequence  
 49.1 17 6 AX422963 Sequence  
 49.1 17 6 AX422964 Sequence  
 49.1 17 6 AX673642 Sequence  
 49.1 17 6 AX690743 Sequence  
 49.1 17 6 AX690744 Sequence  
 49.1 17 6 AX726731 Sequence  
 49.1 17 6 AX733109 Sequence  
 49.1 17 6 AX736377 Sequence  
 49.1 17 6 AX739500 Sequence  
 49.1 17 6 AX783931 Sequence  
 49.1 17 6 AX783932 Sequence  
 49.1 17 6 AX783933 Sequence  
 49.1 17 6 AX783934 Sequence  
 49.1 18 6 AR153222 Sequence  
 49.1 18 6 AR163237 Sequence  
 49.1 18 6 AR210981 Sequence  
 49.1 18 6 AR431662 Sequence  
 49.1 18 6 AX377015 Sequence  
 49.1 19 6 AX378494 Sequence  
 49.1 20 6 AR154498 Sequence  
 49.1 20 6 AR154499 Sequence  
 49.1 20 6 AR162462 Sequence  
 49.1 20 6 E59397 Method for  
 49.1 20 6 I62745 Sequence 8  
 49.1 20 6 AR200654 Sequence  
 49.1 20 6 AR312866 Sequence  
 49.1 20 6 AR313687 Sequence  
 49.1 20 6 AR315005 Sequence  
 49.1 20 6 AR315659 Sequence  
 49.1 20 6 AR400778 Sequence  
 49.1 20 6 AX294196 Sequence  
 49.1 20 6 AX537859 Sequence  
 49.1 20 6 AX765636 Sequence  
 49.1 20 6 BD195743 Method fo  
 49.1 21 6 AR022112 Sequence  
 49.1 21 6 AR036426 Sequence  
 49.1 21 6 AR049045 Sequence  
 49.1 21 6 AR152570 Sequence

## ALIGNMENTS

901 46 bp  
 uence 3 from Patent EP0618292.  
 901  
 901.1 GI:2296119  
 o sapiens (human)  
 o sapiens

REFERENCE  
 1 (bases 1 to 46)  
 AUTHORS  
 Tersikh,A., Pelegriin,A. and Mach,J.  
 TITLE  
 CEA derivatives lacking the Hydrophobic C-terminal domai  
 JOURNAL  
 Patent: EP 0618292-A 3 05-OCT-1994;  
 HOFFMANN LA ROCHE (CH)  
 COMMENT  
 Other publication CA 2116640 940926  
 Other publication JP 6321992 941122.  
 FEATURES  
 Location/Qualifiers  
 1..46  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 71.8%; Score 15.8; DB 6; Length 46;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 AGACAATCACAGTCTCTGC 19  
 ||| ||||| ||||| |||||  
 Db 23 AGAGCATCACAGTCTCTGC 41  
 RESULT 2  
 A39902/c  
 LOCUS  
 A39902  
 DEFINITION  
 Sequence 4 from Patent EP0618292.  
 ACCESSION  
 A39902  
 VERSION  
 A39902.1 GI:2296120  
 KEYWORDS  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Ho  
 1 (bases 1 to 46)  
 AUTHORS  
 Tersikh,A., Pelegriin,A. and Mach,J.  
 TITLE  
 CEA derivatives lacking the Hydrophobic C-terminal doma  
 JOURNAL  
 Patent: EP 0618292-A 4 05-OCT-1994;  
 HOFFMANN LA ROCHE (CH)  
 COMMENT  
 Other publication CA 2116640 940926  
 Other publication JP 6321992 941122.  
 FEATURES  
 Location/Qualifiers  
 1..46  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 71.8%; Score 15.8; DB 6; Length 46;  
 Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 AGACAATCACAGTCTCTGC 19  
 ||| ||||| ||||| |||||  
 Db 28 AGAGCATCACAGTCTCTGC 10  
 RESULT 3  
 167749  
 LOCUS  
 167749  
 DEFINITION  
 Sequence 3 from patent US 5672513.  
 ACCESSION  
 167749  
 VERSION  
 167745.1 GI:2731284  
 KEYWORDS  
 Unknown.  
 SOURCE  
 Unknown.  
 ORGANISM  
 Unclassified.  
 1 (bases 1 to 46)  
 REFERENCES  
 Tersikh,A., Pelegriin,A. and Mach,J.-P.  
 TITLE  
 Carcino-embryonic antigen derivatives lacking the carbo  
 end

09:38:24 2004

us-10-090-326-6.max.rge

it: US 5672513-A 3 30-SEP-1997;  
Location/Qualifiers  
1. .46  
/organism="unknown"  
/mol\_type="unassigned DNA"

71.8%; Score 15.8; DB 6; Length 46;  
ilarity 89.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CAATCAGTCTCTGC 19  
|||||  
GCATCAGTCTCTGC 41

30 nce 4 from patent US 5672513.  
30 46 bp DNA linear PAT 30-DEC-1997  
30.1 GI:2731285

wn.  
wn.  
assified.  
ases 1 to 46)  
ikh,A., Pelegrin,A. and Mach,J.-P.  
no-embryonic antigen derivatives lacking the carboxyl terminal

it: US 5672513-A 4 30-SEP-1997;  
Location/Qualifiers  
1. .46  
/organism="unknown"  
/mol\_type="unassigned DNA"

71.8%; Score 15.8; DB 6; Length 46;  
ilarity 89.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CAATCAGTCTCTGC 19  
|||||  
AGCATCAGTCTCTGC 10

3249 nce 4 from patent US 5948891.  
3249 30 bp DNA linear PAT 28-AUG-2000  
3249.1 GI:10000012

wn.  
wn.  
assified.  
ases 1 to 30)  
ron,D.E. and Salot Harris,E.A.  
plasmic modulators of integrin binding  
nt: US 5948891-A 4 07-SEP-1999;  
Location/Qualifiers  
1. .30  
/organism="unknown"  
/mol\_type="unassigned DNA"

70.9%; Score 15.6; DB 6; Length 30;  
ilarity 81.8%; Pred. No. 2.1e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTCGGA 22  
|||||  
ACAGTCCCACTCTCGAGGA 5

RESULT 6  
AB069564/c  
LOCUS  
DEFINITION  
AB069564  
SYNthetic construct DNA, forward primer for human STS st  
at 1p36.

AB069564.1 GI:15130368  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS  
Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,  
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H  
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M.,  
and Soeda,E.  
A BAC-based STS-content map spanning a 35-Mb region of h  
chromosome 1p35-p36  
Genomics 74 (1), 55-70 (2001)  
21269192  
11374902  
REFERENCE  
2 (bases 1 to 20)  
Horii,A.  
Direct Submission  
TITLE  
Submitted (04-AUG-2001) Akira Horii, Tohoku University S  
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku,  
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp)  
Tel:81-22-717-8042, Fax:81-22-717-8047

FEATURES  
source  
1. .20  
/organism="synthetic construct"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:32630"

misc\_feature  
1. .20  
/note="forward primer for human STS sts-R-359E4  
sts-R-359E4F obtained from clones B359E4, B189F  
B266K22, B287N10, Human BAC library RPCI-11"

ORIGIN  
Query Match 64.5%; Score 14.2; DB 12; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.3e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCAGTCTCTGC 19  
|||||  
DB 20 AGACAATCAGTCTCTGC 2

RESULT 7  
AX688871  
LOCUS  
DEFINITION  
Sequence 1603 from Patent EP1281758.  
ACCESSION  
AX688871  
VERSION  
AX688871.1 GI:29411575  
KEYWORDS  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom  
Shannon,M., Gu,Y. and Nguyen,C.T.  
Four human zinc-finger-containing proteins : mdz3, mdz4,  
mdz12  
Patent: EP 1281758-A 1603 05-FEB-2003;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Aomics, Inc. (US)  
Location/Qualifiers  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

63.6%; Score 14; DB 6; Length 25;  
 ilarity 77.3%; Pred. No. 1.6e+04;  
 Conservative 0; Mismatches 5; Indels 0;  
 Gaps 0;  
 ACAATCACAGTCTCTCGGA 22  
 ||| ||||| |||||  
 TCATTCTCAGTCTCTCGGA 25

8872 25 bp DNA linear PAT 31-MAR-2003  
 Sequence 1604 from Patent EP1281758.  
 8872  
 8872.1 GI:29411576  
 sapiens (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 mon.M., Gu.Y. and Nguyen.C.T.  
 human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
 2  
 nt: EP 1281758-A 1604 05-FEB-2003;  
 nica, Inc. (US)  
 Location/Qualifiers  
 1. .25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

63.6%; Score 14; DB 6; Length 25;  
 ilarity 77.3%; Pred. No. 1.6e+04;  
 Conservative 0; Mismatches 5; Indels 0;  
 Gaps 0;  
 TACATCACAGTCTCTCGGA 22  
 ||| ||||| |||||  
 TCAATTCAGTCTCTCGGA 24

38873 25 bp DNA linear PAT 31-MAR-2003  
 Sequence 1605 from Patent EP1281758.  
 38873  
 38873.1 GI:29411577  
 sapiens (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 mon.M., Gu.Y. and Nguyen.C.T.  
 human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
 12  
 nt: EP 1281758-A 1605 05-FEB-2003;  
 nica, Inc. (US)  
 Location/Qualifiers  
 1. .25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

63.6%; Score 14; DB 6; Length 25;  
 ilarity 77.3%; Pred. No. 1.6e+04;  
 Conservative 0; Mismatches 5; Indels 0;  
 Gaps 0;  
 GCAATCACAGTCTCTCGGA 22  
 ||| ||||| |||||

Db 2 AGTCATTCTCAGTCTCTCGGA 23

RESULT 10  
 AX688874 25 bp DNA linear PAT  
 LOCUS  
 DEFINITION  
 Sequence 1606 from Patent EP1281758.  
 AX688874  
 ACCESSION  
 AX688874.1 GI:29411578  
 VERSION  
 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Hom  
 1  
 Shannon.M., Gu.Y. and Nguyen.C.T.  
 Four human zinc-finger-containing proteins : mdz3, mdz4,  
 mdz12  
 Patent: EP 1281758-A 1606 05-FEB-2003;  
 Aeonica, Inc. (US)  
 Location/Qualifiers  
 1. .25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 63.6%; Score 14; DB 6; Length 25;  
 Best Local Similarity 77.3%; Pred. No. 1.6e+04;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0;  
 Gaps 0;

QY 1 AGACAATCACAGTCTCTCGGA 22  
 ||| ||||| |||||  
 Db 1 AGTCATTCTCAGTCTCTCGGA 22

RESULT 11  
 BX322287 58 bp DNA linear STS  
 LOCUS  
 DEFINITION  
 Arabidopsis thaliana transposon insertion STS SM\_3.3518:  
 tagged site.  
 BX322287  
 BX322287.1 GI:29465926  
 VERSION  
 STS; STS, sequence tagged site.  
 KEYWORDS  
 Arabidopsis thaliana (thale cress)  
 SOURCE  
 Arabidopsis thaliana  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabido  
 1  
 Clarke.J.H., Bowles.B., Carter.J., Jones.J.D.G. and Beva  
 Murphy.G., Langham.S., LeGrys.C., Jones.J.D.G. and Beva  
 Unpublished  
 2 (bases 1 to 58)  
 Clarke.J.H.  
 Direct Submission  
 Submitted (01-APR-2003) Clarke J.H., John Innes Centre,  
 Lane, Norwich, NR4 7UJ, UK  
 Ar denotes an activation tag dissociation transposon wi  
 single line, Ar an enhancer trap dissociation transposo  
 trap dissociation transposon, MT a mis-expression enhan  
 dissociation transposon, SM a defective suppressor muta  
 transposon. 3 denotes a sequence derived from the 3' en  
 transposon. 5 denotes a sequence derived from the 5' en  
 transposon BSRG GARNet, ATIS project  
 On-line seed stock requests: http://nasc.nott.ac.uk/ NA  
 code: NI21894.  
 Location/Qualifiers  
 1. .58  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /variety="Columbia-0 NASC stock code N1092"  
 /db\_xref="taxon:3702"

FEATURES  
 source



09:38:24 2004

us-10-090-326-6.max.rge

/clone="AC069473"  
/note="Derived from superpool 26.33 NASC code Unknown"  
1. .58  
/standard\_name="SM\_3.35183"

63.6%; Score 14; DB 11; Length 58;  
ilarity 77.3%; Pred. No. 1.7e+04;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGAGTCTCTGCGG 22  
|||||  
ACTATCAAAATATCTGTGGA 39

1379 21 bp DNA linear PAT 22-JUN-2001  
ance 477 from Patent WO0138576.  
1379  
1379.1 GI:14535993

sapiens (human)  
sapiens  
cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ill.M., Ireland, J.S. and Lander, E.S.  
a single nucleotide polymorphisms  
it: WO 0138576-A 477 31-MAY-2001;  
HEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

Location/Qualifiers  
1. .21  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

61.8%; Score 13.6; DB 6; Length 21;  
ilarity 92.9%; Pred. No. 2.7e+04;  
Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ACAATCAGATC 14  
|||||  
ACAATCAVAGTC 15

8993 37 bp DNA linear PAT 10-APR-2003  
ence 41 from patent US 6500646.  
8993  
8993.1 GI:29699809

own.  
own.  
assified.  
bases 1 to 37)  
yama, S. and Hasegawa, T.  
membrane-directed drugs  
nt: US 6500646-A 41 31-DEC-2002;  
Location/Qualifiers  
1. .37  
/organism="unknown"  
/mol\_type="genomic DNA"

61.8%; Score 13.6; DB 6; Length 37;  
ilarity 80.0%; Pred. No. 2.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGATCTCTGCGG 21  
|||||

Db 9 GATCTCAGAGTCTCTGCGG 28

RESULT 14  
AX794202  
LOCUS  
DEFINITION  
Sequence 33 from Patent WO02092827.  
ACCESSION  
AX794202  
VERSION  
AX794202.1 GI:32959626  
KEYWORDS  
synthetic construct  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1 Rottier, P.J., de Haan, C.A., Haijema, B.J. and Bosch, B.J.  
TITLE Corona-virus-like particles comprising functionally dele  
JOURNAL Patent: WO 02092827-A 33 21-NOV-2002;  
Universiteit Utrecht (NL); STICHTING VOOR DE TECHNISCHE  
WETENSCHAPPEN (NL)

FEATURES  
1. .50  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="sequence of new junction created in reco  
MHV-virus"

ORIGIN

Query Match 61.8%; Score 13.6; DB 6; Length 50;  
Best Local Similarity 80.0%; Pred. No. 2.8e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

Qy 2 GACAATCAGATCTCTGCGG 21  
|||||  
Db 8 GACTATCAGAGCCCTGCG 27

RESULT 15  
APHCN0V5E 50 bp ss-RNA linear VRL  
LOCUS  
DEFINITION  
Foot and mouth disease virus (serotype C Nov) RNA, 5' en  
ACCESSION  
M10505  
VERSION  
M10505.1 GI:210404  
KEYWORDS  
Foot-and-mouth disease virus  
SOURCE  
Foot-and-mouth disease virus  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Aphthovirus.

REFERENCE  
1 Harris, P.J.  
AUTHORS  
TITLE Comparison of the nucleotide sequence at the 5' end of R  
nine aphthoviruses, including representatives of the Sev  
serotypes  
J. Virol. 36 (3), 659-664 (1980)  
JOURNAL  
MEDLINE  
81119945  
PUBMED  
6257918  
COMMENT  
Original  
FEATURES  
source text: Foot and mouth disease virus RNA.  
Location/Qualifiers  
1. .50  
/organism="Foot-and-mouth disease virus"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:12110"

source

ORIGIN

Query Match 61.8%; Score 13.6; DB 14; Length 50;  
Best Local Similarity 80.0%; Pred. No. 2.8e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

Qy 1 AGACAATCAGATCTCTGCG 20  
|||||  
Db 31 AGCCAACGACAGTCCCTGCG 50

1228 53 bp DNA linear PAT 17-JUL-2003  
 since 59 from Patent WO02092827.  
 1228  
 1228.1 GI:32959634  
 netic construct  
 netic construct  
 ficial sequences.  
 ier,P.J., de Haan,C.A., Haijema,B.J. and Bosch,B.J.  
 as-virus-like particles comprising functionally deleted genomes  
 nt: WO 02092827-A 59 21-NOV-2002;  
 ersiteit Utrecht (NL) ; STICHTING VOOR DE TECHNISCHE  
 NSCHAPPEN (NL)  
 Location/Qualifiers  
 1..53  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="sequence of junction generated in recombinant  
 MHV-virus"  
 61.8%; Score 13.6; DB 6; Length 53;  
 ilarity 80.0%; Pred. No. 2.8e+04;  
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 CAATCACAGTCTCTGCGG 21  
 |||||  
 CTATCACAGCCCTGCGAG 27  
 32308 22 bp DNA linear PAT 20-DEC-2002  
 hence 8 from patent US 6476296.  
 32308  
 52308.1 GI:27300203  
 nown.  
 nown.  
 lassified.  
 (bases 1 to 22)  
 cher,R.L., Choi,Y. and Hannon,M.  
 leic acids that control seed and fruit development in plants  
 ent: US 6476296-A 8 05-NOV-2002;  
 Location/Qualifiers  
 1..22  
 /organism="unknown"  
 /mol\_type="genomic DNA"  
 60.0%; Score 13.2; DB 6; Length 22;  
 ilarity 83.3%; Pred. No. 4.6e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGCG 19  
 |||||  
 ACAATAACCGTCTCTCC 1  
 33429 22 bp DNA linear PAT 18-SEP-2002  
 hod for assaying glutathione S-transferase, and probe and kit  
 refer.  
 33429  
 33429.1 GI:23228374  
 2002058483-A/27.  
 identified  
 identified

unclassified.  
 1 (bases 1 to 22)  
 Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.  
 Method for assaying glutathione S-transferase, and probe  
 therefor  
 Patent: JP 2002058483-A 27 26-FEB-2002;  
 OTSUKA PHARMACEUTICAL FACTORY INC  
 human GSTM2 gene  
 PN JP 2002058483-A/27  
 PD 26-FEB-2002  
 PF 14-AUG-2000 JP 2000245951  
 PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,I  
 PC C12N15/09,C1201/68,G01N21/78,G01N33/53,G0  
 PC C12N15/00  
 CC Method for assaying glutathione S-transferase, and  
 kit therefor  
 CC Key Location/Qualifiers  
 FH Key 1..22  
 FT source /organism="human GSTM2 gene".  
 FT Location/Qualifiers  
 1..22  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"  
 Query Match 60.0%; Score 13.2; DB 6; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 5 AATCACAGTCTCTGCGGA 22  
 |||||  
 DB 22 ACTCACAGTTTCTGCGGA 5  
 RESULT 19  
 120757/C  
 LOCUS 35 bp DNA linear PAT  
 DEFINITION Sequence 10 from patent US 5516637.  
 120757  
 ACCESSION  
 VERSION 120757.1 GI:1601112  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 35)  
 Huang,G.P., Rhode,P.R., Stinson,J.R. and Wong,H.C.  
 Method involving display of protein binding pairs on th  
 bacterial pili and bacteriophage  
 Patent: US 5516637-A 10 14-MAY-1996;  
 Location/Qualifiers  
 1..35  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 60.0%; Score 13.2; DB 6; Length 35;  
 Best Local Similarity 72.2%; Pred. No. 4.7e+04;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0;  
 QY 4 CAATCACAGTCTCTGCGG 21  
 |||||  
 DB 32 CACTCACHGTCTCYKCAG 15  
 RESULT 20  
 AR381829/C  
 LOCUS 35 bp DNA linear PAT  
 DEFINITION Sequence 73 from patent US 6610293.  
 AR381829  
 ACCESSION  
 VERSION AR381829.1 GI:40090090  
 KEYWORDS  
 SOURCE Unknown.

```

wn.
ssified.
ases 1 to 35)
er.G.W., Schuman,R.F., Wong,H. and Stinson,J.R.
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria
it: US 6610293-A 73 26-AUG-2003;
Location/Qualifiers
1. .35
/organism="unknown"
/mol_type="unassigned DNA"

60.0%; Score 13.2; DB 6; Length 35;
larity 72.2%; Pred. No. 4.7e+04;
Conservative 3; Mismatches 2; Indels 0; Gaps 0;
ATCACAGTCTCTGCGG 21
|||||:|:|:|
TCACGCTCTCYKAG 15

'806 35 bp. DNA linear PAT 18-SEP-2002
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria.
'806
'806.1 GI:23202624
02503966-A/39.
ntified
ntified
ssified.
ases 1 to 35)
er.G.W., Schuman,R.F., Wong,H. and Stinson,J.L.
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria
it: JP 2002503966-A 39 05-FEB-2002;
M JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY MEDICINE
Unidentified
JP 2002503966-A/39
05-FEB-2002
16-JUN-1998 JP 1999504633
16-JUN-1997 US 60/049871
GERALD W FISCHER, RICHARD F SCHUMAN, HING WONG, JEFFREY L STINSON
C07K16/12,C07K16/46,A61K39/40,C07K7/00,A61K39/02,C12Q1/18 CC
edness: Single;
Topology: Linear;
/desc = 'primer'.
Key Location/Qualifiers
source
1. .35
/organism='Unidentified'.
Location/Qualifiers
1. .35
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

60.0%; Score 13.2; DB 6; Length 35;
larity 72.2%; Pred. No. 4.7e+04;
Conservative 3; Mismatches 2; Indels 0; Gaps 0;
ATCACAGTCTCTGCGG 21
|||||:|:|:|
ATCACGCTCTCYKAG 15

9738 47 bp DNA linear PAT 12-JUN-2003
ance 1473 from patent US 6537751.
9738

```

```

VERSION AR289738.1 GI:31677022
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 47)
Unclassified.
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1473 25-MAR-2003;
FEATURES
Location/Qualifiers
1. 47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 60.0%; Score 13.2; DB 6; Length 47;
Best Local Similarity 75.0%; Pred. No. 4.7e+04;
Matches 15; Conservative 1; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21
|||||:|:|:|
19 GAGCAYCACACACTCTGCGG 38

Db

RESULT 23
AX199173 51 bp DNA linear PAT:
LOCUS Sequence 103 from Patent WO0151670.
ACCESSION AX199173
VERSION AX199173.1 GI:15389525
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homi-

REFERENCE
1
AUTHORS Shinkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms
methods of use thereof
JOURNAL Patent: WO 0151670-A 103 19-JUL-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (104 is other en-
Accession number CG43093113"

ORIGIN
Query Match 60.0%; Score 13.2; DB 6; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCACAGTCTCTG 18
|||||:|:|:|
27 AGACAATCCATTGTCTG 44

Db

RESULT 24
AX199174 51 bp DNA linear PAT:
LOCUS Sequence 104 from Patent WO0151670.
ACCESSION AX199174
VERSION AX199174.1 GI:15389526
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homi-

REFERENCE
1

```

Kets, R.A. and Leach, M.D.  
 eic acids containing single nucleotide polymorphisms and  
 ods of use thereof  
 nt: WO 0151670-A 104 19-JUL-2001;  
 Gen Corporation (US)  
 Location/Qualifiers  
 1..51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 26  
 /note="2 of 2 allelic variants (103 is other entry)"  
 Accession number CG43093113"

60.0%; Score 13.2; DB 6; Length 51;  
 ilarity 83.3%; Pred. No. 4.7e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACAAATCACAGTCTCTG 18  
 |||||  
 ACAATCCCATGTCGTG 44

'2233 22 bp DNA linear PAT 28-AUG-2000  
 ence 36 from patent US 5948611.  
 '2233  
 '2233.1 GI:9998997

own.  
 own.  
 asified.  
 ases 1 to 22)  
 kop, D.J., Ala-Kokko, L., Williams, C.J., Ritvaniemi, P.,  
 twin, C., Hopkinson, I., and Ahmad, N. Nina.  
 and methods for detecting mutations in the procollagen II  
 (COL2A1) that indicate a genetic predisposition for a  
 AI-associated disease  
 nt: US 5948611-A 36 07-SEP-1999;  
 Location/Qualifiers  
 1..22  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

59.1%; Score 13; DB 6; Length 22;  
 ilarity 76.2%; Pred. No. 5.9e+04;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACAAATCACAGTCTCTGCGG 21  
 |||||  
 ACACTCGCAGTCTCACCTG 1

344 22 bp DNA linear PAT 07-OCT-1996  
 uence 36 from patent US 5558988.  
 344  
 344.1 GI:1606214

own.  
 own.  
 lassified.  
 (bases 1 to 22)  
 ckop, D.J., Ala-Kokko, L. and Ritvaniemi, P.  
 and methods for detecting mutations in the procollagen II  
 e that indicate a genetic predisposition for osteoarthritis  
 nt: US 5558988-A 36 24-SEP-1996;  
 Location/Qualifiers  
 1..22

/organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 59.1%; Score 13; DB 6; Length 22;  
 Best Local Similarity 76.2%; Pred. No. 5.9e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
 |||||  
 Db 21 AGACACTCGCAGTCTCACCTG 1

RESULT 27  
 AX688870 25 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 1602 from Patent EP1281758.  
 ACCESSION AX688870  
 VERSION AX688870.1 GI:29411574  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE  
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4,  
 mdz12  
 JOURNAL Patent: EP 1281758-A 1602 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 25;  
 Best Local Similarity 76.2%; Pred. No. 5.9e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
 |||||  
 Db 5 AGTCATTCTCAGTCTCTCGG 25

RESULT 28  
 AX688875 25 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 1607 from Patent EP1281758.  
 ACCESSION AX688875  
 VERSION AX688875.1 GI:29411579  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE  
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4,  
 mdz12  
 JOURNAL Patent: EP 1281758-A 1607 05-FEB-2003;  
 Aeomica, Inc. (US)  
 FEATURES  
 source  
 1..25  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 25;  
 Best Local Similarity 76.2%; Pred. No. 5.9e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

09:38:24 2004

us-10-090-326-6.max.rge

AATCAGTCTCTCGCGA 22  
|||||  
ATTCTAGTCTCTCGGA 21

1992 28 bp DNA linear PAT 07-SEP-2000  
ence 1112 from patent US 5994076.

1992.1 GI:10017747

own.  
own.  
assified.  
bases 1 to 28)  
chik.A., Johhadze, G. and Bibilashvilli, R.  
ods of assaying differential expression  
t: US 5994076-A 1112 30-NOV-1999;  
Location/Qualifiers  
1. .28  
/organism="unknown"  
/mol\_type="unassigned DNA"

ilarity 59.1%; Score 13; DB 6; Length 28;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGTCTCTCGCG 21  
|||||  
ACAAACATCTCTCAGTG 28

3027 28 bp DNA linear PAT 20-APR-2002  
ence 1112 from patent US 6352829.

3027.1 GI:20247876

own.  
own.  
assified.  
bases 1 to 28)  
chik.A., Johhadze, G. and Bibilashvilli, R.  
ods of assaying differential expression  
nt: US 6352829-A 1112 05-MAR-2002;  
Location/Qualifiers  
1. .28  
/organism="unknown"  
/mol\_type="unassigned DNA"

ilarity 59.1%; Score 13; DB 6; Length 28;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGTCTCTCGCG 21  
|||||  
ACAAACATCTCTCAGTG 28

0181 28 bp DNA linear PAT 20-DEC-2002  
ence 1112 from patent US 6489455.

0181.1 GI:27310692

own.  
own.

Unclassified.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvilli, R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 6489455-A 1112 03-DEC-2002;  
FEATURES Location/Qualifiers  
source 1. .28  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 28;  
Best Local Similarity 76.2%; Pred. No. 6e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCAGTCTCTCGCG 21  
|||||

Db 8 ACACAACATCTCTCAGTGG 28  
|||||

RESULT 32

AX794235 28 bp DNA linear PAT  
LOCUS Sequence 66 from Patent WO02092827.  
DEFINITION AX794235  
ACCESSION AX794235.1 GI:32959641  
VERSION AX794235.1  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Rottier, P.J., de Haan, C.A., Haijema, B.J. and Bosch, B.J.  
TITLE Corona-virus-like particles comprising functionally dele  
JOURNAL Patent: WO 02092827-A 66 21-NOV-2002;  
Universiteit Utrecht (NL); STICHTING VOOR DE TECHNISCHE  
WETENSCHAPPEN (NL)

FEATURES

Location/Qualifiers  
source 1. .28  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="sequence of junction generated in recomb  
MHV-virus"

ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 28;  
Best Local Similarity 76.2%; Pred. No. 6e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAATCAGTCTCTCGCGA 22  
|||||

Db 8 GACTATCACAGCCCCCGCA 28  
|||||

RESULT 33

I92361 34 bp DNA linear PAT  
LOCUS Sequence 13 from patent US 5728519.  
DEFINITION I92361  
ACCESSION I92361  
VERSION I92361.1 GI:3936831  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 34)  
AUTHORS Levenbook, I.S., Chumakov, K.M., Norwood, L.P. and Roninson  
TITLE Assay for virulent revertants of attenuated live vaccine  
therefor  
JOURNAL Patent: US 5728519-A 13 17-MAR-1998;  
FEATURES Location/Qualifiers  
source 1. .34  
/organism="unknown"  
/mol\_type="unassigned DNA"

09:38:24 2004

us-10-090-326-6.max.rge

59.1%; Score 13; DB 6; Length 34;  
ilarity 76.2%; Pred. No. 6e+04; 5; Indels 0; Gaps 0;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
CAATCAGTCTCTGCGGA 22  
|||||  
CAATCAGATGTGTGAGCA 34  
|||||  
8476 40 bp DNA linear PAT 23-NOV-2002  
ence 256 from Patent WO02072846.  
8476 40 bp DNA linear PAT 23-NOV-2002  
8476.1 GI:25270886  
helic construct  
helic construct  
ficial sequences.  
out, D., Reynes, J.P. and Tiraby, G.  
helic genes and bacterial plasmids devoid of cpv  
nt: WO 02072846-A 256 19-SEP-2002;  
A (FR)  
Location/Qualifiers  
1..40  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="assembling oligo for CpG-free LacZ"  
59.1%; Score 13; DB 6; Length 40;  
ilarity 76.2%; Pred. No. 6.1e+04;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
ACATCAGTCTCTGCGGA 22  
|||||  
ACATCAGTGGATGTGGA 38  
|||||  
35024 47 bp DNA linear PAT 28-AUG-2001  
ence 494 from Patent WO0151659.  
35024 47 bp DNA linear PAT 28-AUG-2001  
35024.1 GI:15385671  
o sapiens (human)  
o sapiens  
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
malia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
T., Blumenfeld, M. and Cohen, D.  
helic markers derived from genomic regions carrying genes  
clived in central nervous system disorders  
ent: WO 0151659-A 494 19-JUL-2001;  
SET (FR)  
Location/Qualifiers  
1..47  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
24  
/note="18-856-85 : polymorphic base C or T"  
59.1%; Score 13; DB 6; Length 47;  
milarity 100.0%; Pred. No. 6.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AATCAGTCTCT 17  
|||||  
Db 23 AATCAGTCTCT 11  
|||||  
RESULT 36  
AX234381 50 bp DNA linear PAT  
LOCUS Sequence 31 from Patent WO0162942.  
DEFINITION AX234381  
ACCESSION AX234381  
VERSION AX234381.1 GI:15593382  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.  
AUTHORS Alitalo, K.M. and Jeltsch, M.M.  
TITLE Materials and methods involving hybrid vascular endothel  
factor dhas and proteins and screening methods for modul  
JOURNAL Patent: WO 0162942-A 31 30-AUG-2001;  
FEATURES PATENT: WO 0162942-A 31 30-AUG-2001; (US); Licentia OY  
1..50 Location/Qualifiers  
source  
1..50  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide"  
ORIGIN  
Query Match 59.1%; Score 13; DB 6; Length 50;  
Best Local Similarity 76.2%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
QY 2 GACATCAGTCTCTGCGGA 22  
|||||  
Db 1 GCCATCAGTCTCTGCGGA 21  
|||||  
RESULT 37  
AX158793 51 bp DNA linear PAT  
LOCUS Sequence 2121 from Patent WO0140521.  
DEFINITION AX158793  
ACCESSION AX158793  
VERSION AX158793.1 GI:14540124  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Ho  
Shinketsu, R.A. and Leach, M.  
AUTHORS Nucleic acids containing single nucleotide polymorphism  
TITLE Methods of use thereof  
JOURNAL Patent: WO 0140521-A 2121 07-JUN-2001;  
FEATURES Curagen Corporation (US)  
1..51 Location/Qualifiers  
source  
1..51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
misc\_feature 26  
/note="1 of 2 allelic variants (2122 is other  
Accession number CG38453366"  
ORIGIN  
Query Match 59.1%; Score 13; DB 6; Length 51;  
Best Local Similarity 76.2%; Pred. No. 6.1e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
QY 2 GACATCAGTCTCTGCGGA 22  
|||||  
Db 29 GAAATCAGATCTCTCTGA 49  
|||||

09:38:24 2004

us-10-090-326-6.max.rge

```

794          51 bp      DNA      linear      PAT 22-JUN-2001
nce 2122 from Patent WO0140521.
794          GI:14540125
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ilia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ets,R.A. and Leach,M.
ic acids containing single nucleotide polymorphisms and
ds of use thereof
t: WO 0140521-A 2122 07-JUN-2001;
en Corporation (US)
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/notes="2 of 2 allelic variants (2121 is other entry)
Accession number cg38453366"
59.1%; Score 13; DB 6; Length 51;
larity 76.2%; Pred. No. 6.1e+04;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

AATCACAGTCTCTGCGGA 22
|||||
AATCAGAAATCTCTCTGA 49

795          51 bp      DNA      linear      PAT 22-JUN-2001
nce 2123 from Patent WO0140521.
795          GI:14540126
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ilia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ets,R.A. and Leach,M.
ic acids containing single nucleotide polymorphisms and
ds of use thereof
t: WO 0140521-A 2123 07-JUN-2001;
en Corporation (US)
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
/notes="1 of 2 allelic variants (2124 is other entry)
Accession number cg38453366"
59.1%; Score 13; DB 6; Length 51;
larity 76.2%; Pred. No. 6.1e+04;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

AATCACAGTCTCTGCGGA 22
|||||
AATCAGAAATCTCTCTGA 41
```

```

RESULT 40
AX234390/c
LOCUS          60 bp      DNA      linear      PAT :
DEFINITION
Sequence 40 from Patent WO0162942.
ACCESSION
AX234390
VERSION
AX234390.1 GI:15593391
KEYWORDS
.
SOURCE
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
1
REFERENCE
1
AUTHORS
Alitalo,K.M. and Jeltsch,M.M.
TITLE
Materials and methods involving hybrid vascular endothel:
factor dnas and proteins and screening methods for moduli:
Patent: WO 0162942-A 40 30-AUG-2001;
JOURNAL
LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY
FEATURES
Location/Qualifiers
1..60
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
ORIGIN
Query Match          59.1%; Score 13; DB 6; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY      2 GACAATCACAGTCTCTGCGGA 22
      |||||||
Db      54 GCATTCACACTTCTGCGCA 34

RESULT 41
AX285267/c
LOCUS          20 bp      DNA      linear      PAT :
DEFINITION
Sequence 12 from Patent WO0178773.
ACCESSION
AX285267
VERSION
AX285267.1 GI:17045949
KEYWORDS
.
SOURCE
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
1
REFERENCE
1
AUTHORS
Denich,K.
TITLE
Disassociated pili, their production and use
Patent: WO 0178773-A 12 25-OCT-2001;
JOURNAL
O'Hanley, Peter (US) ; Denich, Kenneth (CA)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match          58.2%; Score 12.8; DB 6; Length 20;
Best Local Similarity 87.5%; Pred. No. 7.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY      1 AGACAATCACAGTCTC 16
      |||||
Db      18 AGAGATCGCAGTCTC 3

RESULT 42
AX302070/c
LOCUS          20 bp      DNA      linear      PAT :
DEFINITION
Sequence 32 from Patent WO0179277.
ACCESSION
AX302070
VERSION
AX302070.1 GI:17383021
KEYWORDS
.
SOURCE
synthetic construct
```

helic construct  
ficial sequences.

ch,K. and Schmidt,M.A.  
nogenic pili presenting foreign peptides, their production and

nt: WO 0179277-A 32 25-OCT-2001;  
nley, Peter (US) ; Denich, Kenneth (CA) ; Schmidt, M. Alexander

Location/Qualifiers

1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

58.2%; Score 12.8; DB 6; Length 20;

ilarity 87.5%; Pred.No. 7.6e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ACAATCACAGTCTC 16

|||||  
AGATCGCAGTCTC 3

7974 24 bp DNA linear PAT 11-MAY-2001  
ence 3097 from Patent WO0129262.

7974.1 GI:14034925

helic construct  
helic construct  
ficial sequences.

ult-Newburg,L. and Pohl,M.  
typing reagents, kits and methods of use thereof  
nt: WO 0129262-A 3097 26-APR-2001;  
id BioSciences, Inc. (US)

Location/Qualifiers

1. .24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

58.2%; Score 12.8; DB 6; Length 24;

ilarity 87.5%; Pred.No. 7.7e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ACAGTCTCTGCGGA 22

|||||  
ACAGTCTTTGCAGA 4

9827 47 bp DNA linear PAT 12-JUN-2003  
ence 1562 from patent US 6537751.

9827.1 GI:31677111

OWN.

OWN.

assified.

bases 1 to 47)

n.D., Chumakov,I. and Blumenfeld,M.  
lelic markers for use in constructing a high density  
quilibrium map of the human genome  
nt: US 6537751-A 1562 25-MAR-2003;

FEATURES source Location/Qualifiers  
1. .47  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 58.2%; Score 12.8; DB 6; Length 47;  
Best Local Similarity 77.8%; Pred.No. 7.9e+04;  
Matches 14; Conservative 1; Mismatches 3; Indels 0;

Qy 4 CAATCACAGTCTCTGCGG 21  
|||||  
38 CAGTCTCAGTCTCTGCCG 21  
|||||

RESULT 45  
AX190056/c  
LOCUS AX190056 51 bp DNA linear PAT  
DEFINITION Sequence 235 from Patent WO0147942.  
ACCESSION AX190056  
VERSION AX190056.1 GI:15143428  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor

REFERENCE 1  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms  
methods of use thereof  
JOURNAL Patent: WO 0147942-A 235 05-JUL-2001;  
Curagen Corporation (US)

FEATURES source Location/Qualifiers  
1. .51  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="1 of 2 allelic variants (236 is other  
entry) -Accession number cg43941884"

ORIGIN

Query Match 58.2%; Score 12.8; DB 6; Length 51;  
Best Local Similarity 87.5%; Pred.No. 7.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 AGACAATCACAGTCTC 16  
|||||  
33 AGACACTCACAGTTTC 18  
|||||

Search completed: February 29, 2004, 09:42:52

Job time : 713.857 secs



09:38:24 2004

us-10-090-326-6.max.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 07:46:14 ; Search time 187.714 Seconds  
(without alignments)  
497.886 Million cell updates/sec

JS-10-090-326-6

22  
1 agacaatcacagtctctgcgga 22

IDENTITY NUC

3apop 10.0 , Gapext 1.0

3373863 seqs, 212409041 residues

hits satisfying chosen parameters: 3308108

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

N: Geneseqn\_29Jan04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	22	6	ABQ82540	Abq82540	Human CEA
71.8	46	2	AAT36494	Aat36494	Carcinoem
70.9	30	2	AAT73719	Aat73719	Beta 7 in
70.9	30	2	AAT06506	Aat06506	Primer NH
69.1	31	4	AAF61364	Aaf61364	Thrombomo
64.5	20	6	AAD34356	Aad34356	Human BSM
64.5	60	6	ABN43232	Abn43232	Human spl
63.6	25	7	ADB00617	Adb00617	Human MDZ
63.6	25	7	ADB00619	Adb00619	Human MDZ
63.6	25	7	ADB00620	Adb00620	Human MDZ
63.6	25	7	ADB00618	Adb00618	Human MDZ
62.7	25	8	ACI53991	Act53991	Human mic
61.8	24	2	AAQ27842	Aaq27842	Short tan
61.8	25	8	ACI61709	Act61709	Human mic
61.8	25	8	ACK26100	Ack26100	Human mic
61.8	25	8	ACH53388	Ach53388	DNA targe
61.8	25	8	ACH53387	Ach53387	DNA targe
61.8	33	6	ABL14371	Ab14371	Human tra
61.8	37	2	AAV40070	Aav40070	PCR prime
61.8	48	2	AAK91822	Aak91822	Porphorym
61.8	50	7	ABX15582	Abx15582	MHV expre
61.8	53	7	ABX15587	Abx15587	MHV expre

57.3	25	8	ACI78821	Human mic	170	12.4	56.4	29	6	ABX14531	ABX14531
57.3	28	6	ABL41270	Diabody a	171	12.4	56.4	29	6	ABX14529	ABX14529
57.3	29	2	AAV37846	sFv23e ge	172	12.4	56.4	29	6	ABK88686	ABK88686
57.3	31	2	AAQ45505	Sequence	173	12.4	56.4	29	6	ABK88688	ABK88688
57.3	35	2	AAI36521	Primer to	174	12.4	56.4	29	6	ABK13406	ABK13406
57.3	35	2	AAK05567	Mouse hea	175	12.4	56.4	29	7	ADA09077	ADA09077
57.3	35	2	AAK82037	Mouse hea	176	12.4	56.4	29	7	ADA09075	ADA09075
57.3	36	9	AAK05567	Mouse hea	177	12.4	56.4	29	7	ADA09075	ADA09075
57.3	36	9	AAK05567	Mouse hea	178	12.4	56.4	30	2	AAQ25323	AAQ25323
57.3	45	4	AAK05567	Mouse hea	179	12.4	56.4	30	2	AAV12042	AAV12042
57.3	47	3	AAK05567	Mouse hea	180	12.4	56.4	30	6	ABK51910	ABK51910
57.3	48	2	AAK05567	Mouse hea	181	12.4	56.4	30	6	ABK51910	ABK51910
57.3	48	2	AAK05567	Mouse hea	182	12.4	56.4	30	6	ABK51910	ABK51910
57.3	48	2	AAK05567	Mouse hea	183	12.4	56.4	30	6	ABK51910	ABK51910
57.3	50	2	AAV18704	Homo sapi	184	12.4	56.4	31	2	AAV67663	AAV67663
57.3	51	4	AAI73139	Human sil	185	12.4	56.4	32	4	AAH24139	AAH24139
57.3	51	4	AAI73139	Human sil	186	12.4	56.4	33	4	ABL55921	ABL55921
57.3	59	2	AAI61569	scFv anti	187	12.4	56.4	34	2	AAI73730	AAI73730
57.3	59	2	AAI61569	scFv anti	188	12.4	56.4	34	2	AAI73731	AAI73731
57.3	60	6	ABN41981	Human spl	189	12.4	56.4	34	2	AAZ06529	AAZ06529
57.3	60	6	ABN41981	Human spl	190	12.4	56.4	34	2	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	191	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	192	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	193	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	194	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	195	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	196	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	197	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	198	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	199	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	200	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	201	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	202	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	203	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	204	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	205	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	206	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	207	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	208	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	209	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	210	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	211	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	212	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	213	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	214	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	215	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	216	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	217	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	218	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	219	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	220	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	221	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	222	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	223	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	224	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	225	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	226	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	227	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	228	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	229	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	230	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	231	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	232	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	233	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	234	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	235	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	236	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	237	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	238	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	239	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	240	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	241	12.4	56.4	35	3	AAZ06528	AAZ06528
57.3	60	6	ABN41981	Human spl	242	12.4	56.4	35	3	AAZ06528	AAZ06528

55.5	32	5	AAE54909	Aaf54909 PCR prime	316	12	54.5	23	8	ADA37834	Ada37834
55.5	32	6	ABL56456	Abf56456 Primer VA	317	12	54.5	23	8	ADA21520	Ada21520
55.5	33	3	AAZ98724	Aaz98724 PCR prime	318	12	54.5	23	8	ADA10307	Ada10307
55.5	33	3	AAZ29868	Aaz29868 SYDV rela	319	12	54.5	23	8	ADA17851	Ada17851
55.5	36	2	AAZ32792	Aaz32792 Reshaped	320	12	54.5	23	8	ADA27959	Ada27959
55.5	37	6	ABQ72442	Abq72442 PCR prime	321	12	54.5	23	8	ADA94539	Ada94539
55.5	38	6	ABQ72426	Abq72426 PCR prime	322	12	54.5	23	8	ADA38764	Ada38764
55.5	38	6	ABQ72443	Abq72443 PCR prime	323	12	54.5	23	8	ADA32885	Ada32885
55.5	38	6	ABQ72444	Abq72444 PCR prime	324	12	54.5	23	8	ACH65489	Ada65489
55.5	38	6	ABQ72448	Abq72448 PCR prime	325	12	54.5	23	8	ADA22446	Ada22446
55.5	38	6	ABQ72440	Abq72440 PCR prime	326	12	54.5	23	8	ADA22446	Ada22446
55.5	38	6	ABQ72441	Abq72441 PCR prime	327	12	54.5	23	8	ADA06612	Ada06612
55.5	41	6	ABQ77937	Abq77937 Human mac	328	12	54.5	23	8	ADA39305	Ada39305
55.5	41	6	ABK11520	Abk11520 Human oxy	329	12	54.5	23	8	ADB96331	Ada96331
55.5	42	6	AAQ23848	Aaq23848 Primer RH	330	12	54.5	23	9	ADC57803	Adc57803
55.5	42	6	AAQ28862	Aad28862 Human ant	331	12	54.5	23	9	ADC55167	Adc55167
55.5	42	9	ADD67340	Add67340 Human ant	332	12	54.5	23	9	ADC12034	Adc12034
55.5	43	2	AAQ37845	Aaq37845 Sequence	333	12	54.5	23	9	ADC56456	Adc56456
55.5	43	2	AAQ69258	Aaq69258 Human cho	334	12	54.5	23	9	ADC07511	Adc07511
55.5	48	2	AAAT63720	Aat63720 Human cho	335	12	54.5	23	9	ADC11501	Adc11501
55.5	48	2	AAAT63720	Aat63720 Human cho	336	12	54.5	23	9	ADC14623	Adc14623
55.5	48	2	AAAT63720	Aat63720 Human cho	337	12	54.5	23	9	ADC08155	Adc08155
55.5	48	6	ABK82499	Abk82499 DNA bindi	338	12	54.5	23	9	ADC08155	Adc08155
55.5	48	10	AD880038	Ad880038 Duplex cl	339	12	54.5	23	9	ADC08155	Adc08155
55.5	49	2	AAQ69329	Aaq69329 Human cho	340	12	54.5	23	9	ADC07622	Adc07622
55.5	49	2	AAAT63791	Aat63791 Human cho	341	12	54.5	23	9	ADC82513	Adc82513
55.5	49	2	AAAT63791	Aat63791 Human cho	342	12	54.5	23	9	ADC84262	Adc84262
55.5	49	6	ABK82570	Abk82570 DNA bindi	343	12	54.5	23	9	ADC83863	Adc83863
55.5	49	10	AD880109	Ad880109 Duplex cl	344	12	54.5	23	9	ADC06942	Adc06942
55.5	50	2	AAZ52154	Aaz52154 Synthetic	345	12	54.5	23	9	ADC06942	Adc06942
55.5	50	2	AAZ52078	Aaz52078 Synthetic	346	12	54.5	23	9	ADC83189	Adc83189
55.5	50	4	AAAL31473	Aal31473 Human SNP	347	12	54.5	23	9	ADD55296	Add55296
55.5	50	6	ABZ04399	Abz04399 Human leu	348	12	54.5	23	9	ADD56254	Add56254
55.5	50	6	ABZ03209	Abz03209 Human leu	349	12	54.5	23	9	ADD54692	Add54692
55.5	51	4	AAH79418	Aah79418 Human DNA	350	12	54.5	23	9	ADD56846	Add56846
55.5	51	5	ABL00984	Abf00984 Human ami	351	12	54.5	23	9	ADD56846	Add56846
55.5	52	2	AAV79391	Aav79391 Staphyloc	352	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN58889	Abn58889 Human spl	353	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN42164	Abn42164 Human spl	354	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN58634	Abn58634 Human spl	355	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN47836	Abn47836 Human spl	356	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN47944	Abn47944 Human spl	357	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN43233	Abn43233 Human spl	358	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN46474	Abn46474 Human spl	359	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN45521	Abn45521 Human spl	360	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN36252	Abn36252 Human spl	361	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN36681	Abn36681 Human spl	362	12	54.5	23	9	ADD56846	Add56846
55.5	60	6	ABN37178	Abn37178 Human spl	363	12	54.5	23	9	ADD56846	Add56846
55.5	20	2	AAZ02867	Aaz02867 PCR prime	364	12	54.5	23	9	ADD56846	Add56846
54.5	20	6	ABL50603	Abf50603 Mouse Nap	365	12	54.5	23	9	ADD56846	Add56846
54.5	20	9	AAZ24128	Aaz24128 Cre recom	366	12	54.5	23	9	ADD56846	Add56846
54.5	21	2	AAZ36544	Aaz36544 PCR prime	367	12	54.5	23	9	ADD56846	Add56846
54.5	21	3	AAZ55812	Aaz55812 Rat FGF-1	368	12	54.5	23	9	ADD56846	Add56846
54.5	21	6	ABS61385	Abf61385 Plasmid d	369	12	54.5	23	9	ADD56846	Add56846
54.5	23	3	AAZ65202	Aaz65202 Primer am	370	12	54.5	23	9	ADD56846	Add56846
54.5	23	4	AAZ90135	Aaz90135 Human PRO	371	12	54.5	23	9	ADD56846	Add56846
54.5	23	5	AAZ44359	Aaz44359 Human PRO	372	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX77918	Abx77918 Human PRO	373	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX80330	Abx80330 Human sec	374	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACA69236	Aca69236 Human sec	375	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX90307	Abx90307 Human sec	376	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX64153	Abx64153 Human PRO	377	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACA64375	Aca64375 Novel hum	378	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACA58037	Aca58037 Human neo	379	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX80834	Abx80834 Human sec	380	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACD44343	Acd44343 Human PRO	381	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX79514	Abx79514 Human sec	382	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACA93535	Aca93535 Novel hum	383	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX81217	Abx81217 Human sec	384	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ACA93033	Aca93033 Novel hum	385	12	54.5	23	9	ADD56846	Add56846
54.5	23	7	ABX17117	Abx17117 Human PRO	386	12	54.5	23	9	ADD56846	Add56846
54.5	23	8	ACA67972	Aca67972 Novel hum	387	12	54.5	23	9	ADD56846	Add56846
54.5	23	8	ACA88421	Aca88421 Human sec	388	12	54.5	23	9	ADD56846	Add56846
54.5	23	8	ACD81928	Acd81928 Human PRO	389	12	54.5	23	9	ADD56846	Add56846

54.5	39	2	AAQ44626	Aac44626 PCR prime	C 462	11.8	53.6	25	8	ACI24500	ACI24500
54.5	39	6	ABA01794	Lambda ZA	463	11.8	53.6	25	8	ACK08170	ACK08170
54.5	40	2	AAQ30862	C-bit mRN	C 464	11.8	53.6	25	8	ACI83606	ACI83606
54.5	40	3	AAZ87244	Murine Ig	465	11.8	53.6	25	8	ACI98520	ACI98520
54.5	40	3	AAZ37327	Human c-k	C 466	11.8	53.6	25	8	ACI34707	ACI34707
54.5	41	2	AAZ91382	Human c-k	C 467	11.8	53.6	25	8	ACI18138	ACI18138
54.5	41	2	AAZ30849	Murine Ig	C 468	11.8	53.6	25	8	ACI26972	ACI26972
54.5	41	6	AAZ45630	Human ser	C 469	11.8	53.6	25	8	ACI77401	ACI77401
54.5	42	2	AAZ35984	MAB 39-1	C 470	11.8	53.6	25	8	ACI35632	ACI35632
54.5	42	2	AAZ37397	Plasmid p	C 471	11.8	53.6	25	8	ACI79934	ACI79934
54.5	42	3	AAZ37796	Oligonucle	C 472	11.8	53.6	25	8	ACI26336	ACI26336
54.5	42	6	ABA94980	AdPac-GAL	C 473	11.8	53.6	25	8	ACI76195	ACI76195
54.5	42	7	AAZ52106	Gal #6 ol	C 474	11.8	53.6	25	8	ACI80544	ACI80544
54.5	42	7	AAZ49815	Gal #6 ol	C 475	11.8	53.6	25	8	ACI18770	ACI18770
54.5	43	8	ACC58587	Anti-tiss	C 476	11.8	53.6	25	8	ACI26519	ACI26519
54.5	47	3	AAZ67126	Human map	C 477	11.8	53.6	25	8	ACI26973	ACI26973
54.5	48	5	ABA10708	Tail adap	478	11.8	53.6	25	8	ACH57449	ACH57449
54.5	49	4	AAZ01416	Human wil	479	11.8	53.6	25	8	ACH62414	ACH62414
54.5	49	5	AAZ57553	Calcium c	480	11.8	53.6	25	8	ACH51321	ACH51321
54.5	50	4	AAZ32032	Human SNP	C 481	11.8	53.6	26	6	ABV99236	ABV99236
54.5	50	6	ABZ03638	Human leu	C 482	11.8	53.6	27	2	AAT28007	AAT28007
54.5	51	4	AAZ27353	Human SNP	C 483	11.8	53.6	27	2	AAZ42308	AAZ42308
54.5	51	4	AAH79579	Human DNA	C 484	11.8	53.6	28	3	AAZ50057	AAZ50057
54.5	51	4	AAH79421	Human DNA	C 485	11.8	53.6	28	3	ABK67096	ABK67096
54.5	52	5	AAZ57567	Calcium c	486	11.8	53.6	29	3	AAZ40885	AAZ40885
54.5	52	7	ABX12970	Human II-	C 487	11.8	53.6	30	2	AAQ42984	AAQ42984
54.5	57	2	AAQ29236	Probe for	C 488	11.8	53.6	30	2	AAQ43500	AAQ43500
54.5	57	2	AAQ20974	AAQ20974	C 489	11.8	53.6	30	2	AAQ28512	AAQ28512
54.5	59	7	ACC41784	Pre-contr	C 490	11.8	53.6	30	2	AAV24251	AAV24251
54.5	60	4	AAH78164	Nucleotid	C 491	11.8	53.6	30	2	AAV00095	AAV00095
54.5	60	6	ABA04540	PCR prime	C 492	11.8	53.6	30	3	AAZ58876	AAZ58876
54.5	60	6	ABX00137	Mouse MAB	C 493	11.8	53.6	30	4	AAZ58876	AAZ58876
54.5	60	6	ABX00137	Human L76	494	11.8	53.6	30	4	AAZ58876	AAZ58876
54.5	60	6	ABX00137	Human L76	C 495	11.8	53.6	30	4	AAZ58876	AAZ58876
54.5	60	6	ABK71343	Thrombopo	C 496	11.8	53.6	30	4	AAH75069	AAH75069
54.5	60	6	ABQ92458	Human lun	C 497	11.8	53.6	30	4	AAH76607	AAH76607
54.5	60	6	ABN36588	Human spl	C 498	11.8	53.6	30	5	AAH74250	AAH74250
54.5	60	6	ABN43331	Human spl	C 499	11.8	53.6	30	5	AAZ58876	AAZ58876
54.5	60	6	ABN58929	Human spl	C 500	11.8	53.6	30	6	ABL94784	ABL94784
54.5	60	6	ABN38189	Human spl	C 501	11.8	53.6	30	6	ABX69366	ABX69366
54.5	60	6	ABN39375	Human spl	C 502	11.8	53.6	30	7	ABT14009	ABT14009
54.5	60	6	ABN42446	Human spl	C 503	11.8	53.6	30	7	ABT14009	ABT14009
54.5	60	6	ABN39043	Human spl	C 504	11.8	53.6	31	2	AAV58064	AAV58064
54.5	60	8	ADA28465	Human lun	505	11.8	53.6	31	2	AAV81121	AAV81121
53.6	17	2	ABT37928	Variable	506	11.8	53.6	31	2	AAV81138	AAV81138
53.6	18	2	AAQ10845	Human PKC	507	11.8	53.6	31	2	AAV81109	AAV81109
53.6	19	8	ADA25296	Human PKC	508	11.8	53.6	31	2	AAV81109	AAV81109
53.6	19	8	ADA25421	Gene dete	C 509	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	2	AAQ53084	Primer AC	C 510	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	2	AAV08609	PCR prime	C 511	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	2	AAZ92961	PCR prime	C 512	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	2	AAZ92964	PCR prime	C 513	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	3	AAZ56683	Murine VH	C 514	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	3	AAZ56685	Murine VH	C 515	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	3	AAZ56685	Murine VH	C 516	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	6	AAZ40436	Human ACE	C 517	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	6	AAZ40436	Human ACE	C 518	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	6	AAZ40436	Human ACE	C 519	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	20	8	AAZ40436	Human ACE	C 520	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	21	2	AAZ70845	Chimeric	C 521	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	21	2	AAZ70845	Chimeric	C 522	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	21	7	ADA18537	Target Ig	C 523	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	22	9	ADD13660	Forward A	C 524	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	22	9	AAZ40335	PCR prime	C 525	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	23	2	AAZ10212	Probe for	C 526	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	2	AAQ62718	Probe for	C 527	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	2	AAQ62718	Probe for	C 528	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	3	AAZ11463	Human dys	C 529	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	3	AAZ36918	Human dys	C 530	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	4	AAZ84114	Human CSG	C 531	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	24	4	AAZ84114	Human CSG	C 532	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6	25	8	ACI35633	Human mic	C 533	11.8	53.6	31	3	AAZ44226	AAZ44226
53.6					C 534	11.8	53.6	31	3	AAZ44226	AAZ44226

53.6	36	4	AAC66984	Aac66984 Bacteriop	608	11.6	52.7	20	3	AAC73804	Aac73804 I
53.6	37	2	AAQ80392	AAQ80392 Mouse hea	609	11.6	52.7	20	4	AAS15171	Aas15171 I
53.6	37	2	AAQ80670	AAQ80670 L243 VH r	610	52.7	52.7	20	6	ABV73630	Abv73630 I
53.6	37	2	AAT07333	Aat07333 Mab 39D10	611	11.6	52.7	20	7	ABX04458	Abx04458 I
53.6	37	2	AAT16943	Aat16943 Murine an	612	11.6	52.7	20	9	ADE14416	Adel14416 I
53.6	37	2	AAX90430	Aax90430 Chimeric	613	11.6	52.7	21	6	ABQ79112	Abq79112 I
53.6	37	6	AAQ31320	AAQ31320 Mouse hea	614	11.6	52.7	21	9	ADD05293	Add05293 I
53.6	38	6	ABQ72438	Abq72438 PCR prime	615	11.6	52.7	22	2	AAX16566	Aax16566 I
53.6	38	6	AAV57502	Aav57502 Antibody	616	52.7	52.7	22	2	AAV23624	Aav23624 I
53.6	38	6	ABQ72429	Abq72429 PCR prime	617	11.6	52.7	23	3	AAT15902	Aat15902 I
53.6	38	6	ABQ72439	Abq72439 PCR prime	618	11.6	52.7	23	3	AA88508	Aa88508 I
53.6	39	4	AAH78402	Aah78402 PCR prime	619	11.6	52.7	24	6	ABQ08771	Abq08771 I
53.6	39	7	ACA49951	Aca49951 Synthetic	620	11.6	52.7	24	6	ABQ02436	Abq02436 I
53.6	40	7	ACA55229	Aca55229 Human IGE	621	11.6	52.7	24	6	ABQ08812	Abq08812 I
53.6	40	7	ACA55211	Aca55211 Human IGE	622	11.6	52.7	25	7	AAV62108	Aav62108 I
53.6	40	7	ACA55191	Aca55191 Canine Ig	623	11.6	52.7	25	7	ADB00624	Adb00624 I
53.6	40	7	ACA55218	Aca55218 Human IGE	624	11.6	52.7	25	8	ACK16869	Ack16869 I
53.6	41	2	AAV50774	Aav50774 Braggica	625	11.6	52.7	25	8	ACK19011	Ack19011 I
53.6	41	3	AAZ87718	Aaz87718 Anti-huma	626	11.6	52.7	25	8	ACI77084	Act177084 I
53.6	41	4	AAF70195	Aaf70195 Oligonucl	627	11.6	52.7	25	8	ACI57014	Act157014 I
53.6	41	5	AAFC93900	Aaf93900 PCR prime	628	11.6	52.7	25	8	ACI65779	Act165779 I
53.6	41	6	AAI69209	Aai69209 Human tyr	629	11.6	52.7	25	8	ACI53105	Act153105 I
53.6	41	7	ACC00157	Acc00157 Probe #2	630	11.6	52.7	25	8	ACK15711	Ack15711 I
53.6	42	6	ABQ72379	Abq72379 PCR prime	631	11.6	52.7	25	8	ACI47944	Act147944 I
53.6	42	3	AAZ49551	Aaz49551 Anticense	632	11.6	52.7	25	8	ACI84694	Act184694 I
53.6	45	2	AAT74974	Aat74974 Anti-tran	633	11.6	52.7	25	8	ACK17311	Ack17311 I
53.6	45	3	AAZ87717	Aaz87717 Anti-huma	634	11.6	52.7	25	8	ACT178125	Act178125 I
53.6	45	4	AAF70194	Aaf70194 Oligonucl	635	11.6	52.7	25	8	ACK13930	Ack13930 I
53.6	46	2	AAQ37398	Aaq37398 Primer Mo	636	11.6	52.7	25	8	ACK18611	Ack18611 I
53.6	47	2	AAV44007	Aav44007 Human Mab	637	11.6	52.7	25	8	ACK189185	Ack189185 I
53.6	47	3	AAZ67762	Aaz67762 Human map	638	11.6	52.7	25	8	ACK23330	Ack23330 I
53.6	47	4	AAH88583	Aah88583 CNS disor	639	11.6	52.7	26	6	ABT09646	Abt09646 I
53.6	48	2	AAV03844	Aav03844 Mouse hea	640	52.7	52.7	28	6	ABL41266	Ab141266 I
53.6	48	2	AAV18533	Aav18533 Mouse hea	641	11.6	52.7	28	6	ACC74146	Acc74146 I
53.6	48	2	AAV18569	Aav18569 Mouse hea	642	11.6	52.7	29	7	AAQ66532	Aaq66532 I
53.6	48	2	AAV82320	Aav82320 Mouse imm	643	11.6	52.7	30	2	AAV35354	Aav35354 I
53.6	48	2	AAZ28184	Aaz28184 Chlamydia	644	11.6	52.7	30	2	AAZ88333	Aaz88333 I
53.6	48	3	AAZ99167	Aaz99167 Chlamydia	645	11.6	52.7	30	3	AAA40187	Aaa40187 I
53.6	48	4	AAH21994	Aah21994 Mouse imm	646	11.6	52.7	30	4	AAF88138	Aaf88138 I
53.6	48	4	AAH22020	Aah22020 Mouse Ig	647	11.6	52.7	30	4	AAF88081	Aaf88081 I
53.6	48	9	ADC65080	Adc65080 Mouse imm	648	11.6	52.7	30	4	ABX13116	Abx13116 I
53.6	48	9	ADC65054	Adc65054 Mouse imm	649	11.6	52.7	30	7	ABX13122	Abx13122 I
53.6	50	2	AAQ37397	Aaq37397 Primer Fo	650	11.6	52.7	31	2	AAZ57793	Aaz57793 I
53.6	50	2	AAQ37416	Aaq37416 Primer MO	651	11.6	52.7	31	4	AAI30568	Aai30568 I
53.6	50	4	AAI73211	Aai73211 Human sil	652	11.6	52.7	31	4	ABN83750	Abn83750 I
53.6	51	2	AAV77111	Aav77111 Staphyloc	653	11.6	52.7	31	6	ABN83753	Abn83753 I
53.6	51	2	AAV33750	Aav33750 Ig-like V	654	11.6	52.7	31	6	ABN83749	Abn83749 I
53.6	51	4	AAI29092	Aai29092 Human SNP	655	11.6	52.7	31	6	AAQ68730	Aaq68730 I
53.6	51	4	AAI77020	Aai77020 Human sil	656	11.6	52.7	33	2	AAQ36969	Aaq36969 I
53.6	51	4	AAI73210	Aai73210 Human sil	657	11.6	52.7	34	2	AAQ36969	Aaq36969 I
53.6	51	4	AAH40412	Aah40412 Human SNP	658	11.6	52.7	36	2	AAQ00981	Aaq00981 I
53.6	51	7	ABX88797	Abx88797 Corn ear-	659	11.6	52.7	36	9	ADD29945	Add29945 I
53.6	53	7	ABZ21173	Abz21173 Variable	660	11.6	52.7	36	9	ADD35983	Add35983 I
53.6	54	2	AAQ78346	Aaq78346 Fv haptan	661	11.6	52.7	36	7	ACD54088	Acd54088 I
53.6	54	2	AAQ86751	Aaq86751 Primer fo	662	11.6	52.7	38	7	ACD54088	Acd54088 I
53.6	54	2	AAV07645	Aav07645 anti-CD22	663	11.6	52.7	39	6	AAQ25718	Aaq25718 I
53.6	56	3	AAZ44228	Aaz44228 Murine CD	664	11.6	52.7	40	2	AAQ36508	Aaq36508 I
53.6	56	3	AAZ58686	Aaz58686 Anti-CD4	665	11.6	52.7	40	2	AAQ54753	Aaq54753 I
53.6	60	2	AAT85649	Aat85649 Canine Im	666	11.6	52.7	40	2	AAQ75893	Aaq75893 I
53.6	60	4	AAE30706	Aae30706 Mouse JH	667	11.6	52.7	40	2	AAT70698	Aat70698 I
53.6	60	6	ABN47743	Abn47743 Human spl	668	11.6	52.7	40	2	AAT28128	Aat28128 I
53.6	60	6	ABN35548	Abn35548 Human spl	671	11.6	52.7	41	6	ABT12238	Abt12238 I
53.6	60	6	ABN33859	Abn33859 Human spl	670	11.6	52.7	41	6	ABT12238	Abt12238 I
53.6	60	6	ABN50576	Abn50576 Human spl	671	11.6	52.7	41	6	ABZ46007	Abz46007 I
53.6	60	6	ABN58845	Abn58845 Human spl	672	11.6	52.7	41	6	ABZ46007	Abz46007 I
53.6	60	6	ABN43038	Abn43038 Human spl	673	11.6	52.7	43	2	AAQ53769	Aaq53769 I
53.6	60	6	ABN47127	Abn47127 Human spl	674	11.6	52.7	43	2	AAT07970	Aat07970 I
53.6	60	6	ABN49635	Abn49635 Human spl	675	11.6	52.7	43	2	AAV00986	Aav00986 I
53.6	68	3	AAZ70326	Aaz70326 Human bia	676	11.6	52.7	43	2	AAV14771	Aav14771 I
52.7	18	6	ABSS59954	Abss59954 Human DNA	677	11.6	52.7	43	2	AAV79846	Aav79846 I
52.7	19	7	ABT33997	Abt33997 Human pig	678	11.6	52.7	43	3	AA92946	Aa92946 I
52.7	20	2	AAT72837	Aat72837 SP24 gene	679	11.6	52.7	43	6	ABK61322	Abk61322 I
52.7	20	3	AAZ76305	Aaz76305 Human bia	680	11.6	52.7	45	2	AAT88664	Aat88664 I

us-10-090-326-6.max.rng

52.7	45	7	ABT34060	Human pig	754	11.4	51.8	18	6	ABT06161
52.7	46	7	ACC47398	G. cirrat	755	11.4	51.8	19	2	AAV30474
52.7	47	2	AACZ11953	Human pot	C 756	11.4	51.8	19	2	AAV58063
52.7	47	4	AHH88587	CNS disor	C 757	11.4	51.8	19	2	AAV81132
52.7	48	2	AAT86302	Primer ol	C 758	11.4	51.8	19	2	AAV81082
52.7	48	2	AAV033965	LDR probe	C 759	11.4	51.8	20	2	AAQ53353
52.7	48	2	ADD27837	GlcNAc-ph	C 760	11.4	51.8	20	2	AAV28294
52.7	50	3	AAA37231	Human DNA	C 761	11.4	51.8	20	2	AAV92224
52.7	50	4	AAAS13202	Tobacco r	C 762	11.4	51.8	20	2	AAV92219
52.7	50	4	AAL28722	Human SNP	C 763	11.4	51.8	20	4	AAAS08838
52.7	50	4	AA134141	Human SNP	C 764	11.4	51.8	20	4	AAAS08747
52.7	50	4	AAL29730	Human SNP	C 765	11.4	51.8	20	6	AAAS97054
52.7	50	4	AAF54340	Probe #30	C 766	11.4	51.8	20	7	ACC45228
52.7	50	6	ABK83306	Human v-e	C 767	11.4	51.8	20	9	AAL60469
52.7	50	6	ABZ01612	Human leu	C 768	11.4	51.8	20	9	ADC10327
52.7	50	6	ABZ07152	Human leu	C 769	11.4	51.8	21	7	ABK69607
52.7	50	6	ABZ03511	Human leu	C 770	11.4	51.8	21	7	ACC68851
52.7	50	6	ABZ04178	Human leu	C 771	11.4	51.8	22	2	AAZ07852
52.7	50	6	ABZ06762	Human leu	C 772	11.4	51.8	22	6	ABK95503
52.7	50	6	ABZ07525	Human leu	C 773	11.4	51.8	22	6	ABT04310
52.7	50	6	ABZ02277	Human leu	C 774	11.4	51.8	23	2	ADC66100
52.7	50	6	ABZ07446	Human leu	C 775	11.4	51.8	23	6	AAAS97990
52.7	50	6	ABZ03481	Human leu	C 776	11.4	51.8	24	2	AAT86450
52.7	50	8	ACD68377	Novel hum	C 777	11.4	51.8	24	2	AAT86611
52.7	50	8	ACH04479	Human sec	C 778	11.4	51.8	24	3	AAAS3238
52.7	50	8	ACD68023	Novel hum	C 779	11.4	51.8	24	5	AAH75985
52.7	50	9	ADC18061	Human PRO	C 780	11.4	51.8	24	7	ABX76693
52.7	50	9	ADD31781	Anti-CEA	C 781	11.4	51.8	24	8	ABX93096
52.7	50	9	ADD70707	Human sec	C 782	11.4	51.8	25	2	AAT84294
52.7	50	9	ADD39784	Human sec	C 783	11.4	51.8	25	4	AAH37783
52.7	50	9	ADD70230	Human sec	C 784	11.4	51.8	25	6	ABQ75556
52.7	50	9	ADD38351	Human sec	C 785	11.4	51.8	25	6	ABK40427
52.7	50	9	ADD39307	Human sec	C 786	11.4	51.8	25	8	ACI60939
52.7	50	9	ADD38830	Human sec	C 787	11.4	51.8	25	8	ACI172655
52.7	50	9	ADD40261	Human sec	C 788	11.4	51.8	25	8	ACI52665
52.7	50	9	ADE50482	Human sec	C 789	11.4	51.8	25	8	ACI93231
52.7	50	9	ADE20094	Human sec	C 790	11.4	51.8	25	8	ACI65791
52.7	50	9	ADE50005	Human sec	C 791	11.4	51.8	25	8	ACK02422
52.7	50	9	ADE21563	Human sec	C 792	11.4	51.8	25	8	ACI09271
52.7	51	4	AAH37908	Human SNP	C 793	11.4	51.8	25	8	ACI28807
52.7	51	4	AAH79918	Human DNA	C 794	11.4	51.8	25	8	ACI64952
52.7	51	2	AAT25558	Human gen	C 795	11.4	51.8	25	8	

1.1.8	30	6	ABN83507	Human alp	900	11.4	51.8	50	6	ABZ03910
1.1.8	30	6	ABN83131	Moloney l	901	11.4	51.8	50	6	ABZ071136
1.1.8	31	2	AAQ62449	vector pv	C 902	11.4	51.8	50	6	ABZ07430
1.1.8	31	2	AAQ39003	Human gen	C 903	11.4	51.8	50	6	ABZ05642
1.1.8	31	4	AAI29711	Human sin	C 904	11.4	51.8	50	6	ABZ06746
1.1.8	31	6	AAI18910	Human CLA	C 905	11.4	51.8	50	9	ADC15776
1.1.8	31	7	ACC69676	Antisense	C 906	11.4	51.8	51	3	AAZ28224
1.1.8	31	9	ADB95122	Primer SK	C 907	11.4	51.8	51	3	AAZ28224
1.1.8	32	2	AAV56631	Feline FL	C 908	11.4	51.8	51	3	AAZ28224
1.1.8	32	3	AAV63829	Human c-f	C 909	11.4	51.8	51	3	AAZ28224
1.1.8	32	5	AAH78297	PCR prime	C 910	11.4	51.8	51	3	AAZ28224
1.1.8	32	6	ABG66558	Primer as	C 911	11.4	51.8	51	3	AAZ28224
1.1.8	32	6	ABA05205	Glub-1 PC	C 912	11.4	51.8	51	3	AAZ28224
1.1.8	32	9	ADC84589	Primer of	C 913	11.4	51.8	51	3	AAZ28224
1.1.8	33	2	AAQ92010	Oligomer	C 914	11.4	51.8	51	3	AAZ28224
1.1.8	33	2	AAQ92010	Sense pri	C 915	11.4	51.8	51	3	AAZ28224
1.1.8	33	2	AAQ91813	Porphyrom	C 916	11.4	51.8	51	3	AAZ28224
1.1.8	33	2	AAZ10952	15D3 VH C	C 917	11.4	51.8	51	3	AAZ28224
1.1.8	33	2	AAH85753	Oligonucle	C 918	11.4	51.8	51	3	AAZ28224
1.1.8	33	3	ABA92909	Angiogeni	C 919	11.4	51.8	51	3	AAZ28224
1.1.8	33	3	AAI64616	Human rib	C 920	11.4	51.8	51	3	AAZ28224
1.1.8	33	3	AAK99419	PCR prime	C 921	11.4	51.8	51	3	AAZ28224
1.1.8	33	6	AAK15995	PCR prime	C 922	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAQ49188	scFvR con	C 923	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAQ67824	Vaccinia	C 924	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAI86395	Sp6 anti-	C 925	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAI86395	Human int	C 926	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAZ08488	Human int	C 927	11.4	51.8	51	3	AAZ28224
1.1.8	34	2	AAZ074603	Murine 5B	C 928	11.4	51.8	51	3	AAZ28224
1.1.8	34	9	ADL15074	PCR prime	C 929	11.4	51.8	51	3	AAZ28224
1.1.8	37	4	ABK05376	Human NOG	C 930	11.4	51.8	51	3	AAZ28224
1.1.8	39	2	AAQ53925	Allele sp	C 931	11.4	51.8	51	3	AAZ28224
1.1.8	40	3	AAZ36260	PCR prime	C 932	11.4	51.8	51	3	AAZ28224
1.1.8	40	3	AAZ43332	Murine T	C 933	11.4	51.8	51	3	AAZ28224
1.1.8	40	3	AAO05317	PCR prime	C 934	11.4	51.8	51	3	AAZ28224
1.1.8	40	6	ABK94858	Fat regul	C 935	11.4	51.8	51	3	AAZ28224
1.1.8	40	8	ADA38341	Salmonell	C 936	11.4	51.8	51	3	AAZ28224
1.1.8	41	2	AAQ36985	VH2, Ox V	C 937	11.4	51.8	51	3	AAZ28224
1.1.8	41	2	AAV50588	Brassica	C 938	11.4	51.8	51	3	AAZ28224
1.1.8	41	4	AAH75452	Human zin	C 939	11.4	51.8	51	3	AAZ28224
1.1.8	41	5	AAH83901	PCR prime	C 940	11.4	51.8	51	3	AAZ28224
1.										

50.9 18 7 ABZ81724  
 50.9 18 8 ADB12819  
 50.9 19 2 AAV10708  
 50.9 20 2 AAQ82523  
 50.9 20 2 AAQ88018  
 50.9 20 2 AAV14498  
 50.9 20 2 AAZ05811  
 50.9 20 2 AAX95167  
 50.9 20 2 AAX93019  
 50.9 20 3 AAA40876  
 50.9 20 3 AAA56679  
 50.9 20 3 AAA56677  
 50.9 20 4 AAF83344  
 50.9 20 4 AAF62056  
 50.9 20 5 ABR82070  
 50.9 20 6 ABK13149  
 50.9 20 6 ABK13359  
 50.9 20 6 ABK22867  
 50.9 20 6 ABQ74717  
 50.9 20 7 ABQ83431  
 50.9 20 7 ABX95291  
 50.9 20 7 ACC45450  
 50.9 20 7 ACF57067  
 50.9 20 8 ACD05104  
 50.9 20 9 ADB98148  
 50.9 20 9 ADC35609  
 50.9 20 9 ADD42146  
 50.9 20 9 ADD42148

## ALIGNMENTS

standard; DNA; 22 BP.

2 (first entry)

PCR primer SEQ ID NO:6.

; carcinoembryonic antigen; adenocarcinoma; oesophagus;  
 ; PCR primer; ss.

ns.

1-A1.

2.

2; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 the stomach comprising conducting a PCR amplification on a DNA sample in  
 a mixture.

Page 33; 141pp; English.

It invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 mixture in first and second amplification stages, each with one  
 or more cycles comprising denaturing, annealing and elongating steps  
 and an elongating step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is condu  
 CC different reaction conditions from that of the first amplificat  
 CC to modulate the relative rate of production of the first amplif  
 CC first primer set and a second amplicon by a second primer set d  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of metas  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio  
 CC decreases the time it takes to carry out a PCR reaction. The p  
 CC sequence represents a PCR primer for human CEA (carcinoembryoni  
 CC antigen), which is used in an example from the present inventio  
 XX  
 SQ Sequence 22 BP; 7 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0;  
 Matches 22; Conservative 0; Mismatches 0;

OY 1 AGACAATCACAGTCTCTCGGA 22  
 |||||  
 Db 1 AGACAATCACAGTCTCTCGGA 22

## RESULT 2

AAT36494/c

ID AAT36494 standard; DNA; 46 BP.

XX AAT36494;

XX 13-NOV-1996 (first entry)

XX Carcinoembryonic antigen gene 3' PCR primer.

XX Carcinoembryonic antigen; immunogen; breast cancer; lung cancer;  
 KW colon cancer; therapy; immunotherapy; vaccine; baculovirus; ve  
 KW Autographa californica nuclear-polyhedrosis virus; Spodoptera f  
 KW insect; pA9080 AcNPV-CEA; primer; PCR; polymerase chain reacti  
 XX Synthetic.

XX WO9532286-A2.

XX 30-NOV-1995.

XX 19-MAY-1995; 95WO-US006373.

XX 20-MAY-1994; 94US-00246981.

XX (MICR-) MICROGENESYS INC.

XX Smith G, Volvovitz F, Hackett C;

XX WPI; 1996-02C581/02.

XX Immunogenic carcinoembryonic antigen produced using insect cel  
 PT baculovirus expression system - useful in cancer therapy.

XX Disclosure; Page 18; 61pp; English.

XX A 3' PCR primer (AAT36494) contains sequences complementary to  
 CC KpnI and BamHI sites and a stop codon and sequences designed t  
 CC the last 72 bp of the human carcinoembryonic antigen (CEA) gen  
 CC codes for the hydrophobic C-terminal region of CEA that is not  
 CC mature CEA expressed in tumour cells. It was used with a 5' pr  
 CC (AAT36493) designed to delete the CEA signal sequence for the  
 CC amplification of human colon adenocarcinoma LS174T (ATCC CL 18  
 CC The PCR product was used to construct vector pA9080 AcNPV-CEA  
 CC AAT36495) which allows prodn. of soluble, immunogenic CEA (AAT  
 CC insect cells

XX Sequence 46 BP; 9 A; 9 C; 15 G; 13 T; 0 U; 0 Other;



71.8%; Score 15.8; DB 2; Length 46;  
 ilarity 89.5%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGC 19  
 |||||  
 AGCATCACAGTCTCTGC 26

undard; DNA; 30 BP.

(first entry)

rin cytoplasmic domain PCR primer NH beta-7 3.

in-like beta 7 integrin binding protein; human; inflammation;  
 .leukocyte; polymerase chain reaction; PCR; primer; ss.

L.

97WO-US000100.  
 96US-00583562.  
 ; CORP.

Harris EA;  
 72863/34.

n-like beta 7 integrin binding protein FLP-1 - used to  
 ulators of inflammatory processes involving leukocytes.

age 10; 84pp; English.

beta-7 3 (AAT73719) and NH beta-7 5 (AAT73718) were used in  
 ification of the beta-7 integrin cytoplasmic domain. The PCR  
 utilised in a 'bait' plasmid in a two-hybrid screening for  
 pressed in a human B cell library which interacted with the C-  
 oplasmic domain of the beta-7 integrin. A claimed coding  
 e AAT73717) for human filamin-like beta-7 integrin binding  
 -1 (AAT19327) was deduced from isolated clones

BP; 4 A; 9 C; 10 G; 7 T; 0 U; 0 Other;  
 70.9%; Score 15.6; DB 2; Length 30;  
 larity 81.8%; Pred. No. 4.7e+02;  
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGCGGA 22  
 |||||  
 ACAGTCCCACTCTCTGAGGA 5

undard; DNA; 30 BP.

(first entry)

a:7 (3') for PCR of beta-7 integrin cytoplasmic domain.

KW inflammatory bowel disease; IBD; mucosal tissue; leukocyte; int  
 KW filamin; lymphocyte; inflammation; PCR; primer; cytoplasmic dom  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX US5948891-A.  
 XX PD 07-SEP-1999.  
 XX  
 XX 06-JAN-1997; 97US-00779113.  
 XX  
 XX 05-JAN-1996; 96US-00583562.  
 XX  
 XX (ICOS-) ICOS CORP.  
 XX Salot Harris EA, Staunton DB;  
 XX WPI; 1999-517974/43.  
 XX  
 XX Cytoplasmic modulators of integrin binding are able to modulate  
 XX inflammatory response.  
 XX  
 XX Example 1; Col 6; 51pp; English.

This is the 3' primer for the PCR of the beta 7 integrin cytopl  
 domain. The 5' primer is sequence AAZ06505. The product from th  
 used in the identification of genes in a B cell library which c  
 beta 7 interacting proteins. This invention relates to a novel  
 like beta 7 integrin binding protein designated FLP-1. Two beta  
 associated integrins have been identified (alpha-4,beta-7 and a  
 e,beta-7). Both are expressed on a sub population of peripheral  
 lymphocytes and their expression is inducible. Both are express  
 macrophages but not monocytes and both appear to function in ho  
 localisation of lymphocytes to mucosal tissue (Jutilla, J. J. Leu  
 Biol. 55:133-140 (1994)). Due to the nature of the binding of o  
 beta 7 integrins to their respective counter-receptor, they may  
 contribute to mucosal immune response as well as inflammatory  
 inflammatory bowel disease, IBD) and autoimmune responses at th  
 Filamin is thought to be important in cell locomotion, cells th  
 low levels of this protein do not form the lamella structures r  
 for locomotion. FLP-1 is structurally similar to filamin, and t  
 observation that integrins cluster in point contacts, gives ris  
 possibility that the beta 7 interaction with FLP-1 and/or filam  
 a crucial step in cell locomotion. Disrupting this interaction  
 useful in preventing the homing of beta 7 positive cells, which  
 certain inflammatory responses such as IBD

XX Sequence 30 BP; 4 A; 9 C; 10 G; 7 T; 0 U; 0 Other;  
 SQ

Query Match 70.9%; Score 15.6; DB 2; Length 30;  
 Best Local Similarity 81.8%; Pred. No. 4.7e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0;  
 QY 1 AGACAATCACAGTCTCTGCGGA 22  
 |||||  
 Db 26 AGACAGTCCCACTCTCTGAGGA 5

RESULT 5  
 AAF61364  
 ID AAF61364 standard; DNA; 31 BP.  
 XX  
 AC AAF61364;  
 XX  
 DT 25-MAY-2001 (first entry)  
 XX  
 DE Thrombomodulin antisense PCR primer.  
 XX  
 KW PCR primer; expression plasmid; leptin; thrombomodulin; NO synt  
 KW prostacyclin synthase; vasotropic; gene therapy; neovascularizat  
 KW restenosis; peripheral arterial occlusive disease; VEGF;  
 KW vascular endothelial growth factor; ss.

d.

A1.

; 99DE-01040012.

; 99DE-01040012.

RBER K.

SEN P.

HOEPE D.

Roesen P, Tschoepe D;

45983/26.

expression plasmid useful for treating peripheral arterial disease, comprises two expression cassettes, one containing the man vascular endothelial growth factor VEGF165.

Page 10; 16pp; German.

ion describes a novel eukaryotic expression plasmid, in presson cassettes, a coding sequence for human VEGF 165 in with at least one human coding sequence selected from leptin, lin, prostacyclin synthase and/or constitutive NO synthase. s of the invention have vasotropic activity and can be used erapy. The plasmid is useful for inducing neovascularization ing restenosis in the treatment of peripheral arterial disease, e.g. in diabetics

BP; 3 A; 11 C; 10 G; 7 T; 0 U; 0 Other;

69.1%; Score 15.2; DB 4; Length 31;

ilarity 85.0%; Pred. No. 7.5e+02;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CAATCAGTCTCTGCGG 21

|||||

CGATCAGTCTCTGCGG 28

andard; DNA; 20 BP.

; (first entry)

gene polymorphism detecting PCR primer, LRGEN17R.

; strength and mineralisation regulatory protein; BSMR; jth; mineralisation; ophthalmological; antidiabetic; y regulating transmembrane receptor; prosthetic device; nplant; diabetic retinopathy; hypertensive retinopathy; steoporosis; prematurity; ocular vessel; eye disorder; ; PCR; primer; ss.

ns.

3-A2.

2.

1; 2001WO-US041788.

0; 2000US-0226119P.

0; 2000US-0234337P.

1; 2001US-0304851P.

XX

(AVET ) AVENTIS PHARMA SA.

PA (HARD ) HARVARD COLLEGE.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX

PI Warman ML, Gong Y, Olsen BR, Rawadi G, Roman-Roman S;

XX

WPI; 2002-329694/36.

DR

Polynucleotide encoding bone strength and mineralization regula

protein useful for diagnosis or therapy of osteoporosis.

PT

Disclosure; Fig 5; 124pp; English.

XX

The invention relates to bone strength and mineralisation regul protein (BSMR) and its corresponding nucleic acid sequence. BSM useful for the diagnosis or therapy of osteoporosis and for reg (increasing) bone strength and mineralisation in a human subjec activating a bone density regulating transmembrane receptor (BS protein). An expression vector comprising a promoter that is of linked to BSMR DNA is useful for modulating bone density and fo enhancing bone strength and mineralisation in a mammal cell. CC comprising a BSMR effector is useful for treating osteoporosis CC useful particularly as a coating for prosthetic devices and su implants. BSMR is useful for screening lead pharmaceutical agei effectors, which may be used to treat a range of eye disorders CC diabetic retinopathy, hypertensive retinopathy and retinopathy CC prematurity, in which normal vascular growth and integrity of vessels is disrupted. The present sequence is a PCR primer usec CC amplify cDNA and gDNA molecules useful for detecting polymorphi CC genes in human

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match

64.5%; Score 14.2; DB 6; Length 20;

Best Local Similarity 84.2%; Pred. No. 2.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 3 ACAATCAGTCTCTGCGG 21

|||||

Db 20 AAAATCAGTCTCTGCGG 2

RESULT 7

ABN43232/c

ID ABN43232 standard; DNA; 60 BP.

XX

AC ABN43232;

XX

DT 15-JUL-2002 (first entry)

XX

Human spliced transcript detection oligonucleotide SEQ ID NO:11

XX

Human; mouse; rat; splice transcript; detection; RNA transcript

splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Homo sapiens.

XX

WO200210449-A2.

PN

07-FEB-2002.

PD

20-JUL-2001; 2001WO-IB001903.

XX

28-JUL-2000; 2000US-0221607P.

PR

02-MAY-2001; 2001US-0287724P.

XX

(COMP-) COMPUGEN INC.

XX

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

WPI; 2002-257383/30.

XX

09:38:24 2004

us-10-090-326-6.max.rng

leotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a full for detecting tissue-, pathology-, and developmental-nes.

SEQ ID NO 15980; 47pp; English.

invention describes oligonucleotide libraries for detecting NAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple on units that populate a genome. The library comprises several tides, each capable of hybridising selectively to a set of NAs transcribed from a given transcription unit of the genome, es one or more messenger RNA splice variants. The tide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or ely characterising the corresponding transcriptome, and in NA transcripts and splice variants of human or animal mes. The libraries may also be used as specialised mini o detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in sue under a specific pathological condition; to detect al specific genes; and to detect RNA transcripts and splice a transcriptome of a patient suffering from a particular .BN27253 to ABN59589 represent oligonucleotide sequences from s and mice, which are used in the exemplification of the ention. N.B. The sequence data for this patent did not form : printed specification, but was obtained in electronic format om WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

BP; 16 A; 13 C; 20 G; 11 T; 0 U; 0 Other;

64.5%; Score 14.2; DB 6; Length 60;

ilarity 84.2%; Pred. No. 2.7e+03; Indels 0; Gaps 0;

Conservative 0; Mismatches 3;

ACAACTACAGTCTCTGC 19

|||||

ACAACTACAGTCTGCAGC 42

andard; DNA; 25 BP.

(first entry)

scanning oligonucleotide SEQ ID 1603.

immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1; 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.

15.

12.

3.

2; 2002EP-00016874.

1; 2001US-00922181.

OMICA INC.

Gu Y, Nguyen C;

423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful i  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity c  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1603; 103pp; English.

XX The present invention relates to novel human zinc finger-conta  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. N  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p2  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at c  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful i  
CC or in manufacturing a medicament for treating or preventing a c  
CC associated with decreased or increased expression or activity c  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. T  
CC acids and proteins are also useful for diagnosing or monitoring  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The  
CC acids can also be used as probes to detect and characterize gro  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The p  
CC useful in constructing microarrays for measuring gene expressio  
CC proteins are useful as therapeutic agents for gene therapy or a  
CC vaccines. The present sequence was used to illustrate the inver

XX Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 7; Length 25;

Best Local Similarity 77.3%; Pred. No. 2.9e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCAGG 22

DB 4 AGTCATTCTCAGTCTCTCGGA 25

RESULT 9

ADB00619

ID ADB00619 standard; DNA; 25 BP.

XX ADB00619;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 1605.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1  
KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1605; 103pp; English.

XX The present invention relates to novel human zinc finger-conta



09:38:24 2004

us-10-090-326-6.max.rng

63.6%; Score 14; DB 7; Length 25;  
larity 77.3%; Pred. No. 2.9e+03;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
CAATCAGTCTCTCGGGA 22  
|||||  
CATTCAGTCTCTCGGGA 24

ndard; DNA; 25 BP.

(first entry)

rway DNA oligonucleotide SEQ ID NO 53982.

be; expressed sequence tag; microarray; gene expression;  
action; biallelic marker; polymorphism; human;  
s comparison.

-Al.

2002US-00098263.

2001US-0276759P.

METRIX INC.

7953/53.

nucleic acid probes, useful for in situ hybridization, in  
thern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

ID NO 53982; 9pp; English.

n discloses a microarray comprising a plurality of nucleic  
including one of 2,018,500 fully defined sequences, or its  
h, perfect mismatch, antisense match or antisense mismatch.  
ed is a method of gene expression analysis. The array is used  
g gene expression levels by hybridisation to a DNA library,  
of genetic variation or in hybridisation of tag-labelled  
he nucleic acid probes are specifically designed for analysis  
one target sequence. The method of analysis comprises  
at least one or more nucleic acids to at least two or more  
probes and detecting the hybridisation. The nucleic acid  
attached to a solid support. The analysis comprises monitoring  
ion levels, identifying biallelic markers or polymorphisms,  
mers of a gene and a cross-species comparison. Each of the  
is further comprises a tag sequence. The array of nucleic acid  
reful in in situ hybridisation, in Southern, Northern or dot-  
sation to identify or detect the sequence or specific  
any gene, in mapping the 5' termini of mRNA molecules by  
usions or in screening cDNA or genomic libraries or subclones  
hal subclones containing segments of DNA that have been  
l previously sequenced. The sequence presented is one of the  
l probes incorporated in the microarray. Note: The sequence  
s patent can also be obtained in electronic format directly  
it seqdata.uspto.gov/sequence.html

BP; 11 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

62.7%; Score 13.8; DB 8; Length 25;

Best Local Similarity 88.2%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACAATCACAGTCTCT 17  
|||||  
Db 6 ATACAATCACAGTCTCT 22

RESULT 13

ABQ77936/c

ID ABQ77936 standard; DNA; 41 BP.

XX

AC ABQ77936;

XX

DT 30-JAN-2003 (first entry)

XX

DE Human macroprotein 21.01 probe, SEQ ID NO:8.

XX

KW Human; macroprotein 21.01; recombinant production; gene therapy;

XX dementia; facial paralysis; probe; ss.

OS Homo sapiens.

XX

PN CN1351053-A.

XX

PD 29-MAY-2002.

XX

PF 26-OCT-2000; 2000CN-00125816.

XX

PR 26-OCT-2000; 2000CN-00125816.

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-708115/77.

XX

PT Human macroprotein 21.01.

XX

PS Example 6; Page 21 (Disclosure); 34pp; Chinese.

XX

CC The invention relates to human macroprotein 21.01 (ABB99891) and  
acids encoding it (ABQ77931). The protein has a molecular weight  
KD. The invention also relates to a method for the recombinant  
of the protein, an antagonist of the protein, and the use of the  
gene and antagonist in therapeutic applications. Macroprotein 21  
be used in the treatment of a variety of diseases such as demen  
facial paralysis. Sequences ABQ77936-ABQ77937 represent human  
macroprotein 21.01 probes used in an exemplification of the inv

XX SQ Sequence 41 BP; 12 A; 8 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 62.7%; Score 13.8; DB 6; Length 41;

Best Local Similarity 88.2%; Pred. No. 4e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 6 ATCAGAGTCTCTGTGGA 22

|||||

Db 26 ATCAGAGTCTCTGTGGA 10

RESULT 14

AAQ27842

ID AAQ27842 standard; DNA; 24 BP.

XX

AC AAQ27842;

XX

DT 25-MAR-2003 (revised)

DT 10-FEB-1993 (first entry)

XX

DE Short tandem repeat sequence primer.

XX

KW STR; polymorphism detection; DNA profiling; typing; identification

09:38:24 2004

us-10-090-326-6.max.rng

forensic; medical; ss.

L.

92WO-US000736.

91US-00647655.

OR COLLEGE MEDICINE.

Edwards AO;

00053/36.

g assay - by detecting polymorphisms in a short tandem repeat and characterising DNA.

ye 49; 75pp; English.

is that of a primer used in a DNA profiling assay for polymorphisms in a short tandem repeat (STR). The assay is internal or external standards, provides higher sensitivity, shorter analysis time, lowers expense, and enables precise identification of alleles. The STRs are amplified with great fidelity and patterns are easily interpreted. The method can be used for STR sequences which show polymorphisms in the number of repeats action or identification of medical and forensic samples, sample origin and tissue origin. See also AAQ27841-Q27864. 25-MAR-2003 to correct PN field.)

BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 2; Length 24;

ilarity 80.0%; Pred.No. 4.6e+03;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TAATCAGTCTCTCGG 21

||||| ||||| |||||

TAATCGTCTCTCGAG 23

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 61700.

be; expressed sequence tag; microarray; gene expression; lation; biallelic marker; polymorphism; human; as comparison.

s.

0-A1.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization; Southern, Northern or dot-blot hybridization to identify or detect sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 61700; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA array. In analysis of genetic variation or in hybridisation of tag-labeled compounds. The nucleic acid probes are specifically designed for at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms or family members of a gene and a cross-species comparison. Each nucleic acid further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules, primer extensions or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is on a nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 8; Length 25;

Best Local Similarity 80.0%; Pred. No. 4.6e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTCGG 21

||||| ||||| |||||

Db 4 GACAACCTCAGTCTCTCGG 23

RESULT 16

ACK26100/c

ID ACK26100 standard; DNA; 25 BP.

XX ACK26100;

XX AC

XX DT

XX DE

XX KW

XX KW

XX KW

XX OS

XX OS

XX PN

XX PD

XX PF

XX PR

XX PR

XX PA

XX PI

XX DR

XX

14-OCT-2003 (first entry)  
Human microarray DNA oligonucleotide SEQ ID NO 126081.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Mittmann MP;

WPI; 2003-567953/53.

XX

09:38:24 2004

us-10-090-326-6.max.rng

nucleic acid probes, useful for in situ hybridization, in  
thern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

ID NO 126081; 9pp; English.

n discloses a microarray comprising a plurality of nucleic  
including one of 2,018,500 fully defined sequences, or its  
h, perfect mismatch, antisense match or antisense mismatch.  
ed is a method of gene expression analysis. The array is used  
g gene expression levels by hybridisation to a DNA library,  
of genetic variation or in hybridisation of tag-labelled  
he nucleic acid probes are specifically designed for analysis  
one target sequence. The method of analysis comprises  
at least one or more nucleic acids to at least two or more  
probes and detecting the hybridisation. The nucleic acid  
traced to a solid support. The analysis comprises monitoring  
ion levels, identifying biallelic markers or polymorphisms,  
mbers of a gene and a cross-species comparison. Each of the  
s further comprises a tag sequence. The array of nucleic acid  
ful in in situ hybridisation, in Southern, Northern or dot-  
sation to identify or detect the sequence or specific  
any gene, in mapping the 5' termini of mRNA molecules by  
sions or in screening cDNA or genomic libraries or subclones  
al subclones containing segments of DNA that have been  
l previously sequenced. The sequence presented is one of the  
l probes incorporated in the microarray. Note: The sequence  
s patent can also be obtained in electronic format directly  
it seqdata.uspto.gov/sequence.html

BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 8; Length 25;

larity 80.0%; Pred. No. 4.6e+03;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAAATCACAGTCTCTGCG 20

|||||

ACATCACAGTTTCGACG 1

undard; DNA; 25 BP.

(first entry)

sequence #2524 useful in array for genetic analyses.

sion analysis; array; hybridisation; genetic variation;  
i compound; gene family; in situ hybridisation;  
sening; Southern hybridisation; northern hybridisation;  
bridisation; gene sequence; mutation detection;  
ance; probe; PCR; primer; ss.

1.

6-A1.

; 2002US-00215112.

; 2001US-0311040P.

TWANN M.

76608/54.

PT New probe array useful e.g. for monitoring gene expression level  
PT analyzing genetic variations, or for hybridizing tag-labeled com  
XX comprises multiple nucleic acid probes.

PS Claim 1; SEQ ID NO 2524; 9pp; English.

XX The present invention relates to nucleic acid sequences that are  
CC complementary to particular genes, and can be used as probes for  
CC variety of analyses such as gene expression analysis. Each probe  
CC comprises 9 or more consecutive nucleotides from at least one of  
CC nucleotide sequences defined in the patent, or their perfect ser  
CC sense mismatch, antisense match or antisense mismatch oligonucle  
CC The probes may be used in an array comprising at least 10 distir  
CC nucleic acid probes. The array is useful in monitoring gene exp  
CC levels by hybridisation to a DNA library, in analysing genetic  
CC variations, and in hybridising tag-labelled compounds. The probe  
CC useful for identifying family members of a gene. The probes are  
CC useful in in situ hybridisations, in screening cDNA or genomic l  
CC (or derived subclones) for additional clones containing segments  
CC that have been previously isolated and sequenced, in Southern, i  
CC or dot-blot hybridisation of genomic DNA to identify or detect  
CC mapping the 5' termini of mRNA molecules by primer extensions. i  
CC nucleic acid sequences of the invention are also useful as PCR i  
CC The invention provides a large collection of nucleic acid sequel  
CC complementary to particular genes with a wide range of analyti  
CC ACH50865-ACH65260 represent the target sequences of the inventi  
CC The sequence data for this patent was obtained in electronic fo  
CC directly from the USPTO web site at seqdata.uspto.gov/psipSDIDEI

XX Sequence 25 BP; 5 A; 4 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 8; Length 25;

Best Local Similarity 80.0%; Pred. No. 4.6e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACATCACAGTCTCTGCGGA 22

|||||

Db 23 ACATCACAGTCTCACCGGA 4

RESULT 18

ACH53387/c

ID ACH53387 standard; DNA; 25 BP.

XX ACH53387;

DT 16-OCT-2003 (first entry)

XX DNA target sequence #2523 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variati  
KW tag-labelled compound; gene family; in situ hybridisation;  
KW library screening; Southern hybridisation; northern hybridisati  
KW dot-blot hybridisation; gene sequence; mutation detection;  
KW target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Mittmann M;

XX WPI; 2003-576608/54.

XX

tide-human transcription arrestin CCCTC-conjugated factor and polynucleotide for encoding such polypeptide.

The present invention describes drug compositions which contain an active component a peptide which has specific affinity to particular phospholipids (such as phosphatidyl ethanolamine or phosphatidyl choline) especially to phospholipids which constitute a lipid bilayer of cortex and of which the concentration in the bilayer increases which are abnormal (e.g. through injury, denaturation or activation). In particular, the peptide contains a sequence having phospholipid and a structure of formula (I): (A1)a-(A2)b-(A3)c, where (A1) is a two specific sequences (see AAWG69516 and AAWG69519), (A2) and (A3) are two specific sequences (see AAWG69516 and AAWG69517) or MEVLGQTYRILRPHQSVWVHGIALR, LRYLRHIFPHQSVWVHGIALR (see AAW69517) or (see AAW69518): a = 0-5; b = 1-5, and c = 0-5. Preferred are the A1-A2-A3; A2-A3; A2-A2-A3; A2-A2-A2 or A2-A2 (especially A2-A2-A2).



A2-A2). The sequence is linked to a peptide such as a blood cially thrombo-modulin, urina-statin or membrane cofactor drugs are used for the treatment and prevention of diseases ood coagulation, inflammatory and immunological disorders. sequence represents a PCR primer used in an example from the ntion

BP; 6 A; 12 C; 10 G; 9 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 2; Length 37;

larity 80.0%; Pred. No. 4.9e+03; Conservativeness 0; Mismatches 4; Indels 0; Gaps 0;

AATCACAGTCTCTGCGG 21

|||||

CCTCAGAGTCTCTGCGG 28

ndard; DNA; 48 BP.

(revised)  
(revised)  
(first entry)

s gingivalis protein PCR primer #21.

s gingivalis; PG; periodontal disease; gingivitis; vaccine;  
CR primer; ss.

s gingivalis.

98WC-AU001023.

97AU-00000839.

97AU-00001182.

98AU-00001546.

98AU-00002264.

98AU-00002911.

98AU-00003128.

98AU-00003338.

98AU-00003654.

98AU-00004917.

98AU-00004963.

98AU-00005028.

LTD.

rr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;  
Webb EA;

5613/32.

orphorymonas gingivalis peptides for preventing gingivitis.

Page 48; 588pp; English.

AA91801 encode two hundred and sixty six antigenic s gingivalis (PG) polypeptide sequences given in AA934318 to X91802 to AA931989 represent PCR primers used in the the PG polypeptides. The PG polypeptides have antibacterial h a vaccine mechanism of action. The PG polypeptides can be ines especially against Porphyromonas gingivalis. Probes can etect Porphyromonas gingivalis in standard hybridisation horymonas gingivalis is involved in periodontal disease

CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR file  
CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 48 BP; 16 A; 12 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 2; Length 48;

Best Local Similarity 80.0%; Pred. No. 5.2e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21

|||||

Db 28 GACAATCACATCATGCGG 47

RESULT 22

ABX15582

ID ABX15582 standard; DNA; 50 BP.

XX

AC ABX15582;

XX

DT 27-MAR-2003 (first entry)

XX

DE MHV expression plasmid junction region #1.

XX

KW MHV; ds; virucide; antibacterial; antiparasitic; VLP;  
KW virus-like particle; coronavirus; attenuated virus; structural f  
KW nucleocapsid protein; membrane protein; envelope protein; spike  
KW immunogen; vaccine; FIPV.

XX

OS Mouse hepatitis virus strain A59.

XX

PN WO200292827-A2.

XX

PD 21-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-NL000318.

XX

PR 17-MAY-2001; 2001EP-00201861.

XX

PA (UYUT-) RIJKSUNIV UTRECHT.

PA (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX

PI Rottier PJM, De Haan CAM, Haijema BJ, Bosch BJ;

XX

WPI; 2003-120691/11.

XX

Novel isolated or recombinant virus-like particle derived from coronavirus for therapeutic and diagnostic purposes, and as immu vaccine, has functionally deleted fragments and is capable of replication.

XX

PS Disclosure; Fig 1A; 138pp; English.

XX

CC The invention relates to isolated or recombinant virus-like part (VLP) capable of replication, derived from coronavirus (e.g. mou hepatitis virus, MHV), having functionally deleted genomes. The functional fragment from nucleic acid encoding viral gene produc than polymerase or structural protein (SP) like nucleocapsid (N) membrane (M), envelope (E) or spike (S) protein, is deleted, or SP do not occur in the order 5'-S-E-M-N-3'. Also included are a composition comprising the VLP, and a carrier for therapeutic an diagnostic use, as an immunogen or vaccine and inhibiting or blo infection with a coronavirus or corona-VLP, by treating an organ a heptad repeat peptide or its functional fragment. The VLP comp is useful for therapeutic and diagnostic purposes, and as an imm vaccine. The VLP is also useful as gene delivery vehicle, and fo eliciting immune response against proteins e.g. viral, bacterial parasitic, and cellular origins. Attenuated MHV VLPs were constr with the ectodomain of the S protein replaced by the correspondi sequence from FIPV (feline infectious peritonitis virus) allowin replication in feline cells. The present sequence is a plasmid j region for the construct

XX

09:38:24 2004

us-10-090-326-6.max.rng

BP; 21 A; 11 C; 10 G; 8 T; 0 U; 0 Other;  
61.8%; Score 13.6; DB 7; Length 50;  
ilarity 80.0%; Pred. NO. 5.2e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CAATCAGCTCTCTGGG 21  
| | | | | | | | | |  
CTATCAGCCCTGCGAG 27  
andard; DNA; 53 BP.  
(first entry)  
ion plasmid junction region #4.  
rucide; antibacterial; antiparasitic; VLP;  
particle; coronavirus; attenuated virus; structural protein;  
d protein; membrane protein; envelope protein; spike protein;  
vaccine.  
itis virus strain A59.  
-A2.  
.;  
.; 2002WO-NL000319.  
.; 2001EP-00201861.  
JKSUNIV UTRECHT.  
CHING TECH WETENSCHAPPEN.  
4, De Haan CAM, Haijema BJ, Bosch BJ;  
L20691/11.  
ated or recombinant virus-like particle derived from  
s for therapeutic and diagnostic purposes, and as immunogen or  
s as functionally deleted fragments and is capable of  
1.  
; Fig 21; 138pp; English.  
ion relates to isolated or recombinant virus-like particle  
ble of replication, derived from coronavirus (e.g. mouse  
virus, MHV), having functionally deleted genomes. The  
fragment from nucleic acid encoding viral gene product other  
erase or structural protein (SP) like nucleocapsid (N),  
M), envelope (E) or spike (S) protein, is deleted, or genes for  
occur in the order 5'-S-E-M-N-3'. Also included are a  
n comprising the VLP, and a carrier for therapeutic and  
use, as an immunogen or vaccine and inhibiting or blocking an  
with a coronavirus or corona-VLP, by treating an organism with  
repeat peptide or its functional fragment. The VLP composition  
for therapeutic and diagnostic purposes, and as an immunogen or  
the VLP is also useful as gene delivery vehicle, and for  
immune response against proteins e.g. viral, bacterial,  
and cellular origins. Attenuated MHV VLPs were constructed  
arranged order of proteins. The present sequence is a plasmid  
region for the S protein region  
13 BP; 22 A; 11 C; 10 G; 10 T; 0 U; 0 Other;  
61.8%; Score 13.6; DB 7; Length 53;  
ilarity 80.0%; Pred. NO. 5.3e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GACAATCAGTCTCTGGG 21  
| | | | | | | | | |  
Db 8 GACTATCAGCCCTGCGAG 27  
RESULT 24  
ABN33343/c  
ID ABN33343 standard; DNA; 60 BP.  
XX AC ABN33343;  
XX DT 15-JUL-2002 (first entry)  
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:60  
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript  
XX KW splice variant; transcriptome; oligonucleotide library; ss.  
XX OS Homo sapiens.  
XX PN WO200210449-A2.  
XX PD 07-FEB-2002.  
XX PF 20-JUL-2001; 2001WO-IB001903.  
XX PR 28-JUL-2000; 2000US-0221607P.  
XX PR 02-MAY-2001; 2001US-0287724P.  
XX PA (COMP-) COMPUGEN INC.  
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
XX WI WIPI; 2002-257383/30.  
XX New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcriptome  
genome, useful for detecting tissue-, pathology-, and developm  
specific genes.  
Example 1; SEQ ID NO 6091; 47pp; English.  
The present invention describes oligonucleotide libraries for  
messenger RNAs that populate a (sub-)transcriptome, where the  
(sub-)transcriptome comprises messenger RNAs transcribed from multi  
transcription units that populate a genome. The library compri  
oligonucleotides, each capable of hybridising selectively to a  
messenger RNAs transcribed from a given transcription unit of  
which encodes one or more messenger RNA splice variants. The  
oligonucleotide libraries are useful for detecting mRNAs from  
biological sample, in expression profiling studies, in qualita  
quantitatively characterising the corresponding transcriptome,  
detecting RNA transcripts and splice variants of human or anim  
transcriptomes. The libraries may also be used as specialised  
libraries to detect transcripts of a sub-transcriptome under a  
biological or pathological state, and so allowing the detectio  
- and pathology-specific genes such as those genes only expres  
specific tissue under a specific pathological condition; to de  
developmental specific genes; and to detect RNA transcripts an  
variants of a transcriptome of a patient suffering from a part  
disorder. ABN27253 to ABN59589 represent oligonucleotide sequ  
rats, humans and mice, which are used in the exemplification o  
present invention. N.B. The sequence data for this patent did  
part of the printed specification, but was obtained in electric  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 60 BP; 14 A; 10 C; 20 G; 16 T; 0 U; 0 Other;  
Query Match 61.8%; Score 13.6; DB 6; Length 60;  
Best Local Similarity 80.0%; Pred. NO. 5.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

AAATCAGAGTCTCTCGGA 22  
|||||  
AAATCAGAGTCTCTCGGA 7

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:10366.

e; rat; splice transcript; detection; RNA transcript;  
ant; transcriptome; oligonucleotide library; ss.

S.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which  
hybridize to mRNAs transcribed from a transcription unit of a  
ful for detecting tissue-, pathology-, and developmental-  
nes.

SEQ ID NO 10366; 47pp; English.

invention describes oligonucleotide libraries for detecting  
NAs that populate a (sub-)transcriptome, where the (sub-  
ome comprises messenger RNAs transcribed from multiple  
on units that populate a genome. The library comprises several  
tides, each capable of hybridizing selectively to a set of  
NAs transcribed from a given transcription unit of the genome,  
as one or more messenger RNA splice variants. The  
tide libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
sily characterizing the corresponding transcriptome, and in  
NA transcripts and splice variants of human or animal  
nes. The libraries may also be used as specialised mini-  
o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
logy-specific genes such as those genes only expressed in  
ssue under a specific pathological condition; to detect  
al specific genes; and to detect RNA transcripts and splice  
a transcriptome of a patient suffering from a particular  
3N27253 to ABN59589 represent oligonucleotide sequen-  
s and mice, which are used in the exemplification of the  
ntion. N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
m WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 20 A; 11 C; 17 G; 12 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 6; Length 60;  
ilarity 80.0%; Pred. No. 5.4e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AAATCAGAGTCTCTCGG 21

Db 56 GACAATCAGTCTCTATACAG 37  
|||||

RESULT 26

ABN41535/c

ID ABN41535 standard; DNA; 60 BP.

XX AC ABN41535;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:14

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcription  
genome, useful for detecting tissue-, pathology-, and developme  
specific genes.

XX PS Example 1; SEQ ID NO 14283; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for d  
messenger RNAs that populate a (sub-)transcriptome, where the (s  
)transcriptome comprises messenger RNAs transcribed from multip  
transcription units that populate a genome. The library compris  
oligonucleotides, each capable of hybridizing selectively to a  
messenger RNAs transcribed from a given transcription unit of t  
which encodes one or more messenger RNA splice variants. The  
oligonucleotide libraries are useful for detecting mRNAs from a  
biological sample, in expression profiling studies, in qualit  
detecting RNA transcripts and splice variants of human or anima  
transcriptomes. The libraries may also be used as specialised m  
libraries to detect transcripts of a sub-transcriptome under a  
biological or pathological state, and so allowing the detection  
- and pathology-specific genes such as those genes only express  
specific tissue under a specific pathological condition; to det  
developmental specific genes; and to detect RNA transcripts and  
variants of a transcriptome of a patient suffering from a parti  
disorder. ABN27253 to ABN59589 represent oligonucleotide sequen  
rats, humans and mice, which are used in the exemplification of  
present invention. N.B. The sequence data for this patent did n  
part of the printed specification, but was obtained in electron  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 60 BP; 15 A; 14 C; 12 G; 19 T; 0 U; 0 Other;

Query Match 61.8%;

Best Local Similarity 80.0%; Score 13.6; DB 6; Length 60;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCAGAGTCTCTCGGA 22  
|||||

1 09:38:24 2004

us-10-090-326-6.max.rng

CAATGACAGTCTCTGGCGA 41

tandard; DNA; 36 BP.

4 (first entry)

in Fv polypeptide associated VH PCR primer #22.

in Fv polypeptide; human albumin; immune diagnostic agent; VH;  
r; ss.

ed.

78-A.

2.

1; 2001JP-00260411.

0; 2000JP-00259436.

FO LTD.

124058/40.

ain Fv polypeptide having human albumin combining activity.

Fig 2; 1lpp; Japanese.

: invention relates to a single chain Fv polypeptide having  
activity specific to human albumin. Also disclosed is the  
:ide sequence encoding the single chain Fv polypeptide, an  
vector containing the polynucleotide, a host cell transformed  
re expression vector, and preparation of a single chain Fv  
; in which the above host cell is cultured and the above single  
lypeptide is separated from the culture. The polypeptide can  
: the preparation of immune diagnostic agents. The present  
presents a PCR primer used in the examples of the present

BP; 9 A; 10 C; 13 G; 4 T; 0 U; 0 Other;

ilarity 60.9%; Score 13.4; DB 9; Length 36;

Conservative 93.3%; Pred. No. 6.2e+03;

0; Mismatches 1; Indels 0; Gaps 0;

ACAGTCTCTGCGG 21

ACTGTCCTGCGG 15

andard; DNA; 50 BP.

(first entry)

ligonucleotide #3230.

essive; immunostimulatory; antiinflammatory; cytostatic;  
tive; antimicrobial; gene therapy; vaccine; amylose; cancer;  
tein; angiotensin; apoptosis related protein; cadherin;  
ymerase; oncogene; histone; kinase; colony stimulating factor;  
related protein; cytochrome; kinase; cytokine; interferon;  
; G-protein coupled receptor; thioesterase; inflammation;  
ial disease; autoimmune disease; infection;

nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US035498.

28-DEC-1999; 99US-0173419P.

27-DEC-2000; 2000US-00173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, pol-  
oncogenes and histones, useful for diagnosing and treating, e.  
autoimmune diseases and infections.

Claim 1; Page 2312; 4143pp; English.

The present invention relates to oligonucleotides encoding pol-  
variants of proteins related to amylases, amyloid proteins, an-  
apoptosis related proteins, cadherin, cyclin, polymerase, onco-  
histones, kinases, colony stimulating factors, complement rela-  
proteins, cytochromes, kinesins, cytokines, interferons, inter-  
protein coupled receptors and thioesterases. The present sequ-  
such oligonucleotide. The oligonucleotides and the peptides en-  
them may be used in the prevention, diagnosis and treatment of  
associated with inappropriate expression of the proteins listed  
Disorders that may be prevented, diagnosed and/or treated incl-  
multifactorial diseases with a genetic component, such as auto-  
diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabet-  
systemic lupus erythematosus and Grave's disease), inflammatio-  
(e.g. cancers of the bladder, brain, breast, colon and kidney,  
leukaemia), diseases of the nervous system and an infection of  
organisms

Sequence 50 BP; 7 A; 19 C; 10 G; 14 T; 0 U; 0 Other;

Query Match Similarity 60.9%; Score 13.4; DB 4; Length 50;

Best Local Similarity 93.3%; Pred. No. 6.5e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 4 CAATCAGTCTCTG 18

DB 19 CACTCAGTCTCTG 33

RESULT 29

ABN36160/c

ID ABN36160 standard; DNA; 60 BP.

AC ABN36160;

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:89  
Human; mouse; rat; splice transcript; detection; RNA transcript  
splice variant; transcriprome; oligonucleotide library; ss.

Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

1. 2001NO-00006251.

[illegible]

09:38:24 2004

us-10-090-326-6.max.rng

ndard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 65769.

be; expressed sequence tag; microarray; gene expression; ation; biallelic marker; polymorphism; human; is comparison.

US-10-090-326-6.

2002US-00098263.

2001US-0276759P.

METRIX INC.

7953/53.

nucleic acid probes, useful for in situ hybridization, in orthern or dot-blot hybridization to identify or detect the specific mutations of any gene.

ID NO 65769; 9pp; English.

n discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, each, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is a method of gene expression analysis. The array is used in gene expression levels by hybridisation to a DNA library, of genetic variation or in hybridisation of tag-labelled nucleic acid probes are specifically designed for analysis one target sequence. The method of analysis comprises at least one or more nucleic acids to at least two or more probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises identifying biallelic markers or polymorphisms, attached to a solid support. The analysis comprises monitoring levels, identifying biallelic markers or polymorphisms, members of a gene and a cross-species comparison. Each of the is further comprises a tag sequence. The array of nucleic acid useful in in situ hybridisation, in Southern, Northern or dot-sonation to identify or detect the sequence or specific any gene, in mapping the 5' termini of mRNA molecules by isons or in screening cDNA or genomic libraries or subclones al subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the probes incorporated in the microarray. Note: The sequence is patent can also be obtained in electronic format directly at seqdata.uspto.gov/sequence.html

BP; 9 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

60.0%; Score 13.2; DB 8; Length 25;

ilarity 83.3%; Pred. No. 7.3e+03;

Conservative 0; Mismatches 3; Indels 0;

TCACAGTCTCTCGGA 22

|||||

TAATAGTCTCTCGGA 23

ACK23331/c

ID ACK23331 standard; DNA; 25 BP.

XX ACK23331;

AC ACK23331;

XX 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 123312.

XX EST; ss; probe; expressed sequence tag; microarray; gene expres;

XX genetic variation; biallelic marker; polymorphism; human;

XX cross-species comparison.

XX Homo sapiens.

XX OS

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridizat

XX Southern, Northern or dot-blot hybridization to identify or dete

XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 123312; 9pp; English.

XX The invention discloses a microarray comprising a plurality of

XX acid probes including one of 2,018,500 fully defined sequences,

XX perfect match, perfect mismatch, antisense match or antisense m

XX Also disclosed is a method of gene expression analysis. The arr

XX in monitoring gene expression levels by hybridisation to a DNA

XX in analysis of genetic variation or in hybridisation of tag-lab

XX compounds. The nucleic acid probes are specifically designed fo

XX of at least one target sequence. The method of analysis compris

XX hybridising at least one or more nucleic acids to at least two

XX nucleic acid probes and detecting the hybridisation. The nucle

XX probes are attached to a solid support. The analysis compris

XX gene expression levels, identifying biallelic markers or polym

XX or family members of a gene and a cross-species comparison. Eac

XX nucleic acids further comprises a tag sequence. The array of nu

XX probes is useful in in situ hybridisation, in Southern, Northern

XX blot hybridisation to identify or detect the sequence or specif

XX mutations of any gene, in mapping the 5' termini of mRNA molecu

XX primer extensions or in screening cDNA or genomic libraries or

XX for additional subclones containing segments of DNA that have b

XX isolated and previously sequenced. The sequence presented is on

XX nucleic acid probes incorporated in the microarray. Note: The s

XX data for this patent can also be obtained in electronic format

XX from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 5 A; 4 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 8; Length 25;

Best Local Similarity 83.3%; Pred. No. 7.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 ACNATCACAGTCTCTCGG 20

|||||

Db 18 ACAAACTCACTCTCTCGG 1

RESULT 36

ACK13931/c

ID ACK13931 standard; DNA; 25 BP.

us-10-090-326-6.max.rnq

array DNA oligonucleotide SEQ ID NO 113912.

5

: 2001US-0276759P.

•

of nucleic acid probes, useful for in situ hybridization, in northern or dot-blot hybridization to identify or detect the specific mutations of any gene.

[illegible]

60.0%; Score 13.2; DB 8; Length 25;

CAATCAGTCTCTGCG 20

.....

Standard; DNA; 25 BP.

Query Match 60.0%; Score 13.2; DB 8; Length 25;  
Best Local Similarity 83.3%; Pred. No. 7.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 4 CAATCACAGTCTCTGCGG 21  
|||  
Db 2 CAATCATATTCTCTTCGG 19  
|||

RESULT 38

AAT08014/C

ID AAT08014 standard; DNA; 35 BP.

AC AAT08014;

DT 24~JUL-1996 (first entry)



09:38:24 2004

us-10-090-326-6.max.rng

heavy chain back primer JS160.

chain reaction; PCR; primer; amplify; traa; leader sequence; in; hormone; enzyme; inhibitor; receptor; antigen; antibody; library; specific binding pair; epitope mapping; vaccine; al vaccine; bacterial display; phage display; TA1; SBP; fication; alpha-CKMB; creatine kinase-MB; ss.

95WO-US007541.

94US-00258026.

INT INC.

thode PR, Stinson JR, Wong HC;

9677/05.

target protein on bacterial cell as fusion protein - with it(s) and peptide leader, used e.g. to select members of ding pairs.

age 42; 74pp; English.

AAT08014 represent amplification primers for the heavy chain lonal antibody alpha-CKMB. Alpha-CKMB is directed against ase-MB. The amplified sequence is used as the DNA encoding a in, for insertion into a chimaeric DNA sequence of the he chimaeric sequence contains a target protein coding when the DNA encoding the traa leader sequence (amplified by AAT08007) and the traa gene product coding sequence sing AAT08006 and AAT08008). The target protein is then a bacterial host cell transformed with a vector containing c sequence. The chimaeric sequence is useful for displaying ins such as hormones, enzymes, inhibitors, receptors, antibodies. It is particularly useful for selecting a target protein from a DNA library, especially members of a ding pair (SBP) or compounds that affect SBP interactions. may also be used for epitope mapping or for use in live cines. The method combines the advantages of bacterial and y and makes possible protein purification without the need ng, panning, etc

BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;

60.0%; Score 13.2; DB 2; Length 35;

larity 72.2%; Pred. No. 7.7e+03;

Conservative 3; Mismatches 2; Indels 0; Gaps 0;

TCACACTCTCTGCGG 21

|||||:|||||

TCACGCTCTCYKAG 15

ndard; DNA; 35 BP.

(first entry)

chain back primer JS160.

ntibody; MAb; lipoteichoic acid; gram positive; bacteria; in; phagocytosis; infection; epitope; peptide mimic;

KW

XX

OS

OS

XX

PN

XX

XX

PD

XX

XX

PF

XX

PR

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Mab 96-110; panning; PCR primer; ss.

Synthetic.

Mus sp.

WO9857994-A2.

23-DEC-1998.

16-JUN-1998; 98WO-US012402.

16-JUN-1997; 97US-0049871P.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Fischer GW, Schuman RF, Wong H, Stinson JL;

WPI; 1999-095329/08.

New antibodies to lipoteichoic acid of gram positive bacteria - develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria.

Example 8; Fig 11; 150pp; English.

The invention relates to a monoclonal antibody (Mab) to lipoteic of gram positive bacteria, where the Mab is a chimeric immunogl comprising at least part of a human immunoglobulin constant regi least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and the bacteria and enhance protection from lethal infection. The acid antibody (encoded by a DNA of the variable region of anti-lil or peptides (encoded by a DNA of the variable region of anti-lil more of the complementarity determining regions (CDRs) of the va region of the antibody) can be used for treating or preventing i caused by gram positive bacteria. They can also be used for the of gram positive bacterial infections. Sequences AAX0561-78 rei PCR primers used for cloning the variable region gene fragments Mab 96-100 antibody of the invention

Sequence 35 BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;

Query Match 60.0%; Score 13.2; DB 2; Length 35;

Best Local Similarity 72.2%; Pred. No. 7.7e+03;

Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCAGCTCTCTGCGG 21

|||||:|||||

32 CASTCAGCTCTCYKAG 15

RESULT 40

AAX82036/c

ID AAX82036 standard; DNA; 35 BP.

XX

AC AAX82036;

XX

DT 10-SEP-1999 (first entry)

XX

DE Mouse heavy chain back primer JS160.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

09:38:24 2004

us-10-090-326-6.max.rng

98WO-US027267.  
97US-0068635P.  
98US-00215163.

NSON J L.  
J H.  
LIEN A D.  
MITT C K.  
TON-CELSA A.

Wong H, O'Brien AD, Schmitt CK, Melton-Celsa A;  
18935/35.

monoclonal antibodies against Shiga toxins, useful for  
against enterohemorrhagic Escherichia coli or other Shiga  
toxin-producing bacteria.

J 5A; 75pp; English.

on relates to humanised monoclonal antibodies (MAB) against  
s. The humanised MAB that binds to Shiga toxin comprises a  
variable region, where: (a) the constant region contains  
part of a human immunoglobulin (Ig) constant region; and (b) the  
region contains at least part of a non-human Ig variable region.  
transformed with vectors encoding a humanised MAB against  
type 2 is useful for treating a patient with an infection  
enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin  
producing bacteria. The humanised MAB can also be used to reduce illness  
caused by EHEC or other Shiga toxin-producing bacteria. EHEC are  
associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic  
colitis) and hemolytic uremic syndrome. In particular, the humanised  
rate edema, thrombocytopenia and uremia associated with EHEC-  
sease. Sequences AAX82030-48 represent PCR primers for  
the variable regions of 11E10 antibody

BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;

ilarity 60.0%; Score 13.2; DB 2; Length 35;  
Conservative 72.2%; Pred. No. 7.7e+03;  
3; Mismatches 2; Indels 0; Gaps 0;

ATCAGTCTCTGCGG 21  
||||:||||:|  
STCAGTCTCTGCGG 15

standard; DNA; 47 BP.

(first entry)

related biallelic marker SEQ ID NO:1562.

e; biallelic marker; high density disequilibrium map;  
; haplotype; phenotype; polymorphic base; genotyping;  
; hybridisation; identification; characterisation; diagnosis;  
eotide polymorphism; SNP; ds.

s.

Location/Qualifiers  
replace(24,T)  
/\*tag= a  
/standard\_name= "single nucleotide polymorphism"

2.

XX 21-APR-1999; 99WO-IB000822.  
XX 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX (GENT ) GENSET.  
XX Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
XX Novel biallelic markers used to construct a high density disequilibrium  
map of the human genome.  
XX Claim 1; Page 563; 2745pp; English.  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the  
invention, which contain a polymorphic base at position 24 of the  
nucleotide sequences. AAZ69579 to AAZ77440 represent amplified  
primers for the biallelic markers. The biallelic markers of the  
have a variety of uses: they can be used for high density mapping  
human genome, and in complex association studies and haplotyping  
which are useful in determining the genetic basis for disease  
compositions and methods of the invention can also be useful for  
identification of the targets for the development of pharmaceutical  
agents and diagnostic methods, as well as the characterisation of  
differential efficacious responses to and side effects from  
pharmaceutical agents acting on a disease as well as other treat-  
ments. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3  
3367, are not actually given a sequence in the Sequence Listing  
present invention  
XX Sequence 47 BP; 14 A; 10 C; 17 G; 6 T; 0 U; 0 Other;  
Query Match 60.0%; Score 13.2; DB 3; Length 47;  
Best Local Similarity 83.3%; Pred. No. 8.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 4 CAATCAGTCTCTGCGG 21  
|||:||||:|  
Db 38 CAGTCTCAGTCTCTGCGG 21

RESULT 42  
ABZ00861/c  
ID ABZ00861 standard; DNA; 50 BP.

XX AC ABZ00861;

XX 09-JAN-2003 (first entry)

Human leukocyte gene expression profiling probe SEQ ID NO 852.  
T7; leukocyte; gene expression profiling; allograft rejection;  
atherosclerosis; congestive heart failure; systemic lupus eryth-  
ematoid arthritis; osteoarthritis; cytomegalovirus; infectio-  
ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

PR 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phill

09:38:24 2004

us-10-090-326-6.max.rng

ard R, Quertermous T, Johnson F;

6525/68.

or leukocyte expression profiling, diagnosing a disease, or the rate of progression of a disease, e.g. atherosclerosis, a heart failure, comprises diagnostic oligonucleotides.

e 352; Opp; English.

n relates to a system for detecting gene expression, which e or two isolated DNA molecules that detect expression of a the gene corresponds to any of 8143 oligonucleotides Z08152) each having 50 base pairs (bp). The system is useful e expression profiling. It is particularly useful for a disease, monitoring (rate of) progression of a disease, herapeutic outcome, determining prognosis for a patient, disease complications in an individual or monitoring response in an individual. The diseases include cardiac allograft kidney allograft rejection, liver allograft rejection, sis, congestive heart failure, systemic lupus erythematosus, rthritis, osteoarthritis or cytomegalovirus infection

BP; 12 A; 10 C; 9 G; 19 T; 0 U; 0 Other;

60.0%; Score 13.2; DB 6; Length 50;

arity 83.3%; Pred. No. 8.3e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CACAGTCTCTGCGGA 22

|||||

'CATAGTCTCTGGGTA 4

undard; DNA; 51 BP.

(first entry)

oietin coding sequence polymorphic site SEQ ID NO: 104.

e nucleotide polymorphism; SNP; paternity test;

it; aberrant protein expression; ds.

;

-A2.

2001WO-US000322.

2000US-0174962P.

AGEN CORP.

Leach MD;

51871/48.

30214.

nan polymucleotides containing single nucleotide

ns, useful for the treatment and diagnosis of e.g. cancer,

nd diabetes.

ge 137; 475pp; English.

invention relates to human nucleic acids containing single polymorphisms (SNPs). These can be used in forensic and assts, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, dial  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vascu  
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arth  
CC meningitis, muscular disorders, dementia, neurological diseases,  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disc  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obes  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention

XX

SQ Sequence 51 BP; 13 A; 17 C; 8 G; 13 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.0%; Score 13.2; DB 4; Length 51;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACATCATCAGTCTCTG 18

|||||

Db 27 AGACATCATCAGTCTG 44

RESULT 44

AAH89322

ID AAH89322 standard; DNA; 51 BP.

XX

AC AAH89322;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human angiotensin coding sequence polymorphic site SEQ ID NO: 1

XX

XX Human; single nucleotide polymorphism; SNP; paternity test;

XX forensic test; aberrant protein expression; ds.

XX

OS Homo sapiens.

XX

PN WO200151670-A2.

XX

PD 19-JUL-2001.

XX

XX 05-JAN-2001; 2001WO-US000322.

XX

XX 07-JAN-2000; 2000US-0174962P.

XX

XX (CURA-) CURAGEN CORP.

XX

XX Shimkets RA, Leach MD;

XX

XX WPI; 2001-451871/48.

XX

XX P-PSDB; AAM00213.

XX

Isolated human polymucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. c infection and diabetes.

XX

PS Claim 1; Page 137; 475pp; English.

XX

The present invention relates to human nucleic acids containing nucleotide polymorphisms (SNPs). These can be used in forensic paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, dial Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vascu CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arth CC meningitis, muscular disorders, dementia, neurological diseases, CC sclerosis, male infertility, hypercalcaemia, blood pressure disc CC osteoporosis, pathogenic infections, hypercholesterolaemia, obes CC autoimmunity. The present sequence is a polymorphism-containing CC oligonucleotide fragment of the invention

XX

SQ Sequence 51 BP; 14 A; 16 C; 8 G; 13 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.0%; Score 13.2; DB 4; Length 51;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

09:38:24 2004

us-10-090-326-6.max.rng

ACATCAGTCTCTG 18  
|||||  
ACATCCATTGCTG 44

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:19346.

a; rat; splice transcript; detection; RNA transcript;  
ant; transcriptome; oligonucleotide library; ss.

S.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which  
hybridize to mRNAs transcribed from a transcription unit of a  
ful for detecting tissue-, pathology-, and developmental-  
nes.

SEQ ID NO 19346; 47pp; English.

invention describes oligonucleotide libraries for detecting  
NAs that populate a (sub-)transcriptome, where the (sub-  
me comprises messenger RNAs transcribed from multiple  
on units that populate a genome. The library comprises several  
tides, each capable of hybridising selectively to a set of  
NAs transcribed from a given transcription unit of the genome,  
as one or more messenger RNA splice variants. The  
side libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
aly characterising the corresponding transcriptome, and in  
NA transcripts and splice variants of human or animal  
nes. The libraries may also be used as specialised mini  
o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
logy-specific genes such as those genes only expressed in  
ssue under a specific pathological condition; to detect  
al specific genes; and to detect RNA transcripts and splice  
a transcriptome of a patient suffering from a particular  
3N27253 to ABN59589 represent oligonucleotide sequences from  
s and mice, which are used in the exemplification of the  
ention. N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 17 A; 12 C; 19 G; 12 T; 0 U; 0 Other;

ilarity 60.0%; Score 13.2; DB 6; Length 60;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CAATCAGTCTCTGCGG 21  
Db 41 CTATCATAGTCTCTGCTG 24

Search completed: February 29, 2004, 09:02:36  
Job time : 224.714 secs

09:38:24 2004

us-10-090-326-6.max.rni

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 08:44:24 ; Search time 41.4286 Seconds  
(without alignments)  
294.698 Million cell updates/sec

S-10-090-326-6  
2

agacaatcacagtctctcgga 22

IDENTITY\_NUC

apop 10.0 , Gapext 1.0

82709 seqs, 277475446 residues

its satisfying chosen parameters: 874574

ngth: 0  
ngth: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA: \*  
: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/PCRUS\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

# SUMMARIES

Query match	Length	DB	ID	Description
71.8	46	1	US-08-217-299-3	Sequence 3, Appli
71.8	46	1	US-08-217-299-4	Sequence 4, Appli
70.9	30	2	US-08-583-562B-4	Sequence 4, Appli
70.9	30	2	US-08-779-113-4	Sequence 4, Appli
61.8	24	1	US-07-647-655C-4	Sequence 41, Appl
61.8	37	4	US-09-331-793-41	Sequence 2, Appli
61.8	44	3	US-08-666-354A-2	Sequence 8, Appli
61.8	52	1	US-07-647-655C-2	Sequence 10, Appl
60.0	22	4	US-09-553-690-8	Sequence 73, Appl
60.0	35	1	US-08-258-026A-10	Sequence 10, Appl
60.0	35	4	US-09-097-055B-73	Sequence 10, Appl
60.0	35	5	PCT-US95-07541-10	Sequence 1473, Ap
60.0	47	4	US-09-422-978-1473	Sequence 36, Appl
59.1	22	1	US-07-977-284A-36	Sequence 36, Appl
59.1	22	2	US-08-256-426B-36	Sequence 1112, Ap
59.1	28	2	US-08-859-998-1112	Sequence 1112, Ap
59.1	28	4	US-09-225-928-1112	Sequence 1112, Ap
59.1	28	4	US-09-225-201B-1112	Sequence 13, Appl
59.1	34	1	US-08-361-337-13	Sequence 1562, Ap
58.2	47	4	US-09-422-978-1562	Sequence 74, Appl
57.3	35	4	US-09-097-055B-74	Sequence 3196, Ap
57.3	47	4	US-09-422-978-3196	Sequence 29, Appl
57.3	48	1	US-08-472-194A-29	Sequence 29, Appl
57.3	48	1	US-08-262-142-29	Sequence 28, Appl
57.3	48	4	US-08-849-567A-29	Sequence 8, Appli
57.3	49	1	US-08-424-874-8	Sequence 11, Appl
57.3	59	3	US-08-983-607-11	

17	4	US-09-586-376-19	Sequence
29	4	US-10-082-260-8	Sequence
29	4	US-10-082-260-10	Sequence
29	4	US-08-815-783-8	Sequence
29	4	US-08-815-783-10	Sequence
29	4	US-09-879-919-8	Sequence
29	4	US-09-879-919-10	Sequence
30	4	US-08-871-488A-6	Sequence
30	4	US-09-123-030-4	Sequence
34	2	US-08-779-113-43	Sequence
34	2	US-08-779-113-44	Sequence
35	4	US-08-899-241-220	Sequence
35	4	US-08-483-695-19	Sequence
40	2	US-07-965-285-19	Sequence
40	2	US-08-487-231-19	Sequence
40	3	US-09-201-912-19	Sequence
47	4	US-09-422-978-2788	Sequence
22	3	US-08-949-155-45	Sequence
22	4	US-09-819-964-45	Sequence
24	3	US-08-949-155-23	Sequence
24	4	US-09-819-964-23	Sequence
29	4	US-09-301-593-70	Sequence
33	3	US-09-116-032-9	Sequence
36	4	US-09-301-593-69	Sequence
37	4	US-09-874-547-78	Sequence
38	4	US-09-874-547-62	Sequence
38	4	US-09-874-547-76	Sequence
38	4	US-09-874-547-77	Sequence
38	4	US-09-874-547-79	Sequence
38	4	US-09-874-547-80	Sequence
38	4	US-09-874-547-84	Sequence
43	1	US-08-071-601-10	Sequence
43	2	US-08-621-100-10	Sequence
48	1	US-08-171-389-8	Sequence
48	1	US-08-123-936-8	Sequence
48	2	US-08-475-228A-8	Sequence
48	3	US-08-482-080A-8	Sequence
48	4	US-09-354-947-8	Sequence
48	5	PCT-US93-12388-8	Sequence
49	1	US-08-171-389-79	Sequence
49	1	US-08-123-936-79	Sequence
49	2	US-08-475-228A-79	Sequence
49	3	US-08-482-080A-79	Sequence
49	5	PCT-US93-12388-79	Sequence
50	4	US-09-554-929-59	Sequence
50	4	US-09-554-929-135	Sequence
52	4	US-08-956-171B-5080	Sequence
52	2	US-08-943-915-24	Sequence
22	4	US-09-019-160-54	Sequence
24	3	US-08-697-610-4	Sequence
24	3	US-08-349-357-4	Sequence
24	4	US-09-786-256C-19	Sequence
24	4	US-09-786-256C-14	Sequence
29	4	US-08-943-915-21	Sequence
30	2	US-08-348-548-44	Sequence
30	5	PCT-US95-15716-44	Sequence
33	4	US-09-668-113A-9	Sequence
35	1	US-08-170-290A-35	Sequence
39	1	US-08-133-011-57	Sequence
39	1	US-08-322-730A-57	Sequence
39	1	US-08-387-874-55	Sequence
39	2	US-08-383-619-57	Sequence
39	3	US-09-293-823-19	Sequence
39	3	US-08-907-739-57	Sequence
39	4	US-09-729-597-57	Sequence
39	4	US-09-726-653-68	Sequence
39	5	PCT-US93-08364-55	Sequence
40	2	US-08-461-286-1	Sequence
40	5	PCT-US92-02854-1	Sequence
41	2	US-08-627-151A-1	Sequence
41	4	US-09-646-691B-2	Sequence
42	1	US-08-250-859-13	Sequence

54.5	42	1	US-08-430-803-13	Sequence 13, Appl	c 174	11.6	52.7	20	4	US-09-422-978-10661	Sequence
54.5	42	2	US-08-379-057-22	Sequence 22, Appl	175	11.6	52.7	22	1	US-08-546-130A-18	Sequence
54.5	42	2	US-08-457-254-24	Sequence 24, Appl	176	11.6	52.7	22	2	US-08-680-395-26	Sequence
54.5	42	2	US-08-484-257-13	Sequence 13, Appl	177	11.6	52.7	22	3	US-09-066-641-28	Sequence
54.5	42	5	PCT-US94-08806-13	Sequence 13, Appl	c 178	11.6	52.7	22	4	US-09-431-705-44	Sequence
54.5	42	5	PCT-US95-01775-13	Sequence 13, Appl	179	11.6	52.7	30	1	US-08-244-376-20	Sequence
54.5	42	5	PCT-US95-16626-24	Sequence 24, Appl	180	11.6	52.7	30	5	PCT-US93-11527-20	Sequence
54.5	48	4	US-09-538-709-998	Sequence 998, App	c 181	11.6	52.7	36	1	US-07-842-349-22	Sequence
54.5	49	2	US-08-627-695-8	Sequence 8, Appl	182	11.6	52.7	36	1	US-07-842-349-23	Sequence
54.5	52	1	US-07-647-655C-1	Sequence 1, Appl	c 183	11.6	52.7	36	1	US-07-756-251A-6	Sequence
54.5	57	1	US-08-050-319B-6	Sequence 6, Appl	184	11.6	52.7	38	4	US-09-474-432B-1366	Sequence
54.5	57	2	US-08-465-982-6	Sequence 6, Appl	185	11.6	52.7	38	4	US-09-476-387-1365	Sequence
53.6	20	1	US-08-167-113-5	Sequence 5, Appl	c 186	11.6	52.7	40	3	US-08-563-501A-33	Sequence
53.6	20	2	US-08-886-161-5	Sequence 5, Appl	c 187	11.6	52.7	42	2	US-09-205-231-33	Sequence
53.6	20	3	US-08-050-159-37	Sequence 37, Appl	188	11.6	52.7	42	2	US-08-389-423-25	Sequence
53.6	20	4	US-09-198-452A-2262	Sequence 2262, Ap	189	11.6	52.7	42	2	US-08-389-423-29	Sequence
53.6	20	4	US-09-198-452A-2265	Sequence 2265, Ap	190	11.6	52.7	42	4	US-09-189-028-25	Sequence
53.6	20	4	US-09-679-299A-155	Sequence 155, App	191	11.6	52.7	42	4	US-09-189-028-29	Sequence
53.6	20	4	US-09-679-299A-156	Sequence 156, App	192	11.6	52.7	43	1	US-07-931-473B-246	Sequence
53.6	24	4	US-09-382-552-180	Sequence 180, App	193	11.6	52.7	43	1	US-07-714-131C-246	Sequence
53.6	27	1	US-08-331-398A-6	Sequence 6, Appl	194	11.6	52.7	43	1	US-08-412-110-246	Sequence
53.6	27	2	US-08-331-397B-6	Sequence 6, Appl	c 195	11.6	52.7	43	1	US-08-467-420A-38	Sequence
53.6	27	3	US-08-759-804A-6	Sequence 6, Appl	c 196	11.6	52.7	43	1	US-08-470-110A-38	Sequence
53.6	27	3	US-09-227-693-6	Sequence 6, Appl	c 197	11.6	52.7	43	1	US-08-409-442A-246	Sequence
53.6	28	2	US-08-859-998-1184	Sequence 1184, Ap	c 198	11.6	52.7	43	2	US-08-667-769A-38	Sequence
53.6	28	4	US-09-225-928-1184	Sequence 1184, Ap	c 199	11.6	52.7	43	2	US-08-469-609A-246	Sequence
53.6	28	4	US-09-225-201B-1184	Sequence 1184, Ap	c 200	11.6	52.7	43	3	US-08-940-371-38	Sequence
53.6	29	4	US-09-304-232-285	Sequence 285, App	c 201	11.6	52.7	43	3	US-09-143-190-246	Sequence
53.6	30	2	US-08-743-637B-148	Sequence 148, App	c 202	11.6	52.7	43	3	US-08-637-647-38	Sequence
53.6	30	3	US-08-526-840B-148	Sequence 148, App	c 203	11.6	52.7	43	4	US-09-502-344-246	Sequence
53.6	31	2	US-08-483-528B-12	Sequence 12, Appl	c 204	11.6	52.7	43	5	PCT-US95-17082A-38	Sequence
53.6	31	3	US-08-673-799C-12	Sequence 12, Appl	c 205	11.6	52.7	45	1	US-08-447-169A-229	Sequence
53.6	31	3	US-09-393-385B-12	Sequence 12, Appl	c 206	11.6	52.7	47	4	US-09-336-643A-61	Sequence
53.6	32	1	US-07-977-696C-8	Sequence 8, Appl	c 207	11.6	52.7	47	4	US-08-778-570B-39	Sequence
53.6	32	1	US-08-129-930B-8	Sequence 8, Appl	c 208	11.6	52.7	47	4	US-09-422-978-1483	Sequence
53.6	32	2	US-08-663-922-2	Sequence 107, App	c 209	11.6	52.7	48	3	US-08-864-473-2	Sequence
53.6	32	3	US-08-783-853A-107	Sequence 107, App	c 210	11.6	52.7	48	3	US-09-440-523-2	Sequence
53.6	32	4	US-08-976-288A-8	Sequence 8, Appl	c 211	11.4	51.8	16	2	US-08-448-418-93	Sequence
53.6	32	4	US-09-344-050-107	Sequence 2, Appl	c 212	11.4	51.8	16	4	US-09-146-979-93	Sequence
53.6	32	4	US-09-313-350-2	Sequence 41, Appl	c 213	11.4	51.8	20	4	US-09-198-452A-1520	Sequence
53.6	33	3	US-08-427-569-41	Sequence 14, Appl	c 214	11.4	51.8	20	2	US-09-198-452A-1525	Sequence
53.6	33	4	US-09-874-547-14	Sequence 11, Appl	c 215	11.4	51.8	22	2	US-08-899-371-17	Sequence
53.6	35	1	US-08-436-463-11	Sequence 21, Appl	c 216	11.4	51.8	24	1	US-08-343-401A-1	Sequence
53.6	35	1	US-08-024-253-21	Sequence 75, Appl	c 217	11.4	51.8	24	1	US-08-445-265A-3	Sequence
53.6	35	4	US-09-097-055B-75	Sequence 6, Appl	c 218	11.4	51.8	24	3	US-08-990-442-3	Sequence
53.6	36	2	US-08-663-922-6	Sequence 17, Appl	c 219	11.4	51.8	24	3	US-09-614-178-2	Sequence
53.6	36	4	US-08-976-183A-17	Sequence 11, Appl	c 220	11.4	51.8	25	3	US-08-510-133A-28	Sequence
53.6	36	4	US-09-318-786-11	Sequence 6, Appl	c 221	11.4	51.8	25	3	US-08-585-895-28	Sequence
53.6	36	4	US-09-313-350-6	Sequence 33, Appl	c 222	11.4	51.8	25	4	US-08-601-132-28	Sequence
53.6	37	2	US-08-765-783A-33	Sequence 2, Appl	c 223	11.4	51.8	25	4	US-08-671-573B-28	Sequence
53.6	37	2	US-08-470-139-2	Sequence 33, Appl	c 224	11.4	51.8	27	4	US-09-601-537-4	Sequence
53.6	37	3	US-08-921-100-33	Sequence 33, Appl	c 225	11.4	51.8	27	6	5215895-5	Patent N
53.6	37	3	US-08-880-142-33	Sequence 33, Appl	c 226	11.4	51.8	28	2	US-08-859-998-537	Sequence
53.6	37	3	US-08-902-201-33	Sequence 35, Appl	c 227	11.4	51.8	28	4	US-09-225-928-537	Sequence
53.6	37	3	US-08-569-147-35	Sequence 33, Appl	c 228	11.4	51.8	28	4	US-09-225-201B-537	Sequence
53.6	37	3	US-09-416-057-33	Sequence 2, Appl	c 229	11.4	51.8	30	1	US-08-273-362-5	Sequence
53.6	37	4	US-09-347-051-2	Sequence 65, Appl	c 230	11.4	51.8	30	1	US-08-273-362-7	Sequence
53.6	38	4	US-08-874-547-55	Sequence 75, Appl	c 231	11.4	51.8	30	3	US-08-975-084-9	Sequence
53.6	38	4	US-08-874-547-75	Sequence 579, App	c 232	11.4	51.8	32	4	US-09-011-143-13	Sequence
53.6	41	2	US-08-350-260A-579	Sequence 15, App	c 233	11.4	51.8	32	4	US-09-302-495-13	Sequence
53.6	41	4	US-09-104-337A-579	Sequence 15, App	c 234	11.4	51.8	32	4	US-10-079-616-13	Sequence
53.6	42	4	US-08-190-199A-5	Sequence 29, Appl	c 235	11.4	51.8	33	1	US-08-475-000-7	Sequence
53.6	46	2	US-09-649-083-29	Sequence 20, Appl	c 236	11.4	51.8	33	2	US-08-483-199-7	Sequence
53.6	47	4	US-09-133-774-20	Sequence 10, Appl	c 237	11.4	51.8	33	2	US-08-902-623-22	Sequence
53.6	48	3	US-09-303-862-20	Sequence 20, Appl	c 238	11.4	51.8	34	2	US-08-484-508-7	Sequence
53.6	48	4	US-09-724-138-10	Sequence 4, Appl	c 239	11.4	51.8	34	2	US-08-184-009-167	Sequence
53.6	50	2	US-08-190-199A-4	Sequence 7257, Ap	c 240	11.4	51.8	34	3	US-08-458-356-167	Sequence
53.6	51	4	US-09-313-294A-7257	Sequence 2800, Ap	c 241	11.4	51.8	34	3	US-08-460-736-167	Sequence
53.6	51	4	US-08-956-171E-2800	Sequence 157, App	c 242	11.4	51.8	38	6	5494663-28	Patent N
52.7	18	4	US-09-422-978-4682	Sequence 157, App	c 243	11.4	51.8	39	2	US-08-193-039B-3	Sequence
52.7	20	3	US-09-280-799-157	Sequence 21, Appl	c 244	11.4	51.8	39	4	US-09-860-761-3	Sequence
52.7	20	3	US-09-277-020-21	Sequence 21, Appl	c 245	11.4	51.8	40	2	US-08-857-946-73	Sequence
52.7	20	3	US-09-277-020-21	Sequence 21, Appl	c 246	11.4	51.8	40	2	US-08-857-946-73	Sequence

31.8	40	3	US-08-970-740-73	Sequence 73, Appl	c 320	11.2	50.9	41	5	PCT-US93-11775-5	Sequence
31.8	41	2	US-08-350-260A-580	Sequence 580, App	321	11.2	50.9	42	3	US-08-813-507-45	Sequence
31.8	41	4	US-09-104-337A-580	Sequence 580, App	322	11.2	50.9	42	3	US-09-464-453-45	Sequence
31.8	42	2	US-08-466-860-41	Sequence 41, Appl	323	11.2	50.9	43	4	US-09-313-221A-8	Sequence
31.8	42	3	US-08-472-040A-41	Sequence 41, Appl	324	11.2	50.9	45	2	US-08-701-124-30	Sequence
31.8	42	3	US-08-276-776-41	Sequence 41, Appl	325	11.2	50.9	45	2	US-08-053-451B-104	Sequence
31.8	42	3	US-08-471-209-41	Sequence 41, Appl	326	11.2	50.9	45	3	US-09-130-225-30	Sequence
31.8	45	2	US-08-659-567-25	Sequence 25, Appl	327	11.2	50.9	45	4	US-09-455-061-30	Sequence
31.8	47	4	US-09-671-317-888	Sequence 888, App	328	11.2	50.9	45	4	US-09-969-192-30	Sequence
31.8	47	4	US-09-422-978-2109	Sequence 2109, Ap	329	11.2	50.9	47	4	US-09-671-317-748	Sequence
31.8	47	4	US-09-422-978-3741	Sequence 3741, Ap	330	11.2	50.9	47	4	US-09-422-978-815	Sequence
31.8	47	4	US-09-422-978-3852	Sequence 3852, Ap	331	11.2	50.9	48	1	US-08-399-696-19	Sequence
31.8	47	4	US-09-724-138-33	Sequence 33, Appl	332	11.2	50.9	59	4	US-09-698-286A-4	Sequence
31.8	50	1	US-08-374-641-40	Sequence 40, Appl	333	11.2	50.9	60	2	US-08-765-512-1	Sequence
31.8	51	4	US-09-443-199C-5	Sequence 5, Appl	334	11.2	50.9	60	2	US-08-914-828-1	Sequence
31.8	51	4	US-09-443-199C-6	Sequence 6, Appl	335	11.2	50.9	60	3	US-08-907-392A-1	Sequence
31.8	51	4	US-09-443-199C-575	Sequence 575, App	336	11.2	50.9	60	3	US-09-121-286-10	Sequence
31.8	51	4	US-09-443-199C-576	Sequence 576, App	337	11	50.0	18	1	US-07-947-120-5	Sequence
31.8	51	4	US-09-443-199C-576	Sequence 576, App	338	11	50.0	18	1	US-08-472-893A-5	Sequence
31.8	51	4	US-09-443-199C-1117	Sequence 1117, Ap	339	11	50.0	18	3	US-08-947-492-5	Sequence
31.8	51	4	US-09-443-199C-1118	Sequence 1118, Ap	340	11	50.0	20	1	US-07-828-444-3	Sequence
31.8	55	3	US-09-264-737-4	Sequence 4, Appl	341	11	50.0	20	2	US-09-676-610B-87	Sequence
31.8	59	5	PCT-US93-01901-36	Sequence 36, Appl	342	11	50.0	20	4	US-08-898-361-60	Sequence
31.8	60	4	US-08-899-279-44	Sequence 44, Appl	343	11	50.0	20	4	US-08-379-078-702	Sequence
31.8	60	4	US-08-899-279-44	Sequence 44, Appl	344	11	50.0	22	1	US-08-379-078-704	Sequence
50.9	16	4	US-09-479-005A-481	Sequence 481, App	345	11	50.0	22	1	US-08-193-039B-26	Sequence
50.9	18	4	US-09-417-485D-26	Sequence 26, Appl	346	11	50.0	23	2	US-09-860-761-26	Sequence
50.9	20	2	US-08-117-952-523	Sequence 523, App	347	11	50.0	24	2	US-08-793-410-13	Sequence
50.9	20	3	US-09-166-186-117	Sequence 117, App	348	11	50.0	24	2	US-08-602-725-19	Sequence
50.9	20	3	US-09-313-932-117	Sequence 117, App	349	11	50.0	24	2	US-08-602-725-20	Sequence
50.9	20	4	US-09-791-211-74	Sequence 74, Appl	350	11	50.0	24	3	US-09-150-133-43	Sequence
50.9	20	4	US-09-198-452A-2320	Sequence 2320, Ap	351	11	50.0	24	3	US-08-338-579A-43	Sequence
50.9	20	4	US-09-198-452A-4493	Sequence 4493, Ap	352	11	50.0	24	3	US-09-150-141-43	Sequence
50.9	23	3	US-08-781-891-120	Sequence 120, App	353	11	50.0	24	3	US-09-009-913-262	Sequence
50.9	23	3	US-09-358-384-3	Sequence 3, Appl	354	11	50.0	24	3	US-09-374-433-43	Sequence
50.9	23	4	US-09-602-586-21	Sequence 21, Appl	355	11	50.0	24	3	US-09-374-824-43	Sequence
50.9	23	4	US-09-618-166-120	Sequence 21, Appl	356	11	50.0	24	3	US-09-374-492-43	Sequence
50.9	23	4	US-09-561-579A-21	Sequence 21, Appl	357	11	50.0	24	3	US-09-785-343-43	Sequence
50.9	24	2	US-09-255-518C-17	Sequence 17, Appl	358	11	50.0	24	4	US-09-724-138-48	Sequence
50.9	26	2	US-08-331-389A-52	Sequence 52, Appl	359	11	50.0	24	4	US-09-382-552-191	Sequence
50.9	27	4	US-09-678-300-21	Sequence 21, Appl	360	11	50.0	24	4	PCT-US94-09851-43	Sequence
50.9	29	2	US-08-960-022-25	Sequence 25, Appl	361	11	50.0	24	5	US-08-859-998-503	Sequence
50.9	29	3	US-09-026-959-14	Sequence 14, Appl	362	11	50.0	25	2	US-09-225-928-503	Sequence
50.9	29	3	US-09-304-232-870	Sequence 870, App	363	11	50.0	25	4	US-09-225-201B-503	Sequence
50.9	30	2	US-08-859-998-226	Sequence 226, App	364	11	50.0	25	4	US-09-301-593-54	Sequence
50.9	30	3	US-09-121-286-11	Sequence 11, Appl	365	11	50.0	27	4	US-08-187-161-5	Sequence
50.9	30	4	US-09-225-928-226	Sequence 226, App	366	11	50.0	28	2	US-08-129-686-23	Sequence
50.9	30	4	US-09-225-201B-226	Sequence 226, App	367	11	50.0	28	3	US-09-566-581-23	Sequence
50.9	31	2	US-08-702-153-6	Sequence 6, Appl	368	11	50.0	28	4	US-09-486-072-27	Sequence
50.9	31	3	US-09-246-277A-9	Sequence 9, Appl	369	11	50.0	28	4	US-08-476-275-11	Sequence
50.9	31	4	US-09-402-401C-10	Sequence 10, Appl	370	11	50.0	29	3	US-09-218-114A-3	Sequence
50.9	32	2	US-08-859-998-425	Sequence 425, App	371	11	50.0	29	3	US-08-475-815B-9	Sequence
50.9	32	4	US-09-225-928-425	Sequence 425, App	372	11	50.0	29	4	US-08-475-813-11	Sequence
50.9	32	4	US-09-225-201B-425	Sequence 225, App	373	11	50.0	29	4	US-08-291-368-16	Sequence
50.9	35	1	US-07-783-861C-22	Sequence 22, Appl	374	11	50.0	30	1	US-08-962-190-16	Sequence
50.9	35	2	US-08-484-891-5	Sequence 5, Appl	375	11	50.0	30	2	US-08-743-637B-77	Sequence
50.9	35	2	US-09-150-811-5	Sequence 5, Appl	376	11	50.0	30	2	US-08-526-840B-77	Sequence
50.9	36	3	US-08-602-632-17	Sequence 17, Appl	377	11	50.0	30	3	US-08-928-361B-22	Sequence
50.9	36	3	US-08-454-098-1	Sequence 1, Appl	378	11	50.0	30	3	US-09-588-995A-22	Sequence
50.9	36	4	US-09-479-005A-785	Sequence 785, App	379	11	50.0	30	4	US-09-097-055B-83	Sequence
50.9	36	5	PCT-US96-01600-1	Sequence 1, Appl	380	11	50.0	30	4	PCT-US95-10310-16	Sequence
50.9	37	2	US-08-933-616-5	Sequence 5, Appl	381	11	50.0	31	3	US-08-836-561-53	Sequence
50.9	37	4	US-09-135-121B-2	Sequence 2, Appl	382	11	50.0	31	4	US-09-434-122-53	Sequence
50.9	38	1	US-07-833-905B-54	Sequence 54, Appl	383	11	50.0	32	3	US-08-341-560B-11	Sequence
50.9	38	2	US-08-700-757-54	Sequence 54, Appl	384	11	50.0	32	3	US-08-811-463-3	Sequence
50.9	38	4	US-09-402-401C-32	Sequence 32, Appl	385	11	50.0	32	5	PCT-US93-03895-11	Sequence
50.9	39	2	US-08-701-124-32	Sequence 32, Appl	386	11	50.0	32	5	US-07-955-726A-34	Sequence
50.9	39	3	US-09-130-225-32	Sequence 32, Appl	387	11	50.0	33	4	US-09-874-547-16	Sequence
50.9	39	4	US-09-455-061-32	Sequence 32, Appl	388	11	50.0	33	4	US-08-151-574-37	Sequence
50.9	39	4	US-09-969-192-32	Sequence 32, Appl	389	11	50.0	34	1	US-08-146-422-4	Sequence
50.9	41	1	US-08-240-081-1	Sequence 1, Appl	390	11	50.0	34	1	US-08-146-424-4	Sequence
50.9	41	1	US-08-240-081-5	Sequence 5, Appl	391	11	50.0	34	1	US-08-626-554-20	Sequence
50.9	41	5	PCT-US93-11775-1	Sequence 1, Appl	392	11	50.0	34	1		

50.0	34	1	US-08-693-709-18	Sequence 18, Appl	c 466	10.8	49.1	18	3	US-09-406-064-31	Sequence
50.0	34	1	US-08-638-448-4	Sequence 4, Appl	c 467	10.8	49.1	18	3	US-09-430-615-60	Sequence
50.0	34	2	US-08-419-448-37	Sequence 37, Appl	c 468	10.8	49.1	18	4	US-09-406-065-65	Sequence
50.0	34	4	US-09-233-510-37	Sequence 37, Appl	c 469	10.8	49.1	18	4	US-09-383-316-81	Sequence
50.0	35	2	US-08-116-778E-29	Sequence 29, Appl	c 470	10.8	49.1	18	4	US-09-788-847-31	Sequence
50.0	35	2	US-08-438-562-29	Sequence 29, Appl	c 471	10.8	49.1	20	1	US-08-317-450B-8	Sequence
50.0	35	2	US-08-483-528B-29	Sequence 29, Appl	c 472	10.8	49.1	20	3	US-08-800-593-8	Sequence
50.0	35	3	US-08-673-799C-29	Sequence 29, Appl	c 473	10.8	49.1	20	3	US-08-800-215C-5	Sequence
50.0	35	3	US-09-393-385B-29	Sequence 29, Appl	c 474	10.8	49.1	20	3	US-08-800-215C-6	Sequence
50.0	36	3	US-09-184-658-46	Sequence 46, Appl	c 475	10.8	49.1	20	3	US-09-487-445-142	Sequence
50.0	36	4	US-09-504-262D-46	Sequence 46, Appl	c 476	10.8	49.1	20	4	US-09-183-636-2	Sequence
50.0	37	2	US-08-629-039-2	Sequence 2, Appl	c 477	10.8	49.1	20	4	US-09-198-452A-3403	Sequence
50.0	37	5	PCT-US94-02342-78	Sequence 78, Appl	c 478	10.8	49.1	20	4	US-09-198-452A-4224	Sequence
50.0	38	4	US-09-294-584A-3	Sequence 3, Appl	c 479	10.8	49.1	20	4	US-09-198-452A-5542	Sequence
50.0	39	2	US-08-002-324-16	Sequence 16, Appl	c 480	10.8	49.1	20	4	US-09-198-452A-6196	Sequence
50.0	39	3	US-08-836-561-52	Sequence 52, Appl	c 481	10.8	49.1	20	4	US-09-434-840-35	Sequence
50.0	39	4	US-09-548-372D-37	Sequence 37, Appl	c 482	10.8	49.1	20	4	US-09-980-052-124	Sequence
50.0	39	4	US-09-548-372D-38	Sequence 38, Appl	c 483	10.8	49.1	21	1	US-07-869-380B-8	Sequence
50.0	39	4	US-09-548-367D-37	Sequence 37, Appl	c 484	10.8	49.1	21	1	US-08-179-738-18	Sequence
50.0	39	4	US-09-548-367D-38	Sequence 38, Appl	c 485	10.8	49.1	21	1	US-08-260-515-5	Sequence
50.0	39	4	US-09-551-853D-37	Sequence 37, Appl	c 486	10.8	49.1	21	1	US-08-513-846-10	Sequence
50.0	39	4	US-09-551-853D-38	Sequence 38, Appl	c 487	10.8	49.1	21	1	US-08-559-303B-34	Sequence
50.0	39	4	US-09-434-122-52	Sequence 52, Appl	c 488	10.8	49.1	21	2	US-08-628-145-18	Sequence
50.0	39	5	PCT-US94-00261-16	Sequence 16, Appl	c 489	10.8	49.1	21	3	US-08-577-081A-31	Sequence
50.0	40	4	US-09-153-310-18	Sequence 18, Appl	c 490	10.8	49.1	21	3	US-08-175-828-34	Sequence
50.0	42	1	US-08-096-762-202	Sequence 202, App	c 491	10.8	49.1	21	3	US-09-380-760-1	Sequence
50.0	42	2	US-08-379-057-26	Sequence 26, App	c 492	10.8	49.1	21	4	US-09-422-978-11273	Sequence
50.0	42	3	US-08-042-353-315	Sequence 315, App	c 493	10.8	49.1	21	4	US-09-060-299-186	Sequence
50.0	42	4	US-08-758-417A-163	Sequence 163, App	c 494	10.8	49.1	21	4	US-09-402-923A-186	Sequence
50.0	42	4	US-09-874-547-17	Sequence 17, Appl	c 495	10.8	49.1	21	4	US-09-750-099-1	Sequence
50.0	45	1	US-08-467-420A-37	Sequence 37, Appl	c 496	10.8	49.1	22	1	US-07-916-034-7	Sequence
50.0	45	1	US-08-467-420A-37	Sequence 37, Appl	c 497	10.8	49.1	22	2	US-08-639-501-41	Sequence
50.0	45	1	US-08-467-769A-37	Sequence 37, Appl	c 498	10.8	49.1	22	2	US-08-634-545-2	Sequence
50.0	45	2	US-08-940-371-37	Sequence 37, Appl	c 499	10.8	49.1	22	3	US-09-044-946-41	Sequence
50.0	45	3	US-08-637-647-37	Sequence 37, Appl	c 500	10.8	49.1	22	3	US-09-044-908-41	Sequence
50.0	45	4	US-09-555-352-33	Sequence 33, Appl	c 501	10.8	49.1	22	3	US-09-287-076A-1	Sequence
50.0	45	5	PCT-US95-17082A-37	Sequence 37, Appl	c 502	10.8	49.1	22	3	US-09-287-076A-2	Sequence
50.0	46	4	US-09-724-138-9	Sequence 9, Appl	c 503	10.8	49.1	23	1	US-08-105-761-21	Sequence
50.0	47	4	US-09-422-978-1374	Sequence 1374, Ap	c 504	10.8	49.1	23	5	PCT-US92-11076-21	Sequence
50.0	47	4	US-09-422-978-2638	Sequence 2638, Ap	c 505	10.8	49.1	24	1	US-08-370-567-34	Sequence
50.0	47	4	US-09-422-978-3015	Sequence 3015, Ap	c 506	10.8	49.1	24	1	US-08-438-759-34	Sequence
50.0	47	4	US-09-422-978-3089	Sequence 3089, Ap	c 507	10.8	49.1	24	1	US-08-538-911-9	Sequence
50.0	47	4	US-09-422-978-3453	Sequence 3453, Ap	c 508	10.8	49.1	24	1	US-08-117-361C-26	Sequence
50.0	49	3	US-08-916-576B-44	Sequence 44, Appl	c 509	10.8	49.1	24	2	US-08-190-199A-12	Sequence
50.0	51	2	US-08-190-199A-14	Sequence 14, Appl	c 510	10.8	49.1	24	2	US-08-716-284-6	Sequence
50.0	51	4	US-09-183-861-27	Sequence 27, Appl	c 511	10.8	49.1	24	3	US-09-135-021-43	Sequence
50.0	51	4	US-09-183-861-27	Sequence 27, Appl	c 512	10.8	49.1	24	3	US-09-135-020-45	Sequence
50.0	51	4	US-09-548-372D-41	Sequence 41, Appl	c 513	10.8	49.1	24	3	US-09-135-010A-45	Sequence
50.0	51	4	US-09-548-372D-42	Sequence 42, Appl	c 514	10.8	49.1	24	4	US-09-444-871-45	Sequence
50.0	51	4	US-09-548-367D-41	Sequence 41, Appl	c 515	10.8	49.1	24	4	US-09-597-735-45	Sequence
50.0	51	4	US-09-548-367D-42	Sequence 42, Appl	c 516	10.8	49.1	24	4	US-09-444-295-45	Sequence
50.0	51	4	US-09-551-974A-27	Sequence 27, Appl	c 517	10.8	49.1	24	4	US-09-597-732-45	Sequence
50.0	51	4	US-09-551-853D-41	Sequence 41, Appl	c 518	10.8	49.1	24	4	US-09-597-731-45	Sequence
50.0	51	4	US-09-551-853D-42	Sequence 42, Appl	c 519	10.8	49.1	24	5	PCT-US94-05591-9	Sequence
50.0	51	4	US-09-565-501A-27	Sequence 27, Appl	c 520	10.8	49.1	24	5	PCT-US94-05684-34	Sequence
50.0	51	4	US-09-619-206A-27	Sequence 27, Appl	c 521	10.8	49.1	25	2	US-08-622-740-16	Sequence
50.0	51	4	US-09-874-923-27	Sequence 27, Appl	c 522	10.8	49.1	25	3	US-08-440-689-16	Sequence
50.0	51	4	US-09-443-199C-590	Sequence 590, App	c 523	10.8	49.1	25	3	US-08-995-451-1	Sequence
50.0	51	4	US-09-443-199C-617	Sequence 617, App	c 524	10.8	49.1	25	3	US-09-312-285-13	Sequence
50.0	53	1	US-08-802-824-6	Sequence 6, Appl	c 525	10.8	49.1	25	3	US-09-312-266-12	Sequence
50.0	53	1	US-08-096-762-206	Sequence 206, App	c 526	10.8	49.1	25	3	US-09-312-038-12	Sequence
50.0	53	3	US-09-042-353-319	Sequence 319, App	c 527	10.8	49.1	25	4	US-09-122-399-16	Sequence
50.0	53	4	US-08-758-417A-167	Sequence 167, App	c 528	10.8	49.1	25	4	US-09-540-014-34	Sequence
50.0	53	4	US-09-057-937-6	Sequence 6, Appl	c 529	10.8	49.1	25	4	US-08-447-985-21	Sequence
50.0	53	6	5240845-30	Patent No. 5240845	c 530	10.8	49.1	25	4	US-09-728-764-13	Sequence
50.0	55	4	US-09-180-432B-20	Sequence 20, Appl	c 531	10.8	49.1	25	4	US-09-312-304B-10	Sequence
50.0	55	4	US-09-180-432B-21	Sequence 21, Appl	c 532	10.8	49.1	25	4	US-09-728-792-12	Sequence
50.0	58	3	US-08-463-903-52	Sequence 52, Appl	c 533	10.8	49.1	25	4	US-09-357-711A-8	Sequence
50.0	58	4	US-07-933-695-52	Sequence 52, Appl	c 534	10.8	49.1	25	4	US-09-850-964-12	Sequence
50.0	60	4	US-08-956-171E-1661	Sequence 1661, Ap	c 535	10.8	49.1	25	4	US-09-078-972A-20	Sequence
49.1	17	4	US-09-586-376-20	Sequence 20, Appl	c 537	10.8	49.1	26	2	US-08-859-998-65	Sequence
49.1	18	3	US-09-358-972-224	Sequence 224, App	c 538	10.8	49.1	26	3	US-09-184-658-66	Sequence



9.1	26	3	US-08-881-038A-5	Sequence 5, Appli	612	10.8	49.1	40	4	US-09-788-847-78	Sequence
9.1	26	3	US-09-433-428D-56	Sequence 56, Appl	613	10.8	49.1	41	3	US-08-813-507-136	Sequence
9.1	26	4	US-09-225-201B-65	Sequence 65, Appl	614	10.8	49.1	41	4	US-09-464-453-136	Sequence
9.1	26	4	US-09-225-201B-65	Sequence 65, Appl	615	10.8	49.1	41	4	US-09-060-239-187	Sequence
9.1	26	4	US-09-646-028B-18	Sequence 18, Appl	616	10.8	49.1	41	4	US-09-402-923A-187	Sequence
9.1	26	4	US-09-504-262D-66	Sequence 66, Appl	617	10.8	49.1	42	1	US-08-719-331-6	Sequence
9.1	27	2	US-08-400-115-11	Sequence 11, Appl	618	10.8	49.1	42	2	US-08-642-406A-8	Sequence
9.1	27	4	US-08-584-040-396	Sequence 396, App	619	10.8	49.1	42	4	US-09-199-534-8	Sequence
9.1	27	4	US-08-584-040-6578	Sequence 6578, Ap	620	10.8	49.1	42	4	US-09-199-534-8	Sequence
9.1	27	4	US-09-658-679A-6	Sequence 6, Appli	621	10.8	49.1	42	4	US-09-408-020-87	Sequence
9.1	28	2	US-08-187-161-5	Sequence 5, Appli	622	10.8	49.1	45	1	US-08-236-520-11	Sequence
9.1	28	6	5258283-16	Patent No. 5258283	623	10.8	49.1	45	2	US-08-659-567-22	Sequence
9.1	29	1	US-07-796-106-20	Sequence 20, Appl	624	10.8	49.1	45	2	US-09-217-847-21	Sequence
9.1	29	4	US-09-304-232-422	Sequence 422, App	625	10.8	49.1	45	3	US-09-264-032-2	Sequence
9.1	29	4	US-09-304-232-577	Sequence 577, App	626	10.8	49.1	45	3	US-09-559-393-2	Sequence
9.1	30	1	US-08-394-210-18	Sequence 3, Appli	627	10.8	49.1	45	3	US-09-559-393-6	Sequence
9.1	30	3	US-09-026-958-3	Sequence 47, Appl	628	10.8	49.1	45	3	US-09-339-159B-41	Sequence
9.1	30	3	US-09-358-972-46	Sequence 46, Appl	629	10.8	49.1	45	4	US-09-339-159B-44	Sequence
9.1	30	3	US-09-358-972-47	Sequence 47, Appl	630	10.8	49.1	45	4	US-09-634-137-28	Sequence
9.1	30	3	US-09-406-147-19	Sequence 19, Appl	631	10.8	49.1	45	4	US-09-724-138-32	Sequence
9.1	30	3	US-09-406-147-20	Sequence 20, Appl	632	10.8	49.1	45	5	PCT-US95-05262-11	Sequence
9.1	30	4	US-09-150-766-9	Sequence 9, Appli	633	10.8	49.1	46	1	US-08-089-755A-14	Sequence
9.1	30	4	US-09-052-919-9	Sequence 9, Appli	634	10.8	49.1	46	1	US-08-421-754-14	Sequence
9.1	30	4	US-09-953-052-9	Sequence 9, Appli	635	10.8	49.1	46	2	US-08-421-791-14	Sequence
9.1	31	1	US-08-452-083-5	Sequence 5, Appli	636	10.8	49.1	46	2	US-09-199-737-40	Sequence
9.1	31	1	US-08-468-557-9	Sequence 18, Appl	637	10.8	49.1	46	4	US-09-058-333A-40	Sequence
9.1	31	2	US-08-742-026-4	Sequence 4, Appli	638	10.8	49.1	47	4	US-09-671-317-589	Sequence
9.1	31	2	US-08-413-593-5	Sequence 5, Appli	639	10.8	49.1	47	4	US-09-422-978-60	Sequence
9.1	31	2	US-08-814-806-24	Sequence 24, Appl	640	10.8	49.1	47	4	US-09-422-978-3440	Sequence
9.1	31	3	US-08-544-381B-128	Sequence 128, App	641	10.8	49.1	48	1	US-08-754-431A-3	Sequence
9.1	31	3	US-08-855-910-15	Sequence 15, Appl	642	10.8	49.1	51	3	US-09-046-247-27	Sequence
9.1	31	3	US-09-595-684B-82	Sequence 82, Appl	643	10.8	49.1	54	3	US-09-365-121-14	Sequence
9.1	31	4	US-09-595-684B-88	Sequence 88, Appl	644	10.8	49.1	54	4	US-09-867-193-14	Sequence
9.1	31	4	US-09-293-854-24	Sequence 24, Appl	645	10.8	49.1	57	2	US-08-002-324-20	Sequence
9.1	31	4	US-09-183-412-50	Sequence 50, Appl	646	10.8	49.1	57	4	US-08-523-030-22	Sequence
9.1	32	4	US-09-084-303B-78	Sequence 78, Appl	647	10.8	49.1	57	5	PCT-US94-00261-20	Sequence
9.1	32	4	US-09-769-864-50	Sequence 50, Appl	648	10.8	49.1	59	3	US-08-951-260A-5	Sequence
9.1	33	1	US-08-398-613A-26	Sequence 26, Appl	650	10.8	49.1	59	4	US-09-430-626A-5	Sequence
9.1	33	1	US-08-398-612A-26	Sequence 26, Appl	651	10.8	49.1	59	4	US-09-621-976-18022	Sequence
9.1	33	1	US-08-398-611A-26	Sequence 26, Appl	652	10.8	49.1	60	3	US-09-358-972-44	Sequence
9.1	33	1	US-08-396-851A-26	Sequence 26, Appl	653	10.8	49.1	60	3	US-09-358-972-45	Sequence
9.1	33	1	US-08-704-582-2	Sequence 2, Appli	654	10.8	49.1	60	3	US-09-406-147-17	Sequence
9.1	33	2	US-08-588-604-7	Sequence 7, Appli	655	10.8	49.1	60	3	US-09-406-147-18	Sequence
9.1	33	2	US-08-491-334A-26	Sequence 26, Appl	656	10.8	49.1	60	4	US-09-085-720-1	Sequence
9.1	33	2	US-08-656-906-15	Sequence 15, Appl	657	10.6	48.2	20	1	US-07-977-284A-120	Sequence
9.1	33	3	US-09-027-449-23	Sequence 23, Appl	658	10.6	48.2	20	1	US-08-589-080-6	Sequence
9.1	33	3	US-08-804-444A-23	Sequence 23, Appl	659	10.6	48.2	20	2	US-08-256-426B-120	Sequence
9.1	33	3	US-09-026-985-23	Sequence 23, Appl	660	10.6	48.2	20	2	US-08-975-211-5	Sequence
9.1	33	3	US-09-217-847-15	Sequence 15, Appl	661	10.6	48.2	20	3	US-08-755-587-125	Sequence
9.1	33	4	US-09-121-952A-23	Sequence 23, Appl	662	10.6	48.2	20	3	US-09-280-799-111	Sequence
9.1	33	4	US-09-234-340A-23	Sequence 23, Appl	663	10.6	48.2	20	3	US-09-282-736-5	Sequence
9.1	34	2	US-08-400-115-12	Sequence 12, Appl	664	10.6	48.2	20	3	US-09-377-309-61	Sequence
9.1	35	1	US-08-208-885-3	Sequence 3, Appli	665	10.6	48.2	20	4	US-09-183-636-2	Sequence
9.1	35	1	US-08-462-177-3	Sequence 3, Appli	666	10.6	48.2	20	4	US-09-780-173A-45	Sequence
9.1	35	2	US-08-833-622-3	Sequence 3, Appli	667	10.6	48.2	20	4	US-09-198-452A-2912	Sequence
9.1	35	2	US-08-360-051A-19	Sequence 19, Appl	668	10.6	48.2	20	4	US-09-649-728-7	Sequence
9.1	35	2	US-08-727-449-3	Sequence 3, Appli	669	10.6	48.2	20	4	US-09-825-497A-5	Sequence
9.1	36	1	US-08-361-337-76	Sequence 76, Appl	670	10.6	48.2	21	3	US-09-168-406A-36	Sequence
9.1	36	1	US-08-106-761-12	Sequence 12, Appl	671	10.6	48.2	21	4	US-09-422-978-5753	Sequence
9.1	38	4	US-09-371-772B-10461	Sequence 10461, A	672	10.6	48.2	21	4	US-09-422-978-8118	Sequence
9.1	38	4	US-09-371-772B-10461	Sequence 10461, A	673	10.6	48.2	21	4	US-09-382-552-221	Sequence
9.1	39	1	US-08-754-431A-5	Sequence 5, Appli	674	10.6	48.2	22	2	US-08-836-137-3	Sequence
9.1	40	1	US-08-208-886C-54	Sequence 54, Appl	675	10.6	48.2	23	1	US-08-004-139B-3	Sequence
9.1	40	1	US-08-704-744-54	Sequence 54, Appl	676	10.6	48.2	23	1	US-08-004-139B-12	Sequence
9.1	40	1	US-08-469-557-54	Sequence 54, Appl	677	10.6	48.2	23	2	US-08-811-492-3	Sequence
9.1	40	1	US-08-290-793B-54	Sequence 28, Appl	678	10.6	48.2	23	2	US-08-811-492-12	Sequence
9.1	40	3	US-08-284-516C-28	Sequence 28, Appl	679	10.6	48.2	23	5	PCT-US96-10545A-3	Sequence
9.1	40	3	US-09-358-972-212	Sequence 212, App	680	10.6	48.2	24	2	PCT-US96-10545A-12	Sequence
9.1	40	3	US-09-406-064-78	Sequence 78, Appl	681	10.6	48.2	24	2	US-08-117-952-22	Sequence
9.1	40	3	US-09-430-615-48	Sequence 48, Appl	682	10.6	48.2	25	2	US-08-808-550-12	Sequence
9.1	40	3	US-09-406-065-53	Sequence 53, Appl	683	10.6	48.2	25	3	US-09-240-918-53	Sequence
9.1	40	4	US-09-537-911A-28	Sequence 28, Appl	684	10.6	48.2	25	4	US-09-289-180-7	Sequence



US-09-371-772B-2063	Sequence 2063, Ap	c 904	10.4	47.3	28	4	US-09-328-174A-50	Sequence
US-09-371-772B-6457	Sequence 6457, Ap	c 905	10.4	47.3	29	1	US-08-149-0990-8	Sequence
US-09-371-772B-6458	Sequence 6458, Ap	c 906	10.4	47.3	29	2	US-08-811-949-30	Sequence
US-09-371-772B-6459	Sequence 6459, Ap	c 907	10.4	47.3	29	2	US-08-478-967A-8	Sequence
US-09-371-772B-6811	Sequence 6811, Ap	c 908	10.4	47.3	29	4	US-09-304-232-128	Sequence
US-09-331-347C-5	Sequence 5, Appli	c 909	10.4	47.3	29	4	US-09-304-232-315	Sequence
US-08-584-040-4473	Sequence 4473, Ap	c 910	10.4	47.3	29	4	US-09-579-845-20	Sequence
US-09-371-772B-2186	Sequence 2186, Ap	c 911	10.4	47.3	29	4	US-09-470-276-27	Sequence
US-07-879-647A-22	Sequence 22, Appl	c 912	10.4	47.3	30	1	US-07-940-861-24	Sequence
US-07-879-584A-22	Sequence 22, Appl	c 913	10.4	47.3	30	1	US-08-459-512-24	Sequence
US-07-879-470A-22	Sequence 22, Appl	c 914	10.4	47.3	30	2	US-08-459-657-24	Sequence
US-07-879-644A-22	Sequence 22, Appl	c 915	10.4	47.3	30	2	US-08-460-132-24	Sequence
US-07-879-640A-22	Sequence 22, Appl	c 916	10.4	47.3	30	2	US-08-950-860-5	Sequence
US-07-879-594A-22	Sequence 22, Appl	c 917	10.4	47.3	30	4	US-09-417-822-36	Sequence
US-07-977-284A-120	Sequence 120, App	c 918	10.4	47.3	30	4	US-09-442-349A-101	Sequence
US-07-879-469A-22	Sequence 22, Appl	c 919	10.4	47.3	30	4	US-09-442-349A-102	Sequence
US-08-256-426B-120	Sequence 120, App	c 920	10.4	47.3	30	4	US-09-318-786-10	Sequence
US-09-289-368-79	Sequence 79, Appl	c 921	10.4	47.3	30	4	US-09-646-028-22	Sequence
US-09-856-539-2	Sequence 2, Appli	c 922	10.4	47.3	30	4	US-09-618-028-22	Sequence
US-09-649-747A-55	Sequence 55, Appl	c 923	10.4	47.3	31	4	PCT-US92-02050-24	Sequence
US-09-422-978-3957	Sequence 3957, Ap	c 924	10.4	47.3	31	4	US-09-815-585-12	Sequence
US-09-422-978-6369	Sequence 6369, Ap	c 925	10.4	47.3	31	4	US-09-689-065B-37	Sequence
US-09-068-506-61	Sequence 61, Appl	c 926	10.4	47.3	32	2	US-08-808-931-34	Sequence
Patent No. 5219727		c 927	10.4	47.3	32	3	US-08-554-840-23	Sequence
US-07-665-960A-40	Sequence 40, Appl	c 928	10.4	47.3	32	3	US-09-050-603A-34	Sequence
US-08-106-802-40	Sequence 40, Appl	c 929	10.4	47.3	32	3	US-09-102-420B-34	Sequence
US-08-319-836B-29	Sequence 29, Appl	c 930	10.4	47.3	32	4	US-09-497-698-34	Sequence
US-08-703-136-40	Sequence 40, Appl	c 931	10.4	47.3	32	4	US-08-925-339-23	Sequence
US-09-045-054-28	Sequence 28, Appl	c 932	10.4	47.3	32	4	US-09-332-595-23	Sequence
US-09-422-978-10757	Sequence 10757, A	c 933	10.4	47.3	33	1	US-08-081-539-63	Sequence
PCT-US95-13142-29	Sequence 29, Appl	c 934	10.4	47.3	33	1	US-08-466-647-63	Sequence
US-09-092-314-10	Sequence 10, Appl	c 935	10.4	47.3	33	1	US-08-338-702-1	Sequence
US-09-791-500-8	Sequence 8, Appli	c 936	10.4	47.3	33	1	US-08-337-339-1	Sequence
US-09-526-738A-7	Sequence 7, Appli	c 937	10.4	47.3	33	2	US-08-724-095-1	Sequence
US-08-905-223-32	Sequence 32, Appl	c 938	10.4	47.3	33	2	US-08-734-591A-104	Sequence
US-09-247-155-32	Sequence 32, Appl	c 939	10.4	47.3	33	3	US-08-914-679A-10	Sequence
US-09-599-360B-18	Sequence 18, Appl	c 940	10.4	47.3	33	3	US-08-470-335-104	Sequence
US-09-663-600A-32	Sequence 32, Appl	c 941	10.4	47.3	33	3	US-08-734-664A-104	Sequence
US-03-621-976-18	Sequence 18, Appl	c 942	10.4	47.3	33	3	US-08-470-339-104	Sequence
US-08-411-796-192	Sequence 192, App	c 943	10.4	47.3	33	4	US-08-467-602-104	Sequence
US-08-691-814B-69	Sequence 69, Appl	c 944	10.4	47.3	33	4	US-09-868-758-21	Sequence
US-08-471-039-192	Sequence 192, App	c 945	10.4	47.3	33	4	US-09-868-758-22	Sequence
US-08-559-390-192	Sequence 192, App	c 946	10.4	47.3	33	5	PCT-US95-14262-1	Sequence
PCT-US93-11198-192	Sequence 192, App	c 947	10.4	47.3	33	5	PCT-US95-14378-1	Sequence
US-08-435-350-54	Sequence 54, Appl	c 948	10.4	47.3	34	3	US-09-305-408-4	Sequence
US-08-902-623-21	Sequence 21, Appl	c 949	10.4	47.3	35	2	US-08-467-603-37	Sequence
US-09-704-611-8	Sequence 8, Appli	c 950	10.4	47.3	35	2	US-08-466-793-37	Sequence
US-09-866-108A-12021	Sequence 12021, A	c 951	10.4	47.3	35	2	US-08-491-861A-37	Sequence
US-09-866-108A-12022	Sequence 12022, A	c 952	10.4	47.3	35	4	US-09-374-671A-37	Sequence
US-09-866-108A-12023	Sequence 12023, A	c 953	10.4	47.3	35	4	US-09-661-596A-5	Sequence
US-08-866-108A-12024	Sequence 12024, A	c 954	10.4	47.3	36	4	US-09-371-772B-14119	Sequence
US-09-866-108A-12025	Sequence 12025, A	c 955	10.4	47.3	37	1	US-08-105-483-315	Sequence
US-09-866-108A-12026	Sequence 12026, A	c 956	10.4	47.3	37	1	US-08-285-936-20	Sequence
US-08-859-998-415	Sequence 415, App	c 957	10.4	47.3	37	1	US-08-709-209-315	Sequence
US-08-859-998-1139	Sequence 1139, Ap	c 958	10.4	47.3	37	1	US-08-458-101-315	Sequence
US-08-245-041-74	Sequence 74, Appl	c 959	10.4	47.3	37	4	US-09-163-025B-191	Sequence
US-09-225-928-415	Sequence 415, App	c 960	10.4	47.3	37	4	US-09-595-386-14	Sequence
US-09-225-928-1139	Sequence 1139, Ap	c 961	10.4	47.3	37	4	US-10-037-282-191	Sequence
US-09-225-201B-415	Sequence 415, App	c 962	10.4	47.3	37	4	US-09-993-525-14	Sequence
US-09-225-201B-1139	Sequence 1139, Ap	c 963	10.4	47.3	38	1	US-08-383-756-12	Sequence
US-08-435-434-9	Sequence 9, Appli	c 964	10.4	47.3	38	2	US-08-895-939-2	Sequence
US-08-435-436-9	Sequence 9, Appli	c 965	10.4	47.3	38	2	US-08-448-418-40	Sequence
US-08-438-863-9	Sequence 7, Appli	c 966	10.4	47.3	38	2	US-08-460-898-12	Sequence
US-08-438-863-13	Sequence 9, Appli	c 967	10.4	47.3	38	3	US-09-188-820-2	Sequence
US-08-562-114B-7	Sequence 13, Appl	c 968	10.4	47.3	38	4	US-09-163-025B-190	Sequence
US-08-438-862-9	Sequence 7, Appli	c 969	10.4	47.3	38	4	US-09-163-025B-192	Sequence
US-08-628-747-13	Sequence 13, Appl	c 970	10.4	47.3	38	4	US-09-163-025B-194	Sequence
US-08-402-253-13	Sequence 13, Appl	c 971	10.4	47.3	38	4	US-09-163-025B-195	Sequence
US-08-443-866B-13	Sequence 13, Appl	c 972	10.4	47.3	38	4	US-09-163-025B-196	Sequence
US-08-943-731-644	Sequence 644, App	c 973	10.4	47.3	38	4	US-09-146-979-40	Sequence
US-08-729-594A-7	Sequence 7, Appli	c 974	10.4	47.3	38	4	US-10-037-282-190	Sequence
US-08-937-993-7	Sequence 7, Appli	c 975	10.4	47.3	38	4	US-10-037-282-192	Sequence
		c 976	10.4	47.3	38	4	US-10-037-282-194	Sequence

Sequence 195, App  
Sequence 196, App  
Sequence 42, Appl  
Sequence 42, Appl  
Sequence 9, Appl  
Sequence 17, Appl  
Sequence 9, Appl  
Sequence 17, Appl  
Sequence 9, Appl  
Sequence 17, Appl  
Sequence 33, Appl  
Sequence 41, Appl  
Sequence 12, Appl  
Sequence 103, Appl  
Sequence 62, Appl  
Sequence 62, Appl  
Sequence 5, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 5, Appl  
Sequence 7, Appl  
Sequence 588, Appl  
Sequence 7, Appl  
Sequence 7, Appl

38 4 US-10-037-282-195  
47.3 38 4 US-10-037-282-196  
47.3 39 1 US-08-285-936-42  
47.3 39 1 US-08-487-860-42  
47.3 39 3 US-08-392-459-9  
47.3 39 3 US-08-392-459-17  
47.3 39 4 US-09-854-799-9  
47.3 39 4 US-09-854-799-17  
47.3 39 5 PCT-US91-08525-9  
47.3 39 5 PCT-US91-08525-17  
47.3 39 5 PCT-US93-04384-33  
47.3 39 5 PCT-US93-04384-41  
47.3 40 3 US-08-675-773B-12  
47.3 40 4 US-09-485-737B-103  
47.3 41 1 US-08-081-539-62  
47.3 41 1 US-08-466-647-62  
47.3 41 1 US-08-122-546-5  
47.3 41 1 US-08-137-117D-7  
47.3 41 1 US-08-436-717-7  
47.3 41 2 US-08-764-938-5  
47.3 41 2 US-08-553-501A-7  
47.3 41 2 US-08-350-260A-588  
47.3 41 2 US-08-765-783A-7  
47.3 41 3 US-08-921-100-7

ALIGNMENTS

plication US/08217299

2513

ATION:

Mach, J. P.

Pelegriin, A.

Tersklkh, A.

VENTION: Carcinoembryonic Antigen Derivatives

SEQUENCES: 4

NCE ADDRESS:

: Hoffmann-La Roche Inc.

340 Kingsland Street

tley

J

USA

10

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.25

LICATION DATA:

ON NUMBER: US/08/217,299

TE:

ATION: 435

CATION DATA:

ON NUMBER: EP 93810214.2

TE: 25-MAR-1993

ENT INFORMATION:

kras, Bruce A.

ION NUMBER: 32,748

;/DOCKET NUMBER: RAN 4093/096

ATION INFORMATION:

: (201) 235-5801

OR SEQ ID NO: 3:

CHARACTERISTICS:

46 base pairs

nucleic acid

NESS: single

: linear

?PE: CDNA

AL: NO

: ANTI-SENSE: NO

: ORIGINAL SOURCE:

: ORGANISM: Homo sapiens

US-08-217-299-3

Query Match

71.8%; Score 15.8; DB 1; Length 46;

Best Local Similarity 89.5%; Pred. No. 63;

Matches 17; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACATCAGCTCTCTGC 19

Db 23 AGACATCAGCTCTCTGC 41

RESULT 2

US-08-217-299-4/c

: Sequence 4, Application US/08217299

: Patent No. 5672513

: GENERAL INFORMATION:

: APPLICANT: Mach, J. P.

: APPLICANT: Pelegriin, A.

: APPLICANT: Tersklkh, A.

: TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives

: NUMBER OF SEQUENCES: 4

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Hoffmann-La Roche Inc.

: STREET: 340 Kingsland Street

: CITY: Nutley

: STATE: NJ

: COUNTRY: USA

: ZIP: 07110

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patentin Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/217,299

: FILING DATE:

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: EP 93810214.2

: FILING DATE: 25-MAR-1993

: ATTORNEY/AGENT INFORMATION:

: NAME: Pokras, Bruce A.

: REGISTRATION NUMBER: 32,748

: REFERENCE/DOCKET NUMBER: RAN 4093/096

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (201) 235-5801

: TELEFAX: (201) 235-3500

: INFORMATION FOR SEQ ID NO: 4:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 46 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: CDNA

: HYPOTHETICAL: NO

: ANTI-SENSE: NO

: ORIGINAL SOURCE:

: ORGANISM: Homo sapiens

US-08-217-299-4

Query Match

71.8%; Score 15.8; DB 1; Length 46;

Best Local Similarity 89.5%; Pred. No. 63;

Matches 17; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACATCAGCTCTCTGC 19

Db 28 AGACATCAGCTCTCTGC 10

RESULT 3

09:38:24 2004

us-10-090-326-6.max.rni

```
'C
Application US/08583562B
570
ATION:
Staunton, Donald
Harris, Edith
ENTION: Cytoplasmic Modulators of Integrin
ENTION: Binding
SEQUENCES: 36
ICE ADDRESS:
: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sears Tower
icago
Illinois
USA
6
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
ICATION DATA:
IN NUMBER: US/08/583,562B
PE:
ATION: 536
ENT INFORMATION:
liams Jr., Joseph A.
ON NUMBER: 38,659
/DOCKET NUMBER: 27866/33033
ATION INFORMATION:
: 312-474-6300
312-474-0448
R SEQ ID NO: 4:
ARACTERISTICS:
10 base pairs
leic acid
SS: single
linear
PE: cDNA

70.9%; Score 15.6; DB 2; Length 30;
larity 81.8%; Pred. No. 73;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTGCGGA 22
|||||
CAGTCCCACTCTCTGAGGA 5

Application US/08779113
891
ATION:
Staunton, Donald E.
Harris, Edith S.
ENTION: Cytoplasmic Modulators of Integrin
ENTION: Binding
SEQUENCES: 65
ICE ADDRESS:
: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sears Tower
icago
Illinois
United States of America
6
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
ICATION DATA:
```

```
;
; APPLICATION NUMBER: US/08/779,113
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Greta E. No. 594889land
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33773
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-779-113-4

Query Match 70.9%; Score 15.6; DB 2; Length 30;
Best Local Similarity 81.8%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCAGTCTCTGCGGA 22
Db 26 AGACGTCCCACTCTCTGAGGA 5

RESULT 5
US-07-647-655C-4
; Sequence 4, Application US/07647655C
; Patent No. 5364759
; GENERAL INFORMATION:
; APPLICANT: Albert O. Edwards and
; APPLICANT: Charles Thomas Caskey
; TITLE OF INVENTION: DNA profiling with short
; TITLE OF INVENTION: tandem repeat polymorphisms and identifica
; TITLE OF INVENTION: STRS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski Patent Department
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk 3.5 inch (1.44MB)
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: BASIC
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/647,655C
; FILING DATE: 19910131
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: THOMAS D. PAUL
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 651-5325
; TELEFAX: (713) 651-5246
; TELEX: WESTERN UNION 762829
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Synthetic DNA
```

61.8%; Score 13.6; DB 1; Length 24;  
ilarity 80.0%; Pred. No. 6.9e+02;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTGCGG 21  
|||||  
GAATCGTGTCTCTGCGG 23

pplication US/09331793  
0646  
ATION:  
URIYAMA, Shinichi  
ASEGAWA, Takashi  
NTION: CELL MEMBRANE DIRECTED DRUGS  
E: 1110-253P  
CATION NUMBER: US/09/331,793  
G DATE: 1999-06-25  
ID NOS: 67  
atentIn version 3.0

nthetic DNA Primers

61.8%; Score 13.6; DB 4; Length 37;  
ilarity 80.0%; Pred. No. 7.4e+02;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTGCGG 21  
|||||  
TCTCAGTCTCTGCGG 28

/C  
plication US/08666354A  
0141  
MATION:  
KLAUSER, THOMAS  
KRAMER, JOACHIM  
MEYER, THOMAS F.  
POHLNER, JOHANNES  
VENTION: BACTERIA USED TO PRODUCE STABLE FUSION  
VENTION: PROTEINS AND METHOD FOR THEIR IDENTIFICATION  
SEQUENCES: 18  
NCE ADDRESS:  
BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
P.O. BOX 747  
LLS CHURCH  
A  
USA  
140-0747  
ADABLE FORM:  
PE: Floppy disk  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
PLICATION DATA:  
ION NUMBER: US/08/666,354A  
TE: 23-SEP-1996  
ATION: 435  
ENT INFORMATION:  
FENSON, LEONARD R.  
TION NUMBER: 30,330  
DOCKET NUMBER: 147-157P  
CATION INFORMATION:  
3: 703-205-8000

TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OLIGONUCLEOTIDE PRIMER"  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-666-354A-2

Query Match 61.8%; Score 13.6; DB 3; Length 44;  
Best Local Similarity 80.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACATCAGTCTCTGCGG 22  
Db 29 ACTGTCACTGTCTCTGCGAA 10

RESULT 8  
US-07-647-655C-2  
Sequence 2, Application US/07647655C  
Patent No. 5364759  
GENERAL INFORMATION:  
APPLICANT: Albert O. Edwards and  
APPLICANT: Charles Thomas Caskey  
TITLE OF INVENTION: DNA profiling with short  
TITLE OF INVENTION: tandem repeat polymorphisms and identific  
TITLE OF INVENTION: STRS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski Patent Department  
STREET: 1301 McKinney, Suite 5100  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3.5 inch (1.44MB)  
COMPUTER: IBM PC/AT  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: BASIC  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/647,655C  
FILING DATE: 19910131  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: THOMAS D. PAUL  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5217  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 651-5325  
TELEFAX: (713) 651-5246  
TELEX: WESTERN UNION 762829  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Synthetic DNA  
US-07-647-655C-2

Query Match 61.8%; Score 13.6; DB 1; Length 52;  
Best Local Similarity 80.0%; Pred. No. 7.8e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

AATCAGTCTCTGCGG 21  
|||||  
AATCGTGTCTCTGCGAG 51

lication US/09553690  
296

TION:  
scher, Robert L.  
oi, Yeonhee  
mon, Mike

e Regents of the University of California  
TION: Nucleic Acids That Control Seed and  
TION: Fruit Development in Plants

: 023070-099900US  
TION NUMBER: US/09/553,690

DATE: 2000-04-21

ID NOS: 50

tSEQ for Windows Version 3.0

ificial Sequence

TION: primer SKB-8

60.0%; Score 13.2; DB 4; Length 22;  
larity 83.3%; Pred. No. 1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AATCAGTCTCTGCG 19

|||||  
AATACCGTCTCTCC 1

/c  
plication US/08258026A  
637

ATION:  
Huang, Grace P.  
Rhode, Peter R.  
Stinson, Jeffrey R.  
Wong, Hing C.

ENTION: A METHOD FOR DISPLAYING PROTEINS

QUENCES: 26

CE ADDRESS:

David G. Conlin; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
30 WATER STREET

TON

SSACHUSETTS

US

9

DABLE FORM:

E: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

ICATION DATA:

N NUMBER: US/08/258,026A

E: 10-JUN-1994

TION: 435

NT INFORMATION:

nick, David R.

ON NUMBER: 34235

DOCKET NUMBER: 42838

ATION INFORMATION:

(617) 523-3400

(617) 523-6400

TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

US-08-258-026A-10

Query Match

Best Local Similarity 60.0%; Score 13.2; DB 1; Length 35;

Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCAGTCTCTGCGG 21

|||||

Db 32 CASTCAGTCTCYKAG 15

RESULT 11

US-09-097-055B-73/c

; Sequence 73, Application US/09097055B

; Patent No. 6610293

; GENERAL INFORMATION:

APPLICANT: Fischer, Gerald W.

Schuman, Richard F.

Wong, Hing

Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND

CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEI

POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

DUNNER, LLP

STREET: 1300 I Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,055B

FILING DATE: 15-Jun-1998

ATTORNEY/AGENT INFORMATION:

NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 73:

US-09-097-055B-73

Query Match

Best Local Similarity 60.0%; Score 13.2; DB 4; Length 35;

Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCAGTCTCTGCGG 21

|||||

Db 32 CASTCAGTCTCYKAG 15

09:38:24 2004

us-10-090-326-6.max.rni

3/c  
Application PC/TUS9507541  
ATION: Huang, Grace P.  
Rhode, Peter R.  
Stinson, Jeffrey R.  
Wong, Hing C.  
VENTION: A METHOD FOR DISPLAYING  
SEQUENCES: 24  
NCE ADDRESS:  
: David G. Conlin; DIKE, BRONSTEIN,  
: ROBERTS & CUSHMAN  
130 WATER STREET  
STON  
ASSACHUSETTS  
US  
09  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patentin Release #1.0, Version #1.25  
ICATION DATA:  
ON NUMBER: PCT/US95/07541  
TE:  
ATION:  
ATION DATA:  
ON NUMBER: US 08/258,026  
TE: 10-JUN-1994  
ENT INFORMATION:  
snick, David R.  
ION NUMBER: 34235  
/DOCKET NUMBER: 42838  
ATION INFORMATION:  
: (617) 523-3400  
(617) 523-6400  
00291 STRE UR  
OR SEQ ID NO: 10:  
APACTERISTICS:  
35 base pairs  
leic acid  
SSS: unknown  
unknown  
0  
ilarity 60.0%; Score 13.2; DB 5; Length 35;  
Conservative 72.2%; Pred. No. 1.2e+03;  
3; Mismatches 2; Indels 0; Gaps 0;  
ATCAGTCTCTGCGG 21  
STCAGTCTCTGCGG 15  
73  
Application US/09422978  
7751  
ATION:  
hen, Daniel  
unfeld, Marta  
umakov, Ilya  
ATION: Biallelic markers for use in constructing a high density...  
E: GENSET.020CPI  
CATION NUMBER: US/09/422,978  
G DATE: 1999-10-20  
CATION NUMBER: US 09/298,850  
G DATE: 1999-04-21  
CATION NUMBER: US 60/109,732  
G DATE: 1998-11-23

; EARLIER APELICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1473  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-25379-389 : polymorphic base C or T  
US-09-422-978-1473  
Query Match 60.0%; Score 13.2; DB 4; Length 47;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 1; Mismatches 4; Indels 0;  
QY 2 GACAATCAGTCTCTGCGG 21  
DB 19 GAGCAYCACACTCTGCGG 38  
RESULT 14  
US-07-977-284A-36/c  
; Sequence 36, Application US/07977284A  
; Patent No. 5558988  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; APPLICANT: Ala-Kokko, Leena  
; APPLICANT: Williams, Charlene J.  
; APPLICANT: Ritvaniemi, Pertti  
; APPLICANT: Baldwin, Clinton  
; APPLICANT: Hopkinson, Ian  
; APPLICANT: Ahmad, Nilofar Nina  
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC  
; TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS  
; NUMBER OF SEQUENCES: 261  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,284A  
; FILING DATE: 13-NOV-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeLuca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-0697  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: LINEAR  
; ANTI-SENSE: YES  
US-07-977-284A-36  
Query Match 59.1%; Score 13; DB 1; Length 22;



us-10-090-326-6.max.rni

GENERAL INFORMATION:  
 APPLICANT: Chenchik, Alex  
 APPLICANT: Jokhadze, George

APPLICANT: Jokhadze, George  
 APPLICANT: Bibilashvili, Robert  
 TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
 TITLE OF INVENTION: EXPRESSION  
 NUMBER OF SEQUENCES: 1375

ADDRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA

STATE: CA  
COUNTRY: US  
ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEO for Windows

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21 MAY 1997

FILING DATE: 21-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE: \_\_\_\_\_  
 ATTORNEY/AGENT NAME: Field Bret E

REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001

TELECOMMUNICATION INFORMATION  
TELEPHONE: 415-322-507  
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1112:  
SEQUENCE CHARACTERISTICS.

LENGTH: 28 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA

**FEATURE:** OTHER INFORMATION. Click

5-08-859-998-1112

Query Match 59.1%

Best Local Similarity 76.24  
Matches 16; Conservative

AGACAAATCACAGTCTCTC

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

8 ACACAAACACATTTCTCA

RESULT 17

4-09-225-928-1112  
Sequence 1112 Application 1112

Patent No. 6352829

GENERAL INFORMATION:  
APPLICANT: Chenchik, A

Jokhadze, O  
Bibilashvili

TITLE OF INVENTION: MEM EX

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESSEE: ADDRESSEE: Fish &

STREET: 2200 Sand  
CITY: Menlo Park

STATE: CA  
COUNTRY: US

COUNTRY: US  
ZIP: 94025

COMPUTER READABLE FORM  
MEDIUM TYPE: Disk

09:38:24 2004

us-10-090-326-6.max.rni

MPUTER: IBM Compatible  
ERATING SYSTEM: Windows95  
FTWARE: FastSEQ for Windows Version 2.0  
APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
LING DATE: 05-Jan-1999  
ASSIFICATION: <Unknown>  
PLICATION DATA:  
PLICATION NUMBER: 08/859,998  
LING DATE: 21-MAY-1997  
Y/AGENT INFORMATION:  
ME: Field, Bret E.  
GISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
MUNICATION INFORMATION:  
LEPHONE: 415-322-5070  
LEFAX: 415-854-0875  
FOR SEQ ID NO: 1112:  
E CHARACTERISTICS:  
NGTH: 28 base pairs  
PE: nucleic acid  
RANDEDNESS: single  
POLOGY: linear  
E TYPE: DNA  
:  
HER INFORMATION: oligonucleotide primer  
E DESCRIPTION: SEQ ID NO: 1112:  
12  
59.1%; Score 13; DB 4; Length 28;  
ilarity 76.2%; Pred. No. 1.4e+03;  
Conservative 0; Mismatches 5; Indels 0;  
ACAATCACAGTCTCTGCGG 21  
|||||  
ACAAACACATCTCAGTGG 28  
112  
Application US/09225201B  
9455  
3MATION:  
NT: Chenchik, Alex  
Jokhadze, George  
Bibilashvili, Robert  
F INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
OF SEQUENCES: 1375  
NDENCE ADDRESS:  
RESSEE: Fish & Richardson, P.C.  
REET: 2200 Sand Hill Road, Suite 100  
TY: Menlo Park  
ATE: CA  
NTRY: US  
P: 94025  
R READABLE FORM:  
IUM TYPE: Diskette  
PUTER: IBM Compatible  
RATING SYSTEM: Windows95  
TWARE: FastSEQ for Windows Version 2.0  
APPLICATION DATA:  
PLICATION NUMBER: US/09/225,201B  
LING DATE: 05-Jan-1999  
ASSIFICATION: <Unknown>  
PLICATION DATA:  
PLICATION NUMBER: US/08/859,998  
LING DATE: 21-MAY-1997  
Y/AGENT INFORMATION:  
ME: Field, Bret E.  
ISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
MUNICATION INFORMATION:

TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 1112:  
US-09-225-201B-1112  
Query Match 59.1%; Score 13; DB 4; Length 28;  
Best Local Similarity 76.2%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
Qy 1 AGACATCACAGTCTCTGCGG 21  
Db 8 ACACAAACATCTCAGTGG 28  
|||||  
RESULT 19  
US-08-361-337-13  
Sequence 13, Application US/08361337  
Patent No. 5728519  
GENERAL INFORMATION:  
APPLICANT: Levenbook, Inessa S.  
APPLICANT: Chumakov, Konstantin M.  
APPLICANT: No. 5728519wood, Laurie P.  
APPLICANT: Roninson, Igor  
TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF  
ATTENUATED LIVE VACCINES  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: 127 Peachtree Street, N.E.  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,337  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perryman, David G.  
REGISTRATION NUMBER: 33,438  
REFERENCE/DOCKET NUMBER: 1414.634  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-361-337-13  
Query Match 59.1%; Score 13; DB 1; Length 34;  
Best Local Similarity 76.2%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
Qy 2 GACAATCACAGTCTCTGCGGA 22  
|||||

09:38:24 2004

us-10-090-326-6.max.rni

AATCAGATTCTGAGCA 34

2/c  
Application US/09422978

751

ION:

en, Daniel

nenfeld, Marta

nakov, Ilya

ION: Biallelic markers for use in constructing a high density...

: GENSEI.020CPI

ATION NUMBER: US/09/422,978

DATE: 1999-10-20

ATION NUMBER: US 09/298,850

DATE: 1999-04-21

ATION NUMBER: US 60/109,732

DATE: 1998-11-23

ATION NUMBER: US 60/082,614

DATE: 1998-04-21

ID NOS: 11796

o Sapiens

ele

TION: 99-4679-240 : polymorphic base C or T

2

58.2%; Score 12.8; DB 4; Length 47;

larity 77.8%; Pred. No. 1.9e+03;

Conservative 1; Mismatches 3; Indels 0; Gaps 0;

TCACAGTCTCTCGGG 21

|||||

TCTCAGTCTCTCCG 21

/c  
plication US/09097055B

293

MATION:

T: Fischer, Gerald W.

Schuman, Richard F.

Wong, Hing

Stinson, Jeffrey L.

INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND  
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM  
POSITIVE BACTERIA

F SEQUENCES: 89

NDENCE ADDRESS:

RESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

DUNNER, LLP

EET: 1300 I Street, NW

Y: Washington

TE: DC

NTY: USA

: 20005-3315

READABLE FORM:

IUM TYPE: Floppy disk

PUTER: IBM PC compatible

RATING SYSTEM: PC-DOS/MS-DOS

TWARE: Patent in Release #1.0, Version #1.30

APPLICATION DATA:

LICATION NUMBER: US/09/097,055B

ING DATE: 15-Jun-1998

/AGENT INFORMATION:

E: Einaudi, Carol P.

ISTRATION NUMBER: 32,220

; REFERENCE/DOCKET NUMBER: 04995.0041-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-097-055B-74

Query Match

Best Local Similarity 57.3%; Score 12.6; DB 4; Length 35;

Matches 13; Conservative 3; Mismatches 3; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 21

|||||

Db 33 ACKSTCACHGTCTCYKAG 15

RESULT 22

US-09-422-978-3196/c

; Sequence 3196, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a hi

; FILE REFERENCE: GENSEI.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 3196

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 99-24480-44 : polymorphic base A or C

US-09-422-978-3196

Query Match

Best Local Similarity 57.3%; Score 12.6; DB 4; Length 47;

Matches 12; Conservative 2; Mismatches 1; Indels 0;

QY 8 CACAGTCTCTCTGCGGA 22

|||||

Db 16 CACAGTCTCTGCGSM 2

RESULT 23

US-08-472-194A-29

; Sequence 29, Application US/08472194A

; Patent No. 5807718

; GENERAL INFORMATION:

; APPLICANT: Joyce, Gerald F

; APPLICANT: Breaker, Ronald R

; TITLE OF INVENTION: ENZYMAIC DNA MOLECULES

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

09:38:24 2004

us-10-090-326-6.max.rni

Patent Counsel  
.0550 No. 5807718th Torrey Pines Road, TPC 8  
Jolla

USA  
ADABLE FORM:  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
ICATION DATA: US/08/472,194A

IN NUMBER: US/08/472,194A

IE: 07-JUN-1995

ATION: 536

ATION DATA:

IN NUMBER: US 08/349,023

IE: 02-DEC-1994

ENT INFORMATION:

iting, Thomas

ON NUMBER: 34,163

DOCKET NUMBER: TSRI 463.1

ATION INFORMATION:

619-784-2937

619-784-9399

OR SEQ ID NO: 29:

ARACTERISTICS:

18 base pairs

leic acid

3SS: single

linear

2E: DNA (genomic)

,

ilarity 57.3%; Score 12.6; DB 1; Length 48;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTCTGC 19

||||| ||| |||

TCCATCACACTCTGTGC 29

Application US/09262142B

462

ATION:

bas, Carlos F.

/ce, Gerald

atoro, Stephen W.

adasamy, Sakthivel

ATION: ENZYMATIC DNA MOLECULES THAT CONTAIN MODIFIED

ATION: NUCLEOTIDES

3: SCR21448

ATION NUMBER: US/09/262,142B

3 DATE: 1999-03-03

ID NOS: 58

antIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: DNA enzyme

ilarity 57.3%; Score 12.6; DB 3; Length 48;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTCTGC 19

||||| ||| |||

Db 11 AGTCCATCACACTCTGTGC 29

RESULT 25

US-08-849-567A-29

; Sequence 29, Application US/08849567A

; Patent No. 6326174

; GENERAL INFORMATION:

; APPLICANT: Joyce, Gerald F.

; APPLICANT: Breaker, Ronald R.

; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES

; FILE REFERENCE: SCR1943S

; CURRENT APPLICATION NUMBER: US/08/849,567A

; CURRENT FILING DATE: 1997-08-25

; PRIOR APPLICATION NUMBER: PCT/US95/15580

; PRIOR FILING DATE: 1995-12-01

; PRIOR APPLICATION NUMBER: 08/472,194

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/349,023

; PRIOR FILING DATE: 1994-12-02

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29

; LENGTH: 48

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNA enzy

US-08-849-567A-29

Query Match

Best Local Similarity 57.3%; Score 12.6; DB 4; Length 48;

Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCACAGTCTGTGC 19

||||| ||| |||

Db 11 AGTCCATCACACTCTGTGC 29

RESULT 26

US-08-424-874-8/c

; Sequence 8, Application US/08424874

; Patent No. 5718915

; GENERAL INFORMATION:

; APPLICANT: Virtanen, Jorma A.

; APPLICANT: Virtanen, Sinikka

; TITLE OF INVENTION: BINDING MOLECULE MULTI ENZYME COMPLEXES

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,874

; FILING DATE: 19-APR-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 8218-006

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-3660

; TELEFAX: 415-854-3694

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 8:

09:38:24 2004

us-10-090-326-6.max.rni

RACTERISTICS:

9 base pairs  
leic acid  
SS: unknown  
unknown  
E: DNA (genomic)

misc feature

25..26

RMATION: /note= "Where Y =

RMATION: FMOC-DMT-SER-CEDIPPA = N-Fluorenylmethoxycarbonyl

RMATION: O-dimethoxytriphenyl serinyl cyanoethyl

RMATION: N,N-diisopropylphosphoramidite"

57.3%; Score 12.6; DB 1; Length 49;

larity 71.4%; Pred. No. 2.4e+03;

Conservative 1; Mismatches 5; Indels 0; Gaps 0;

AATCAGAGTCTGCGGA 22

|||||

AATCTAGACTGCGCA 12

plication US/08983607

470

ATION:

Alan Garen

Xiaohong Cai

ENTION: Human Anti-Tumor Monoclonal Anti-

ENTION: bodies

QUENCES: 51

CE ADDRESS:

Department of Molecular Biophysics

and Biochemistry, Yale University

66 Whitney Avenue

Haven

nnecticut

United States of America

0-8114

DABLE FORM:

E: 3.5" 1.44 Mb diskette

IBM PC

SYSTEM: MS DOS

Word Processing

ICATION DATA:

N NUMBER: US/08/983,607

E: April 27, 1998

TION: 435

ATION DATA:

N NUMBER: PCT/IB96/01032

E: June 28, 1996

TION: 435

NT INFORMATION:

/ M. Krinsky

ON NUMBER: 32423

DOCKET NUMBER: OCR-679

ATION INFORMATION:

203-773-9544

203-773-1183

R SEQ ID NO: 11:

RACTERISTICS:

9 residues

leic acid

SS: single

linear

E: DNA

N: primer used in constructs

57.3%; Score 12.6; DB 3; Length 59;

Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0;

Qy 6 ATCAGAGTCTGCGGA 22

|||||

Db 33 ATCAGAGTCTGYSYGA 49

RESULT 28

US-09-586-376-19/c

; Sequence 19, Application US/09586376

; Patent No. 6492115

; GENERAL INFORMATION:

; APPLICANT: Guida, Marco

; APPLICANT: Hall, Jeff

; TITLE OF INVENTION: GENETIC TYPING OF THE HUMAN CYTOCHROME P450 2

; TITLE OF INVENTION: AND RELATED MATERIALS AND METHODS

; FILE REFERENCE: 4389-20

; CURRENT APPLICATION NUMBER: US/09/586,376

; CURRENT FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-586-376-19

Query Match

56.4%; Score 12.4; DB 4; Length 17;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

Qy 1 AGACAATCACAGTC 14

|||||

Db 17 AGACCATCACAGTC 4

RESULT 29

US-10-082-260-8

; Sequence 8, Application US/10082260

; Patent No. 6506882

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang, et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

; FILE REFERENCE: PF253D1

; CURRENT APPLICATION NUMBER: US/10/082,260

; CURRENT FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 08/815,783

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812

; PRIOR FILING DATE: 1996-03-14

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 29

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-10-082-260-8

Query Match

56.4%; Score 12.4; DB 4; Length 29;

Best Local Similarity 92.9%; Pred. No. 2.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

Qy 3 ACAATCACAGTCTC 16

|||||

Db 10 ACAATCACAGTTTC 23

RESULT 30

US-10-082-260-10

; Sequence 10, Application US/10082260

16882  
 TATION:  
 I, Guo-Liang, et al.  
 INTION: Human Tumor Necrosis Factor Delta and Epsilon  
 E: PF253D1  
 CATION NUMBER: US/10/082,260  
 IG DATE: 2002-02-26  
 TION NUMBER: 08/815,783  
 DATE: 1997-03-12  
 TION NUMBER: 60/016,812  
 DATE: 1996-03-14  
 ID NOS: 10  
 entIn Ver. 2.1

## tificial Sequence

ACTION: Primer

56.4%; Score 12.4; DB 4; Length 29;  
 ilarity 92.9%; Pred. No. 2.8e+03;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AATCACAGTCTC 16  
 |||||  
 AATCACAGTTTC 23

plication US/08815783  
 9170

MATION:  
 NI, JIAN  
 YU, GUO-LIANG  
 GENTZ, REINER  
 DILLON, PATRICK  
 VENTION: HUMAN TUMOR NECROSIS FACTOR DELTA AND  
 VENTION: EPSILON  
 EQUENCES: 10  
 NCE ADDRESS:  
 : HUMAN GENOME SCIENCES, INC.  
 9410 KEY WEST AVENUE  
 CKVILLE  
 D  
 US  
 50

ADABLE FORM:  
 PE: Floppy disk  
 IBM PC compatible  
 SYSTEM: PC-DOS/MS-DOS  
 PatentIn Release #1.0, Version #1.30  
 CATION DATA:  
 ON NUMBER: US/08/815,783  
 IE:

ATION: 514  
 ENT INFORMATION:  
 BALL, PAUL C  
 ION NUMBER: 34,610  
 /DOCKET NUMBER: PF253  
 CATION INFORMATION:  
 : (301) 309-8504  
 (301) 309-8512  
 OR SEQ ID NO: 8:  
 ARACTERISTICS:  
 29 base pairs  
 leic acid  
 3SS: single  
 linear  
 PE: DNA (genomic)

Query Match 56.4%; Score 12.4; DB 4; Length 29;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16  
 |||||  
 Db 10 ACAATCACAGTTTC 23

## RESULT 32

US-08-815-783-10  
 ; Sequence 10, Application US/08815783  
 ; Patent No. 6509170  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: YU, GUO-LIANG  
 ; APPLICANT: GENTZ, REINER  
 ; APPLICANT: DILLON, PATRICK  
 ; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR DELTA AND  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 ; STREET: 9410 KEY WEST AVENUE  
 ; CITY: ROCKVILLE  
 ; STATE: MD  
 ; COUNTRY: US  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/815,783  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KIMBALL, PAUL C  
 ; REGISTRATION NUMBER: 34,610  
 ; REFERENCE/DOCKET NUMBER: PF253  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 29 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-815-783-10

Query Match 56.4%; Score 12.4; DB 4; Length 29;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16  
 |||||  
 Db 10 ACAATCACAGTTTC 23

## RESULT 33

US-09-879-919-8  
 ; Sequence 8, Application US/09879919  
 ; Patent No. 6541224  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Guo-Liang, et al.  
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
 ; FILE REFERENCE: PF253P1  
 ; CURRENT APPLICATION NUMBER: US/09/879,919  
 ; CURRENT FILING DATE: 2001-06-14

09:38:24 2004

us-10-090-326-6.max.rn1

ION NUMBER: 60/293,499  
DATE: 2001-05-25  
ION NUMBER: 60/277,978  
DATE: 2001-03-23  
ION NUMBER: 60/276,248  
DATE: 2001-03-16  
ION NUMBER: 60/254,875  
DATE: 2000-12-13  
ION NUMBER: 60/241,952  
DATE: 2000-10-23  
ION NUMBER: 60/211,537  
DATE: 2000-06-15  
ION NUMBER: 08/815,783  
DATE: 1997-03-12  
ION NUMBER: 60/016,812  
DATE: 1996-03-14  
ID NOS: 26  
ntIn Ver. 2.1

no sapiens

56.4%; Score 12.4; DB 4; Length 29;  
larity 92.9%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LATCACAGTCTC 16  
|||||  
LATCACAGTCTC 23

pplication US/09879919

224  
ATION:

Guo-Liang, et al.  
ATION: Human Tumor Necrosis Factor Delta and Epsilon

3: PF253P1

ATION NUMBER: US/09/879,919

; DATE: 2001-06-14

ION NUMBER: 60/293,499

DATE: 2001-05-25

ION NUMBER: 60/277,978

DATE: 2001-03-23

ION NUMBER: 60/276,248

DATE: 2001-03-16

ION NUMBER: 60/254,875

DATE: 2000-12-13

ION NUMBER: 60/241,952

DATE: 2000-10-23

ION NUMBER: 60/211,537

DATE: 2000-06-15

ION NUMBER: 08/815,783

DATE: 1997-03-12

ION NUMBER: 60/016,812

DATE: 1996-03-14

ID NOS: 26

ntIn Ver. 2.1

no sapiens

56.4%; Score 12.4; DB 4; Length 29;  
larity 92.9%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LATCACAGTCTC 16  
|||||

Db 10 ACAATCACAGTCTC 23

RESULT 35

US-08-871-488A-6

; Sequence 6, Application US/08871488A

; Patent No. 6358710

; GENERAL INFORMATION:

; APPLICANT: Graves, Scott S.

; APPLICANT: Reno, John M.

; APPLICANT: Mallett, Robert W.

; APPLICANT: Hylarides, Mark D.

; APPLICANT: Searle, Stephen M.J.

; APPLICANT: Henry, Andrew H.

; APPLICANT: Pedersen, Jan T.

; APPLICANT: Rees, Anthony R.

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE

; TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THE

; TITLE OF INVENTION: PRETARGETING METHODS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; City: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/871,488A

; FILING DATE: 09-JUN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey Ph.D., Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 690022.527C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-871-488A-6

Query Match 56.4%; Score 12.4; DB 4; Length 30;

Best Local Similarity 92.9%; Pred. No. 2.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16

|||||

Db 15 ACCATCACAGTCTC 28

RESULT 36

US-09-123-030-4/c

; Sequence 4, Application US/09123030

; Patent No. 6365337

; GENERAL INFORMATION:

; APPLICANT: Letts, Verity A.

; APPLICANT: Frankel, Wayne N.

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Felix, Ricardo

; APPLICANT: Biddlecome, Gloria

; TITLE OF INVENTION: Genes Encoding Neuronal Voltage-Gated Calcium

; TITLE OF INVENTION: Gamma Subunits

; FILE REFERENCE: US App. 09/123,030

09:38:24 2004

us-10-090-326-6.max.rni

ATION NUMBER: US/09/123,030  
; DATE: 1998-07-27  
ID NOS: 40  
ntIn Ver. 2.0

inae gen. sp.

56.4%; Score 12.4; DB 4; Length 30;  
ilarity 72.7%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ACAATCACAGTCTCTGCGGA 22  
| | | | |  
3CCCTCAGCGCCCTGCGGA 9

pplication US/08779113

3891  
MARION:  
Staunton, Donald E.  
Harris, Edith S.  
VENTION: Cytoplasmic Modulators of Integrin  
VENTION: Binding  
SEQUENCES: 65

NCE ADDRESS:  
: Marshall, O'Toole, Gerstein, Murray & Borun  
233 South Wacker Drive, 6300 Sears Tower  
icago  
llinois  
United States of America

06  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
LOCATION DATA:  
ON NUMBER: US/08/779,113

TE:  
ATION: 536  
ENT INFORMATION:  
eta E. No. 594889land  
ION NUMBER: 35,302  
/DOCKET NUMBER: 27866/33773  
CATION INFORMATION:  
: 312-474-6300  
312-474-0448  
OR SEQ ID NO: 43:  
A CHARACTERISTICS:  
34 base pairs  
cleic acid  
ESS: single  
linear  
PE: other nucleic acid

56.4%; Score 12.4; DB 2; Length 34;  
ilarity 72.7%; Pred. No. 2.9e+03;  
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

IACAATCACAGTCTCTGCGGA 22  
| | | | |  
IACCTGACCCACTCTCTGAGGA 34

I/C  
pplication US/08779113

; Patent No. 5948891  
; GENERAL INFORMATION:  
; APPLICANT: Staunton, Donald E.  
; APPLICANT: Harris, Edith S.  
; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin  
; TITLE OF INVENTION: Binding  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,113  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Greca E. No. 594889land  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33773  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; US-08-779-113-44

Query Match 56.4%; Score 12.4; DB 2; Length 34;  
Best Local Similarity 72.7%; Pred. No. 2.9e+03;  
Matches 16; Cnervative 0; Mismatches 6; Indels 0;

Qy 1 AGACATCACAGTCTCTGCGGA 22  
| | | | |  
Db 22 AGACTGACCCACTCTCTGAGGA 1

RESULT 39  
US-08-899-241-220/c  
; Sequence 220, Application US/08899241A  
; Patent No. 6322995  
; GENERAL INFORMATION:  
; APPLICANT: Hohmann, Hans-Peter  
; APPLICANT: Huembelin, Markus  
; APPLICANT: van Loon, Adolphus  
; APPLICANT: Schurter, Walter  
; TITLE OF INVENTION: Improved Riboflavin Production  
; FILE REFERENCE: Improved Riboflavin Prod  
; CURRENT APPLICATION NUMBER: US/08/899,241A  
; CURRENT FILING DATE: 1997-07-23  
; EARLIER APPLICATION NUMBER: 96111905.4  
; EARLIER FILING DATE: 1996-07-24  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 220  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Bacillus subtilis  
; US-08-899-241-220

Query Match 56.4%; Score 12.4; DB 4; Length 35;  
Best Local Similarity 92.9%; Pred. No. 2.9e+03;



09:38:24 2004

us-10-090-326-6.max.rni

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ACAGCTCTGC 19  
|||||  
ACAGCTCTGC 4

Application US/08483695  
;139

ATION:  
Brechot, Christian  
Kremsdorf, Dina

Porchon, Colette

ENTION: Nucleotide and Peptide Sequences of a  
ENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
SEQUENCES: 46

ICE ADDRESS:  
Finnegan, Henderson, Farabow, Garrett &  
Dunner  
300 I Street, N.W.  
Washington

USA

5-3315

ADABLE FORM:

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25

ICATION DATA:

N NUMBER: US/08/483,695

E:

ATION:

N NUMBER: US/07/965,285

E: 18-MAR-1993

N NUMBER: FR 91 06 882

E: 06-JUN-1991

NT INFORMATION:

ers, Kenneth J.

ON NUMBER: 25,146

DOCKET NUMBER: 05286-0001-00000

ATION INFORMATION:

202-408-4000

202-408-4400

R SEQ ID NO: 19:

ACTERISTICS:

0 base pairs

leic acid

SS: single

linear

E: Other

N: DNA probe

56.4%; Score 12.4; DB 2; Length 40;

larity 72.7%; Pred. No. 2.9e+03;

Conservative 0; Mismatches 6; Indels 0; Gaps 0;

CAATCAGCTCTCTGCGGA 22

|||||

CAATCAGCTCTCTGCGGA 34

plication US/07965285

904

ATION:

Brechot, Christian

APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/965,285

FILING DATE: 18-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 06 882

FILING DATE: 06-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05286-0001-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other

DESCRIPTION: DNA probe

US-07-965-285-19

Query Match

Best Local Similarity 56.4%; Score 12.4; DB 2; Length 40;

Matches 16; Conservative 0; Mismatches 6; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGGA 22

Db 13 AGACAATCACAGTCTCTGCGGA 34

RESULT 42

US-08-487-231-19

; Sequence 19, Application US/08487231

; Patent No. 5919454

; GENERAL INFORMATION:

APPLICANT: Brechot, Christian

APPLICANT: Kremsdorf, Dina

APPLICANT: Porchon, Colette

TITLE OF INVENTION: Nucleotide and Peptide Sequences of a

TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and T

TITLE OF INVENTION: Applications

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

09:38:24 2004

us-10-090-326-6.max.rni

PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patentin Release #1.0, Version #1.25  
LICATON DATA:  
ON NUMBER: US/08/487,231  
TE: 07-JUNE-1995  
ATION: 435  
CATION DATA:  
ON NUMBER: US 07/965,285  
TE: 18-MAR-1993  
ATION: 435  
CATION DATA:  
ON NUMBER: FR 91 06 882  
TE: 06-JUN-1991  
ENT INFORMATION:  
yers, Kenneth J.  
ION NUMBER: 25,146  
/DOCKET NUMBER: 05286-0001-02000  
CATION INFORMATION:  
: 202-408-4000  
: 202-408-4400  
OR SEQ ID NO: 19:  
ARACTERISTICS:  
40 base pairs  
cleic acid  
ESS: single  
linear  
PE: Other  
ON: DNA probe  
56.4%; Score 12.4; DB 2; Length 40;  
ilarity 72.7%; Pred. No. 2.9e+03;  
Conservative 0; Mismatches 6; Indels 0;  
Gaps 0;  
JACAAATCACAGTCTCTGCGGA 22  
|||||  
JACAAATCACGCTCCCGCAGGA 34  
Application US/09201912  
0962  
INATION:  
Brechot, Christian  
Kremsdorf, Dina  
Porchon, Colette  
VENTION: Nucleotide and Peptide Sequences of a  
VENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
SEQUENCES: 46  
NCE ADDRESS:  
3: Finnegan, Henderson, Farabow, Garret &  
3: Dunner  
1300 I Street, N.W.  
ashington  
DC  
USA  
005-3315  
EADABLE FORM:  
YPE: Floppy disk  
: IBM PC compatible  
3 SYSTEM: PC-DOS/MS-DOS  
: Patentin Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/09/201,912  
ATE:  
CATION:  
ICATION DATA:  
ION NUMBER: 07/965,285  
ATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-09-201-912-19  
Query Match 56.4%; Score 12.4; DB 3; Length 40;  
Best Local Similarity 72.7%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0;  
QY 1 AGACAATCACAGTCTCTGCGGA 22  
DB 13 AGACAATCACGCTCCCGCAGGA 34  
RESULT 44  
US-09-422-978-2788/c  
Sequence 2788, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a  
FILE REFERENCE: GENSET 020CPI  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2788  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-18717-319 : polymorphic base T or A  
US-09-422-978-2788  
Query Match 56.4%; Score 12.4; DB 4; Length 47;  
Best Local Similarity 81.2%; Pred. No. 3e+03;  
Matches 13; Conservative 1; Mismatches 2; Indels 0;  
QY 7 TCACAGTCTCTGCGGA 22  
DB 34 TCACATTCCTGCTGA 19  
RESULT 45  
US-08-949-155-45/c  
Sequence 45, Application US/08949155  
Patent No. 6271436  
GENERAL INFORMATION:  
APPLICANT: Piedrahita, Jorge A  
APPLICANT: Bazer, Fuller W  
TITLE OF INVENTION: Compositions and Methods for the  
Generation of Transgenic Animal Species

09:38:24 2004

us-10-090-326-6.max.rni

SEQUENCES: 51  
DE ADDRESS:  
ARNOLD, WHITE AND DURKEE  
O. Box 4433  
ston  
JS  
0-4433  
TABLE FORM:  
3: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
LOCATION DATA:  
4 NUMBER: US/08/949,155  
3: Concurrently Herewith  
TION: 800  
ATION DATA:  
4 NUMBER: US 60/027,338  
3: 11-OCT-1996  
ATION DATA:  
4 NUMBER: US 60/046,094  
3: 09-MAY-1997  
NT INFORMATION:  
ler, David W.  
ON NUMBER: 41,071  
DOCKET NUMBER: TANK:177  
ATION INFORMATION:  
(512) 418-3000  
(713) 789-2679  
R SEQ ID NO: 45:  
ACTERISTICS:  
2 base pairs  
leic acid  
SS: single  
linear  
55.5%; Score 12.2; DB 3; Length 22;  
larity 82.4%; Pred. No. 3.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
ATCACAGTCTCTGC 19  
|||||  
ATGACAGCCACTGC 3  
February 29, 2004, 11:22:04  
5 secs

09:38:24 2004

us-10-090-326-6.max.rnpb

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 09:43:45 ; Search time 135.143 Seconds  
(without alignments)  
587.262 Million cell updates/sec

S-10-090-326-6

agacaatcacagtctctgcgga 22

IDENTITY NUC

apop 10.0 , Gapext 1.0

353733 seqs, 1803733377 residues

its satisfying chosen parameters: 1448676

ngth: 0  
ngth: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Published Applications NA:\*

: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/ECT\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/ECTUS\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

SUMMARIES

#	query	arch	Length	DB	ID	Description
64.5	20	10	US-09-931-375A-36			Sequence 36, Appl
64.5	60	10	US-09-908-975-15980			Sequence 15980, A
62.7	25	14	US-10-098-263B-53982			Sequence 53982, A
61.8	25	14	US-10-215-112-2523			Sequence 2523, Ap
61.8	25	14	US-10-215-112-2524			Sequence 2524, Ap
61.8	25	14	US-10-098-263B-61700			Sequence 61700, A
61.8	25	14	US-10-098-263B-126081			Sequence 126081, A
61.8	37	15	US-10-298-796-41			Sequence 41, Appl
61.8	60	10	US-09-908-975-6091			Sequence 6091, Ap
61.8	60	10	US-09-908-975-10366			Sequence 10366, A
61.8	60	10	US-09-908-975-14283			Sequence 14283, A
60.9	60	10	US-09-908-975-8908			Sequence 8908, Ap
60.0	20	15	US-10-189-256-66			Sequence 66, Appl
60.0	20	15	US-10-190-366-135			Sequence 135, App
60.0	20	15	US-10-190-366-332			Sequence 332, App

C	16	13.2	60.0	22	10	US-09-840-743-77	Sequence
	17	13.2	60.0	25	14	US-10-098-263B-65769	Sequence
C	18	13.2	60.0	25	14	US-10-098-263B-113912	Sequence
	19	13.2	60.0	25	14	US-10-098-263B-115691	Sequence
C	20	13.2	60.0	25	14	US-10-098-263B-123312	Sequence
C	21	13.2	60.0	35	9	US-09-893-615-73	Sequence
C	22	13.2	60.0	35	10	US-09-215-163-28	Sequence
C	23	13.2	60.0	35	15	US-10-601-171-73	Sequence
C	24	13.2	60.0	47	15	US-10-349-143-1473	Sequence
C	25	13.2	60.0	50	15	US-10-131-827-852	Sequence
C	26	13.2	60.0	60	10	US-09-908-975-19346	Sequence
C	27	13	59.1	25	14	US-10-098-263B-65781	Sequence
C	28	13	59.1	25	14	US-10-098-263B-113313	Sequence
C	29	13	59.1	25	14	US-10-098-263B-113314	Sequence
C	30	13	59.1	50	9	US-09-795-006A-31	Sequence
C	31	13	59.1	50	15	US-10-131-827-505	Sequence
C	32	13	59.1	60	9	US-09-795-006A-40	Sequence
C	33	13	59.1	60	10	US-09-908-975-19195	Sequence
C	34	13	59.1	60	10	US-09-908-975-20408	Sequence
C	35	13	59.1	60	10	US-09-908-975-20972	Sequence
C	36	13	59.1	60	10	US-09-908-975-23253	Sequence
C	37	12.8	58.2	17	14	US-10-156-306-4767	Sequence
C	38	12.8	58.2	17	14	US-10-156-306-5763	Sequence
C	39	12.8	58.2	20	9	US-09-833-087-16	Sequence
C	40	12.8	58.2	20	9	US-09-833-079-21	Sequence
C	41	12.8	58.2	22	9	US-09-797-207-16	Sequence
C	42	12.8	58.2	22	12	US-10-445-318-16	Sequence
C	43	12.8	58.2	25	14	US-10-098-263B-12151	Sequence
C	44	12.8	58.2	25	14	US-10-098-263B-33483	Sequence
C	45	12.8	58.2	25	14	US-10-098-263B-86605	Sequence
C	46	12.8	58.2	35	15	US-10-323-903-12	Sequence
C	47	12.8	58.2	47	15	US-10-349-143-1562	Sequence
C	48	12.8	58.2	56	15	US-10-403-337-34	Sequence
C	49	12.8	58.2	56	15	US-10-351-890-34	Sequence
C	50	12.8	58.2	60	10	US-09-908-975-7592	Sequence
C	51	12.8	58.2	60	10	US-09-908-975-18033	Sequence
C	52	12.6	57.3	60	10	US-09-908-975-22535	Sequence
C	53	12.6	57.3	24	10	US-09-940-185-1219	Sequence
C	54	12.6	57.3	25	14	US-10-098-263B-78812	Sequence
C	55	12.6	57.3	25	14	US-10-032-585-5037	Sequence
C	56	12.6	57.3	35	9	US-09-893-615-74	Sequence
C	57	12.6	57.3	35	10	US-09-215-163-29	Sequence
C	58	12.6	57.3	35	15	US-10-601-171-74	Sequence
C	59	12.6	57.3	39	9	US-09-263-959-166	Sequence
C	60	12.6	57.3	47	15	US-10-349-143-3196	Sequence
C	61	12.6	57.3	59	14	US-10-085-959-6	Sequence
C	62	12.6	57.3	60	10	US-09-908-975-14347	Sequence
C	63	12.6	57.3	60	10	US-09-908-975-14729	Sequence
C	64	12.6	57.3	60	10	US-09-908-975-15029	Sequence
C	65	12.6	57.3	60	10	US-09-908-975-16438	Sequence
C	66	12.6	57.3	60	10	US-09-908-975-22908	Sequence
C	67	12.4	56.4	17	14	US-10-232-634-19	Sequence
C	68	12.4	56.4	17	14	US-10-156-306-4765	Sequence
C	69	12.4	56.4	17	14	US-10-156-306-4766	Sequence
C	70	12.4	56.4	17	14	US-10-339-782-373	Sequence
C	71	12.4	56.4	24	9	US-09-978-295A-111	Sequence
C	72	12.4	56.4	24	9	US-09-978-697-111	Sequence
C	73	12.4	56.4	24	9	US-09-978-192A-111	Sequence
C	74	12.4	56.4	24	9	US-09-999-832A-111	Sequence
C	75	12.4	56.4	24	10	US-09-978-189-111	Sequence
C	76	12.4	56.4	24	10	US-09-978-608A-111	Sequence
C	77	12.4	56.4	24	10	US-09-978-585A-111	Sequence
C	78	12.4	56.4	24	10	US-09-978-191A-111	Sequence
C	79	12.4	56.4	24	10	US-09-978-403A-111	Sequence
C	80	12.4	56.4	24	10	US-09-978-564A-111	Sequence
C	81	12.4	56.4	24	10	US-09-999-833A-111	Sequence
C	82	12.4	56.4	24	10	US-09-981-915A-111	Sequence
C	83	12.4	56.4	24	10	US-09-978-824-111	Sequence
C	84	12.4	56.4	24	10	US-09-918-585A-111	Sequence
C	85	12.4	56.4	24	10	US-09-978-423A-111	Sequence
C	86	12.4	56.4	24	10	US-09-978-193A-111	Sequence
C	87	12.4	56.4	24	10	US-09-999-830A-111	Sequence
C	88	12.4	56.4	24	10	US-09-978-757A-111	Sequence

56.4	24	10	US-09-978-187B-111	Sequence 111, App	162	12.4	56.4	50	15	US-10-131-827-7596	Sequence
56.4	24	10	US-09-978-643A-111	Sequence 111, App	163	12.4	56.4	60	10	US-09-908-975-5192	Sequence
56.4	24	10	US-09-978-375A-111	Sequence 111, App	164	12.4	56.4	60	10	US-09-908-975-7100	Sequence
56.4	24	10	US-09-978-298A-111	Sequence 111, App	165	12.4	56.4	60	10	US-09-908-975-14708	Sequence
56.4	24	10	US-09-978-188A-111	Sequence 111, App	166	12.4	56.4	60	10	US-09-908-975-16665	Sequence
56.4	24	10	US-09-978-681A-111	Sequence 111, App	167	12.4	56.4	60	10	US-09-908-975-18083	Sequence
56.4	24	10	US-09-978-194A-111	Sequence 111, App	168	12.4	56.4	60	10	US-09-908-975-19802	Sequence
56.4	24	10	US-09-999-829A-111	Sequence 111, App	169	12.4	56.4	60	10	US-09-908-975-32238	Sequence
56.4	24	10	US-09-978-299A-111	Sequence 111, App	170	12.2	55.5	20	14	US-10-219-834-53	Sequence
56.4	24	10	US-09-978-544A-111	Sequence 111, App	171	12.2	55.5	20	14	US-10-219-834-151	Sequence
56.4	24	10	US-09-978-665A-111	Sequence 111, App	172	12.2	55.5	23	9	US-09-969-373-3963	Sequence
56.4	24	10	US-09-978-802A-111	Sequence 111, App	173	12.2	55.5	25	14	US-10-215-112-6834	Sequence
56.4	24	12	US-10-164-749A-111	Sequence 111, App	174	12.2	55.5	25	14	US-10-098-263B-424	Sequence
56.4	24	14	US-10-017-081A-111	Sequence 111, App	175	12.2	55.5	25	14	US-10-098-263B-1730	Sequence
56.4	24	14	US-10-167-749-111	Sequence 111, App	176	12.2	55.5	25	14	US-10-098-263B-37626	Sequence
56.4	24	14	US-10-013-921A-111	Sequence 111, App	177	12.2	55.5	25	14	US-10-098-263B-50612	Sequence
56.4	24	14	US-10-013-929A-111	Sequence 111, App	178	12.2	55.5	25	14	US-10-098-263B-53981	Sequence
56.4	24	14	US-10-016-177A-111	Sequence 111, App	179	12.2	55.5	25	14	US-10-098-263B-56309	Sequence
56.4	24	14	US-10-166-709A-111	Sequence 111, App	180	12.2	55.5	25	14	US-10-098-263B-68715	Sequence
56.4	24	14	US-10-143-031A-111	Sequence 111, App	181	12.2	55.5	25	14	US-10-098-263B-85815	Sequence
56.4	24	14	US-10-143-030A-111	Sequence 111, App	182	12.2	55.5	25	14	US-10-098-263B-120767	Sequence
56.4	24	14	US-10-002-967A-111	Sequence 111, App	183	12.2	55.5	25	14	US-10-032-585-4381	Sequence
56.4	24	14	US-10-017-083A-111	Sequence 111, App	184	12.2	55.5	29	13	US-10-114-893-225	Sequence
56.4	24	14	US-10-145-128A-111	Sequence 111, App	185	12.2	55.5	29	14	US-10-159-006-70	Sequence
56.4	24	14	US-10-017-191A-111	Sequence 111, App	186	12.2	55.5	36	14	US-09-874-547-78	Sequence
56.4	24	14	US-10-143-028A-111	Sequence 111, App	187	12.2	55.5	37	9	US-09-874-547-62	Sequence
56.4	24	14	US-10-143-029A-111	Sequence 111, App	188	12.2	55.5	38	9	US-09-874-547-76	Sequence
56.4	24	14	US-10-145-089A-111	Sequence 111, App	189	12.2	55.5	38	9	US-09-874-547-77	Sequence
56.4	24	14	US-10-165-067A-111	Sequence 111, App	190	12.2	55.5	38	9	US-09-874-547-79	Sequence
56.4	24	14	US-10-145-017A-111	Sequence 111, App	191	12.2	55.5	38	9	US-09-874-547-80	Sequence
56.4	24	14	US-10-164-728A-111	Sequence 111, App	192	12.2	55.5	38	9	US-09-874-547-84	Sequence
56.4	24	14	US-10-013-926A-111	Sequence 111, App	193	12.2	55.5	42	9	US-09-910-120-58	Sequence
56.4	24	14	US-10-165-247A-111	Sequence 111, App	194	12.2	55.5	42	14	US-10-341-226-58	Sequence
56.4	24	14	US-10-145-124A-111	Sequence 111, App	195	12.2	55.5	48	10	US-09-993-346-8	Sequence
56.4	24	14	US-10-160-502A-111	Sequence 111, App	196	12.2	55.5	49	10	US-09-993-346-79	Sequence
56.4	24	14	US-10-145-087A-111	Sequence 111, App	197	12.2	55.5	50	14	US-10-322-360-59	Sequence
56.4	24	14	US-10-017-086A-111	Sequence 111, App	198	12.2	55.5	50	14	US-10-322-360-135	Sequence
56.4	24	14	US-10-164-829A-111	Sequence 111, App	199	12.2	55.5	50	15	US-10-131-827-3200	Sequence
56.4	24	14	US-10-164-929A-111	Sequence 111, App	200	12.2	55.5	50	15	US-10-131-827-4390	Sequence
56.4	24	14	US-10-013-922A-111	Sequence 111, App	201	12.2	55.5	52	8	US-08-781-986A-5080	Sequence
56.4	24	14	US-10-020-445A-111	Sequence 111, App	202	12.2	55.5	59	14	US-10-315-515-116	Sequence
56.4	24	15	US-10-013-924A-111	Sequence 111, App	203	12.2	55.5	60	10	US-09-908-975-9000	Sequence
56.4	24	15	US-10-017-084A-111	Sequence 111, App	204	12.2	55.5	60	10	US-09-908-975-9429	Sequence
56.4	24	15	US-10-017-085A-111	Sequence 111, App	205	12.2	55.5	60	10	US-09-908-975-9926	Sequence
56.4	24	15	US-10-013-916A-111	Sequence 111, App	206	12.2	55.5	60	10	US-09-908-975-14912	Sequence
56.4	24	15	US-10-143-026B-111	Sequence 111, App	207	12.2	55.5	60	10	US-09-908-975-15981	Sequence
56.4	24	15	US-10-013-918A-111	Sequence 111, App	208	12.2	55.5	60	10	US-09-908-975-18269	Sequence
56.4	24	15	US-10-013-928A-111	Sequence 111, App	209	12.2	55.5	60	10	US-09-908-975-19222	Sequence
56.4	24	15	US-10-162-522A-111	Sequence 111, App	210	12.2	55.5	60	10	US-09-908-975-20584	Sequence
56.4	24	15	US-10-013-923A-111	Sequence 111, App	211	12.2	55.5	60	10	US-09-908-975-20692	Sequence
56.4	24	15	US-10-013-925A-111	Sequence 111, App	212	12.2	55.5	60	10	US-09-908-975-31382	Sequence
56.4	24	15	US-10-013-927A-111	Sequence 111, App	213	12.2	55.5	60	10	US-09-908-975-31637	Sequence
56.4	24	15	US-10-145-093A-111	Sequence 111, App	214	12.2	55.5	21	13	US-10-035-098-27	Sequence
56.4	24	15	US-10-013-919A-111	Sequence 111, App	215	12	54.5	22	9	US-09-891-332A-54	Sequence
56.4	24	15	US-10-013-920A-111	Sequence 111, App	216	12	54.5	23	9	US-09-889-722-323	Sequence
56.4	25	14	US-10-098-263B-30812	Sequence 30812, A	217	12	54.5	23	9	US-09-889-723-323	Sequence
56.4	25	14	US-10-098-263B-31196	Sequence 31196, A	218	12	54.5	23	9	US-09-889-729-323	Sequence
56.4	25	14	US-10-098-263B-46888	Sequence 46888, A	219	12	54.5	23	9	US-09-889-727-323	Sequence
56.4	25	14	US-10-098-263B-75692	Sequence 75692, A	220	12	54.5	23	9	US-09-889-731-323	Sequence
56.4	25	14	US-10-098-263B-83493	Sequence 83493, A	221	12	54.5	23	9	US-09-889-732-323	Sequence
56.4	25	14	US-10-098-263B-83494	Sequence 83494, A	222	12	54.5	23	9	US-09-889-732-323	Sequence
56.4	25	14	US-10-098-263B-84586	Sequence 84586, A	223	12	54.5	23	9	US-09-889-732-323	Sequence
56.4	25	14	US-10-098-263B-101733	Sequence 101733, A	224	12	54.5	23	9	US-09-889-732-323	Sequence
56.4	28	9	US-09-895-141-49	Sequence 49, Appl	225	12	54.5	23	9	US-09-991-163-323	Sequence
56.4	29	9	US-09-879-919-8	Sequence 8, Appl	226	12	54.5	23	9	US-09-991-163-323	Sequence
56.4	29	9	US-09-879-919-10	Sequence 10, Appl	227	12	54.5	23	9	US-09-993-604-323	Sequence
56.4	29	13	US-10-082-260-8	Sequence 8, Appl	228	12	54.5	23	9	US-09-990-456-323	Sequence
56.4	29	13	US-10-082-260-10	Sequence 10, Appl	229	12	54.5	23	9	US-09-989-721-323	Sequence
56.4	29	14	US-10-268-951-8	Sequence 8, Appl	230	12	54.5	23	9	US-09-992-598-323	Sequence
56.4	30	14	US-10-268-951-10	Sequence 10, Appl	231	12	54.5	23	9	US-09-989-293A-323	Sequence
56.4	30	14	US-10-056-794-6	Sequence 6, Appl	232	12	54.5	23	9	US-09-989-735-323	Sequence
56.4	30	14	US-10-296-995-5	Sequence 5, Appl	233	12	54.5	23	9	US-09-990-444-323	Sequence
56.4	47	15	US-10-349-143-2788	Sequence 2788, Ap	234	12	54.5	23	9	US-09-991-181-323	Sequence

54.5	23	9	US-09-990-436-323	Sequence 323, App	c 308	12	54.5	52	14	US-10-090-827-21	Sequence
54.5	23	9	US-09-993-687-323	Sequence 323, App	309	12	54.5	59	14	US-10-222-654-46	Sequence
54.5	23	10	US-09-989-734-323	Sequence 323, App	310	12	54.5	60	9	US-09-735-705-375	Sequence
54.5	23	10	US-09-997-653-323	Sequence 323, App	311	12	54.5	60	9	US-09-850-716A-375	Sequence
54.5	23	10	US-09-997-653-323	Sequence 323, App	312	12	54.5	60	9	US-09-897-778-375	Sequence
54.5	23	10	US-09-997-428-323	Sequence 323, App	313	12	54.5	60	10	US-09-908-975-9336	Sequence
54.5	23	10	US-09-997-666-323	Sequence 323, App	314	12	54.5	60	10	US-09-908-975-10937	Sequence
54.5	23	10	US-09-990-438-323	Sequence 323, App	315	12	54.5	60	10	US-09-908-975-11791	Sequence
54.5	23	10	US-09-990-562-323	Sequence 323, App	316	12	54.5	60	10	US-09-908-975-12123	Sequence
54.5	23	10	US-09-990-711-323	Sequence 323, App	317	12	54.5	60	10	US-09-908-975-15194	Sequence
54.5	23	10	US-09-989-726-323	Sequence 323, App	318	12	54.5	60	10	US-09-908-975-16079	Sequence
54.5	23	10	US-09-998-156-323	Sequence 323, App	319	12	54.5	60	14	US-10-117-982-375	Sequence
54.5	23	10	US-09-990-437-323	Sequence 323, App	320	12	54.5	60	15	US-10-313-986-375	Sequence
54.5	23	10	US-09-991-157-323	Sequence 323, App	321	12	54.5	60	20	US-09-770-107-31	Sequence
54.5	23	10	US-09-997-573-323	Sequence 323, App	322	11.8	53.6	20	14	US-10-006-883A-51	Sequence
54.5	23	10	US-09-991-172-323	Sequence 323, App	323	11.8	53.6	20	15	US-10-159-856-17	Sequence
54.5	23	10	US-09-990-726-323	Sequence 323, App	324	11.8	53.6	20	15	US-10-159-856-94	Sequence
54.5	23	10	US-09-997-559-323	Sequence 323, App	325	11.8	53.6	20	15	US-10-289-762-2262	Sequence
54.5	23	10	US-09-997-601-323	Sequence 323, App	326	11.8	53.6	20	15	US-10-289-762-2265	Sequence
54.5	23	10	US-09-990-443-323	Sequence 323, App	327	11.8	53.6	20	15	US-10-202-675-10	Sequence
54.5	23	10	US-09-991-854-323	Sequence 323, App	328	11.8	53.6	23	14	US-09-730-018-8	Sequence
54.5	23	10	US-09-997-628-323	Sequence 323, App	329	11.8	53.6	24	10	US-09-382-860-180	Sequence
54.5	23	10	US-09-997-683-323	Sequence 323, App	330	11.8	53.6	24	14	US-10-431-842-8	Sequence
54.5	23	10	US-09-989-729A-323	Sequence 323, App	331	11.8	53.6	25	14	US-10-215-112-457	Sequence
54.5	23	10	US-09-997-349-323	Sequence 323, App	332	11.8	53.6	25	14	US-10-215-112-6585	Sequence
54.5	23	10	US-09-997-440-323	Sequence 323, App	333	11.8	53.6	25	14	US-10-215-112-11550	Sequence
54.5	23	10	US-09-997-542-323	Sequence 323, App	334	11.8	53.6	25	14	US-10-098-263B-18129	Sequence
54.5	23	10	US-09-990-440-323	Sequence 323, App	335	11.8	53.6	25	14	US-10-098-263B-18761	Sequence
54.5	23	10	US-09-993-463-323	Sequence 323, App	336	11.8	53.6	25	14	US-10-098-263B-24491	Sequence
54.5	23	10	US-09-997-542-323	Sequence 323, App	337	11.8	53.6	25	14	US-10-098-263B-26327	Sequence
54.5	23	10	US-09-993-748-323	Sequence 323, App	338	11.8	53.6	25	14	US-10-098-263B-26327	Sequence
54.5	23	10	US-09-990-439-323	Sequence 323, App	339	11.8	53.6	25	14	US-10-098-263B-26510	Sequence
54.5	23	10	US-09-990-427-323	Sequence 323, App	340	11.8	53.6	25	14	US-10-098-263B-26963	Sequence
54.5	23	10	US-09-989-328-323	Sequence 323, App	341	11.8	53.6	25	14	US-10-098-263B-26964	Sequence
54.5	23	10	US-09-993-583-323	Sequence 323, App	342	11.8	53.6	25	14	US-10-098-263B-34698	Sequence
54.5	23	10	US-09-941-992-323	Sequence 323, App	343	11.8	53.6	25	14	US-10-098-263B-35623	Sequence
54.5	23	10	US-09-992-521-323	Sequence 323, App	344	11.8	53.6	25	14	US-10-098-263B-35624	Sequence
54.5	23	10	US-09-997-384-323	Sequence 323, App	345	11.8	53.6	25	14	US-10-098-263B-76186	Sequence
54.5	23	10	US-09-998-041-323	Sequence 323, App	346	11.8	53.6	25	14	US-10-098-263B-77392	Sequence
54.5	23	10	US-09-997-585-323	Sequence 323, App	347	11.8	53.6	25	14	US-10-098-263B-79925	Sequence
54.5	23	10	US-09-997-614-323	Sequence 323, App	348	11.8	53.6	25	14	US-10-098-263B-80535	Sequence
54.5	23	10	US-09-989-862-323	Sequence 323, App	349	11.8	53.6	25	14	US-10-098-263B-83597	Sequence
54.5	23	10	US-09-997-529-323	Sequence 323, App	350	11.8	53.6	25	14	US-10-098-263B-98511	Sequence
54.5	23	10	US-09-989-725-323	Sequence 323, App	351	11.8	53.6	25	14	US-10-098-263B-108151	Sequence
54.5	23	11	US-09-989-733-323	Sequence 323, App	352	11.8	53.6	29	14	US-09-452-599-148	Sequence
54.5	23	11	US-09-992-643-323	Sequence 323, App	353	11.8	53.6	30	9	US-09-423-800-8	Sequence
54.5	23	13	US-10-001-054-76	Sequence 76, Appl	354	11.8	53.6	30	14	US-10-182-018-8	Sequence
54.5	23	15	US-10-219-538-323	Sequence 323, App	355	11.8	53.6	30	14	US-10-169-003-8	Sequence
54.5	24	9	US-09-757-041-4	Sequence 4, Appl	356	11.8	53.6	30	14	US-10-337-981-8	Sequence
54.5	25	14	US-10-215-112-2649	Sequence 2649, Ap	357	11.8	53.6	30	14	US-10-121-120-148	Sequence
54.5	25	14	US-10-215-112-2650	Sequence 2650, Ap	358	11.8	53.6	31	14	US-10-195-752-12	Sequence
54.5	25	14	US-10-215-112-3113	Sequence 3113, Ap	359	11.8	53.6	31	14	US-10-300-215-189	Sequence
54.5	25	14	US-10-098-263B-7214	Sequence 7214, Ap	360	11.8	53.6	31	14	US-10-300-215-212	Sequence
54.5	25	14	US-10-098-263B-12733	Sequence 12733, A	361	11.8	53.6	31	14	US-10-300-215-225	Sequence
54.5	25	14	US-10-098-263B-22557	Sequence 22557, A	362	11.8	53.6	31	14	US-10-300-215-242	Sequence
54.5	25	14	US-10-098-263B-22792	Sequence 22792, A	363	11.8	53.6	32	9	US-09-965-099-107	Sequence
54.5	25	14	US-10-098-263B-29311	Sequence 29311, A	364	11.8	53.6	32	10	US-09-947-839-8	Sequence
54.5	25	14	US-10-098-263B-61699	Sequence 61699, A	365	11.8	53.6	32	13	US-10-051-852-107	Sequence
54.5	25	14	US-10-098-263B-66399	Sequence 66399, A	366	11.8	53.6	32	15	US-10-430-176-107	Sequence
54.5	25	14	US-10-098-263B-95422	Sequence 95422, A	367	11.8	53.6	33	9	US-09-874-547-14	Sequence
54.5	25	14	US-10-098-263B-97119	Sequence 97119, A	368	11.8	53.6	34	9	US-09-333-527-13	Sequence
54.5	25	14	US-10-098-263B-126082	Sequence 126082, A	369	11.8	53.6	34	14	US-10-127-427-13	Sequence
54.5	26	10	US-09-468-147-157	Sequence 157, App	370	11.8	53.6	34	15	US-10-374-531-66	Sequence
54.5	32	9	US-09-993-164-17	Sequence 17, Appl	371	11.8	53.6	35	9	US-09-893-615-75	Sequence
54.5	34	10	US-09-215-163-38	Sequence 38, Appl	372	11.8	53.6	35	10	US-09-215-163-30	Sequence
54.5	36	10	US-09-215-163-15	Sequence 15, Appl	373	11.8	53.6	35	15	US-10-601-171-75	Sequence
54.5	39	9	US-09-974-973-15	Sequence 15, Appl	374	11.8	53.6	36	14	US-10-222-028A-11	Sequence
54.5	39	15	US-10-273-973-57	Sequence 57, Appl	375	11.8	53.6	37	9	US-09-855-271-2	Sequence
54.5	43	10	US-09-990-586-32	Sequence 32, Appl	376	11.8	53.6	37	9	US-09-730-857-33	Sequence
54.5	43	14	US-10-310-113-28	Sequence 28, Appl	377	11.8	53.6	37	9	US-09-949-559-53	Sequence
54.5	43	14	US-10-230-880-32	Sequence 32, Appl	378	11.8	53.6	37	10	US-09-875-221A-53	Sequence
54.5	50	15	US-10-131-827-3629	Sequence 3629, Ap	379	11.8	53.6	38	9	US-09-874-547-65	Sequence

53.6	38	9	US-09-874-547-75	Sequence 75, Appl	454	11.6	52.7	50	14	US-10-012-121A-192	Sequenc
53.6	38	10	US-09-898-121A-2	Sequence 2, Appl	455	11.6	52.7	50	14	US-10-006-116A-192	Sequenc
53.6	39	14	US-10-231-452-66	Sequence 66, Appl	456	11.6	52.7	50	14	US-10-006-117A-192	Sequenc
53.6	41	9	US-09-988-899-66	Sequence 61, Appl	457	11.6	52.7	50	14	US-10-017-527A-192	Sequenc
53.6	41	14	US-10-160-232-22	Sequence 22, Appl	458	11.6	52.7	50	14	US-10-013-913A-192	Sequenc
53.6	42	9	US-09-874-547-15	Sequence 15, Appl	459	11.6	52.7	50	14	US-10-007-194A-192	Sequenc
53.6	43	9	US-09-924-099-30	Sequence 30, Appl	460	11.6	52.7	50	14	US-10-013-430A-192	Sequenc
53.6	44	15	US-10-412-703A-40	Sequence 40, Appl	461	11.6	52.7	50	14	US-10-011-671A-192	Sequenc
53.6	45	14	US-10-160-232-21	Sequence 21, Appl	462	11.6	52.7	50	14	US-10-012-755A-192	Sequenc
53.6	47	8	US-08-969-140-29	Sequence 29, Appl	463	11.6	52.7	50	14	US-10-015-386A-192	Sequenc
53.6	47	8	US-08-781-986A-2800	Sequence 2800, Ap	464	11.6	52.7	50	14	US-10-011-692A-192	Sequenc
53.6	51	9	US-09-147-142-25	Sequence 25, Appl	465	11.6	52.7	50	14	US-10-006-768A-192	Sequenc
53.6	60	10	US-09-908-975-6607	Sequence 6607, Ap	466	11.6	52.7	50	14	US-10-017-610A-192	Sequenc
53.6	60	10	US-09-908-975-8296	Sequence 8296, Ap	467	11.6	52.7	50	14	US-10-006-063A-192	Sequenc
53.6	60	10	US-09-908-975-15786	Sequence 15786, A	468	11.6	52.7	50	14	US-10-020-063A-192	Sequenc
53.6	60	10	US-09-908-975-19875	Sequence 19875, A	469	11.6	52.7	50	14	US-10-015-391A-192	Sequenc
53.6	60	10	US-09-908-975-20491	Sequence 20491, A	470	11.6	52.7	50	14	US-10-017-407A-192	Sequenc
53.6	60	10	US-09-908-975-22383	Sequence 22383, A	471	11.6	52.7	50	14	US-10-011-833A-192	Sequenc
53.6	60	10	US-09-908-975-23324	Sequence 23324, A	472	11.6	52.7	50	14	US-10-006-041A-192	Sequenc
53.6	60	10	US-09-908-975-23324	Sequence 23324, A	473	11.6	52.7	50	14	US-10-015-822A-192	Sequenc
53.6	60	10	US-09-908-975-31593	Sequence 31593, A	474	11.6	52.7	50	14	US-10-015-387A-192	Sequenc
52.7	18	9	US-09-969-373-4506	Sequence 4506, Ap	475	11.6	52.7	50	14	US-10-006-130A-192	Sequenc
52.7	18	9	US-09-969-373-4510	Sequence 4510, Ap	476	11.6	52.7	50	14	US-10-006-172A-192	Sequenc
52.7	18	15	US-10-349-143-4682	Sequence 4682, Ap	477	11.6	52.7	50	14	US-10-017-253A-192	Sequenc
52.7	19	14	US-10-005-956-140	Sequence 140, App	478	11.6	52.7	50	14	US-10-015-392A-192	Sequenc
52.7	20	9	US-09-734-847A-21	Sequence 21, Appl	479	11.6	52.7	50	14	US-10-017-306A-192	Sequenc
52.7	20	9	US-09-800-629A-157	Sequence 157, App	480	11.6	52.7	50	14	US-10-017-867A-192	Sequenc
52.7	20	14	US-10-126-355-18	Sequence 18, Appl	481	11.6	52.7	50	14	US-10-012-064A-192	Sequenc
52.7	20	15	US-10-349-143-10661	Sequence 10661, A	482	11.6	52.7	50	14	US-10-013-909A-192	Sequenc
52.7	21	9	US-09-835-232-14	Sequence 14, Appl	483	11.6	52.7	50	14	US-10-015-671A-192	Sequenc
52.7	21	14	US-10-308-485-14	Sequence 14, Appl	484	11.6	52.7	50	14	US-10-015-610A-192	Sequenc
52.7	22	8	US-08-731-499-30	Sequence 30, Appl	485	11.6	52.7	50	14	US-10-012-137A-192	Sequenc
52.7	24	10	US-09-940-185-2443	Sequence 2443, Ap	486	11.6	52.7	50	14	US-10-012-752A-192	Sequenc
52.7	25	14	US-10-098-263B-47935	Sequence 47935, A	487	11.6	52.7	50	14	US-10-012-754A-192	Sequenc
52.7	25	14	US-10-098-263B-53096	Sequence 53096, A	488	11.6	52.7	50	14	US-10-013-910A-192	Sequenc
52.7	25	14	US-10-098-263B-57005	Sequence 57005, A	489	11.6	52.7	50	14	US-10-013-911A-192	Sequenc
52.7	25	14	US-10-098-263B-57770	Sequence 57770, A	490	11.6	52.7	50	14	US-10-013-912A-192	Sequenc
52.7	25	14	US-10-098-263B-77075	Sequence 77075, A	491	11.6	52.7	50	14	US-10-015-653A-192	Sequenc
52.7	25	14	US-10-098-263B-78116	Sequence 78116, A	492	11.6	52.7	50	14	US-10-012-101B-192	Sequenc
52.7	25	14	US-10-098-263B-84685	Sequence 84685, A	493	11.6	52.7	50	14	US-10-015-480A-192	Sequenc
52.7	25	14	US-10-098-263B-89176	Sequence 89176, A	494	11.6	52.7	50	14	US-10-015-715A-192	Sequenc
52.7	25	14	US-10-098-263B-90102	Sequence 90102, A	495	11.6	52.7	50	14	US-10-012-237A-192	Sequenc
52.7	25	14	US-10-098-263B-113911	Sequence 113911, A	496	11.6	52.7	50	14	US-10-013-906A-192	Sequenc
52.7	25	14	US-10-098-263B-115692	Sequence 115692, A	497	11.6	52.7	50	14	US-10-015-388A-192	Sequenc
52.7	25	14	US-10-098-263B-116850	Sequence 116850, A	498	11.6	52.7	50	14	US-10-012-753A-192	Sequenc
52.7	25	14	US-10-098-263B-117292	Sequence 117292, A	499	11.6	52.7	50	14	US-10-015-385A-192	Sequenc
52.7	25	14	US-10-098-263B-118592	Sequence 118592, A	500	11.6	52.7	50	14	US-10-007-236A-192	Sequenc
52.7	25	14	US-10-098-263B-123311	Sequence 123311, A	501	11.6	52.7	50	14	US-10-015-389A-192	Sequenc
52.7	26	14	US-10-213-288-7	Sequence 7, Appl	502	11.6	52.7	50	15	US-10-015-519A-192	Sequenc
52.7	31	9	US-09-845-160-10	Sequence 10, Appl	503	11.6	52.7	50	15	US-10-013-915A-192	Sequenc
52.7	31	9	US-09-845-160-11	Sequence 11, Appl	504	11.6	52.7	50	15	US-10-015-394A-192	Sequenc
52.7	38	10	US-09-825-805-1365	Sequence 1365, Ap	505	11.6	52.7	50	15	US-10-015-390A-192	Sequenc
52.7	38	10	US-09-877-478-4504	Sequence 4504, Ap	506	11.6	52.7	50	15	US-10-006-746A-192	Sequenc
52.7	39	9	US-09-263-959-167	Sequence 167, App	507	11.6	52.7	50	15	US-10-011-795A-192	Sequenc
52.7	41	14	US-10-005-956-203	Sequence 203, App	508	11.6	52.7	50	15	US-10-131-827-1603	Sequenc
52.7	42	9	US-09-735-787-25	Sequence 25, Appl	509	11.6	52.7	50	15	US-10-131-827-2268	Sequenc
52.7	42	9	US-09-735-787-29	Sequence 29, Appl	510	11.6	52.7	50	15	US-10-131-827-3472	Sequenc
52.7	42	14	US-10-138-870-25	Sequence 25, Appl	511	11.6	52.7	50	15	US-10-131-827-3502	Sequenc
52.7	42	14	US-10-138-870-29	Sequence 29, Appl	512	11.6	52.7	50	15	US-10-131-827-4169	Sequenc
52.7	43	14	US-10-037-986-246	Sequence 246, App	513	11.6	52.7	50	15	US-10-131-827-6753	Sequenc
52.7	43	14	US-10-408-085-246	Sequence 246, App	514	11.6	52.7	50	15	US-10-131-827-7143	Sequenc
52.7	45	10	US-09-860-474-229	Sequence 229, App	515	11.6	52.7	50	15	US-10-131-827-7437	Sequenc
52.7	45	14	US-10-409-565-229	Sequence 229, App	516	11.6	52.7	50	15	US-10-131-827-7516	Sequenc
52.7	46	9	US-09-263-959-130	Sequence 130, App	517	11.6	52.7	50	15	US-10-012-231A-192	Sequenc
52.7	47	14	US-10-121-746-61	Sequence 61, Appl	518	11.6	52.7	60	10	US-09-908-975-5800	Sequenc
52.7	47	15	US-10-349-143-1483	Sequence 1483, Ap	519	11.6	52.7	60	10	US-09-908-975-6300	Sequenc
52.7	48	10	US-09-918-156-2	Sequence 2, Appl	520	11.6	52.7	60	10	US-09-908-975-6473	Sequenc
52.7	48	10	US-09-158-106-35	Sequence 35, Appl	521	11.6	52.7	60	10	US-09-908-975-7710	Sequenc
52.7	48	14	US-10-023-888-29	Sequence 29, Appl	522	11.6	52.7	60	10	US-09-908-975-10650	Sequenc
52.7	50	10	US-09-946-374-192	Sequence 192, App	523	11.6	52.7	60	10	US-09-908-975-10750	Sequenc
52.7	50	14	US-10-006-856A-192	Sequence 192, App	524	11.6	52.7	60	10	US-09-908-975-10936	Sequenc
52.7	50	14	US-10-006-818A-192	Sequence 192, App	525	11.6	52.7	60	10	US-09-908-975-12204	Sequenc
52.7	50	14	US-10-015-393A-192	Sequence 192, App	526	11.6	52.7	60	10	US-09-908-975-13055	Sequenc
52.7	50	14	US-10-015-393A-192	Sequence 192, App	527	11.6	52.7	60	10		

32.7	60	10	US-09-908-975-13340	Sequence 13340, A	600	11.4	51.8	41	9	US-09-988-899-62	Sequence
32.7	60	10	US-09-908-975-13617	Sequence 13617, A	c 601	11.4	51.8	41	10	US-09-892-949-71	Sequence
32.7	60	10	US-09-908-975-14381	Sequence 14381, A	c 602	11.4	51.8	41	15	US-10-351-157-41	Sequence
32.7	60	10	US-09-908-975-15216	Sequence 15216, A	c 603	11.4	51.8	42	9	US-09-817-487A-5	Sequence
32.7	60	10	US-09-908-975-15441	Sequence 15441, A	c 604	11.4	51.8	42	14	US-10-300-215-174	Sequence
32.7	60	10	US-09-908-975-16790	Sequence 16790, A	c 605	11.4	51.8	42	15	US-10-417-476-19	Sequence
32.7	60	10	US-09-908-975-18148	Sequence 18148, A	c 606	11.4	51.8	45	9	US-09-859-053-1	Sequence
32.7	60	10	US-09-908-975-18153	Sequence 18153, A	c 607	11.4	51.8	46	9	US-09-263-959-124	Sequence
32.7	60	10	US-09-908-975-18931	Sequence 18931, A	c 608	11.4	51.8	47	9	US-09-780-929-121	Sequence
32.7	60	10	US-09-908-975-18988	Sequence 18988, A	c 609	11.4	51.8	47	15	US-10-349-143-2109	Sequence
32.7	60	10	US-09-908-975-19495	Sequence 19495, A	c 610	11.4	51.8	47	15	US-10-349-143-3741	Sequence
32.7	60	10	US-09-908-975-19638	Sequence 19638, A	c 611	11.4	51.8	47	15	US-10-349-143-3852	Sequence
32.7	60	10	US-09-908-975-19938	Sequence 19938, A	c 612	11.4	51.8	48	8	US-08-779-784-15	Sequence
32.7	60	10	US-09-908-975-20360	Sequence 20360, A	c 613	11.4	51.8	50	10	US-09-950-442-40	Sequence
32.7	60	10	US-09-908-975-22707	Sequence 22707, A	c 614	11.4	51.8	50	15	US-10-298-695-40	Sequence
32.7	60	10	US-09-908-975-31650	Sequence 31650, A	c 615	11.4	51.8	50	15	US-10-131-827-3901	Sequence
32.7	60	10	US-10-156-306-4366	Sequence 4366, Ap	c 616	11.4	51.8	50	15	US-10-131-827-5633	Sequence
32.7	60	10	US-10-300-215-183	Sequence 183, App	c 617	11.4	51.8	50	15	US-10-131-827-6737	Sequence
32.7	60	10	US-10-300-215-236	Sequence 236, App	c 618	11.4	51.8	50	15	US-10-131-827-7127	Sequence
32.7	60	10	US-09-956-712-88	Sequence 88, Appl	c 619	11.4	51.8	50	15	US-10-131-827-7421	Sequence
32.7	60	10	US-10-633-913-88	Sequence 88, Appl	c 620	11.4	51.8	50	15	US-10-131-827-7500	Sequence
32.7	60	10	US-10-281-479A-13	Sequence 13, Appl	c 621	11.4	51.8	51	10	US-09-977-797A-93	Sequence
32.7	60	10	US-10-275-180A-13	Sequence 13, Appl	c 622	11.4	51.8	51	10	US-09-155-106-36	Sequence
32.7	60	10	US-10-286-132A-13	Sequence 13, Appl	c 623	11.4	51.8	56	14	US-10-222-654-28	Sequence
32.7	60	10	US-10-289-762-1520	Sequence 1520, Ap	c 624	11.4	51.8	57	9	US-09-845-899A-21	Sequence
32.7	60	10	US-10-289-762-1525	Sequence 1525, Ap	c 625	11.4	51.8	60	10	US-09-908-975-5035	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 144, App	c 626	11.4	51.8	60	10	US-09-908-975-5554	Sequence
32.7	60	10	US-09-144-886-29	Sequence 29, Appl	c 627	11.4	51.8	60	10	US-09-908-975-6874	Sequence
32.7	60	10	US-10-098-263B-118	Sequence 118, App	c 628	11.4	51.8	60	10	US-09-908-975-8504	Sequence
32.7	60	10	US-10-098-263B-313	Sequence 313, App	c 629	11.4	51.8	60	10	US-09-908-975-8612	Sequence
32.7	60	10	US-10-098-263B-4298	Sequence 4298, Ap	c 630	11.4	51.8	60	10	US-09-908-975-10411	Sequence
32.7	60	10	US-10-098-263B-9262	Sequence 9262, Ap	c 631	11.4	51.8	60	10	US-09-908-975-11950	Sequence
32.7	60	10	US-10-098-263B-10915	Sequence 10915, A	c 632	11.4	51.8	60	10	US-09-908-975-13477	Sequence
32.7	60	10	US-10-098-263B-14341	Sequence 14341, A	c 633	11.4	51.8	60	10	US-09-908-975-14337	Sequence
32.7	60	10	US-10-098-263B-14341	Sequence 14341, A	c 634	11.4	51.8	60	10	US-09-908-975-15010	Sequence
32.7	60	10	US-10-098-263B-18798	Sequence 18798, A	c 635	11.4	51.8	60	10	US-09-908-975-16613	Sequence
32.7	60	10	US-10-098-263B-33617	Sequence 33617, A	c 636	11.4	51.8	60	10	US-09-908-975-17703	Sequence
32.7	60	10	US-10-098-263B-33710	Sequence 33710, A	c 637	11.4	51.8	60	10	US-09-908-975-17867	Sequence
32.7	60	10	US-10-098-263B-41681	Sequence 41681, A	c 638	11.4	51.8	60	10	US-09-908-975-18115	Sequence
32.7	60	10	US-10-098-263B-41682	Sequence 41682, A	c 639	11.4	51.8	60	10	US-09-908-975-18157	Sequence
32.7	60	10	US-10-098-263B-52656	Sequence 52656, A	c 640	11.4	51.8	60	10	US-09-908-975-18623	Sequence
32.7	60	10	US-10-098-263B-54534	Sequence 54534, A	c 641	11.4	51.8	60	10	US-09-908-975-20961	Sequence
32.7	60	10	US-10-098-263B-60930	Sequence 60930, A	c 642	11.4	51.8	60	10	US-09-908-975-21870	Sequence
32.7	60	10	US-10-098-263B-64943	Sequence 64943, A	c 643	11.4	51.8	60	10	US-09-908-975-23372	Sequence
32.7	60	10	US-10-098-263B-65782	Sequence 65782, A	c 644	11.4	51.8	60	10	US-10-047-403-44	Sequence
32.7	60	10	US-10-098-263B-72646	Sequence 72646, A	c 645	11.2	50.9	17	10	US-09-818-875-4062	Sequence
32.7	60	10	US-10-098-263B-75025	Sequence 75025, A	c 646	11.2	50.9	17	10	US-09-818-875-4063	Sequence
32.7	60	10	US-10-098-263B-77024	Sequence 77024, A	c 647	11.2	50.9	17	14	US-10-238-700-426	Sequence
32.7	60	10	US-10-098-263B-93222	Sequence 93222, A	c 648	11.2	50.9	17	14	US-10-238-700-1205	Sequence
32.7	60	10	US-10-098-263B-99368	Sequence 99368, A	c 649	11.2	50.9	17	15	US-10-209-787-4062	Sequence
32.7	60	10	US-10-098-263B-102403	Sequence 102403, A	c 650	11.2	50.9	17	15	US-10-209-787-4063	Sequence
32.7	60	10	US-10-098-263B-105600	Sequence 105600, A	c 651	11.2	50.9	17	15	US-10-261-185-4062	Sequence
32.7	60	10	US-10-098-263B-107073	Sequence 107073, A	c 652	11.2	50.9	17	15	US-10-261-185-4063	Sequence
32.7	60	10	US-10-098-263B-107074	Sequence 107074, A	c 653	11.2	50.9	18	14	US-10-304-095-26	Sequence
32.7	60	10	US-10-098-263B-109484	Sequence 109484, A	c 654	11.2	50.9	20	9	US-09-817-814-18	Sequence
32.7	60	10	US-10-098-263B-126948	Sequence 126948, A	c 655	11.2	50.9	20	10	US-09-824-322B-117	Sequence
32.7	60	10	US-10-210-951-209	Sequence 209, App	c 656	11.2	50.9	20	14	US-10-006-430-81	Sequence
32.7	60	10	US-10-121-884-17	Sequence 17, App	c 657	11.2	50.9	20	14	US-10-174-394-18	Sequence
32.7	60	10	US-10-121-759-17	Sequence 17, Appl	c 658	11.2	50.9	20	14	US-10-332-059-3	Sequence
32.7	60	10	US-10-056-229-198	Sequence 198, App	c 659	11.2	50.9	20	15	US-10-289-762-2320	Sequence
32.7	60	10	US-10-114-153-251	Sequence 251, App	c 660	11.2	50.9	20	15	US-10-289-762-4493	Sequence
32.7	60	10	US-09-333-527-26	Sequence 26, Appl	c 661	11.2	50.9	20	16	US-10-210-479-37	Sequence
32.7	60	10	US-09-976-935-7	Sequence 7, Appl	c 662	11.2	50.9	20	16	US-10-210-479-105	Sequence
32.7	60	10	US-10-127-427-26	Sequence 26, Appl	c 663	11.2	50.9	23	9	US-09-969-373-3863	Sequence
32.7	60	10	US-09-978-244A-53	Sequence 53, Appl	c 664	11.2	50.9	23	10	US-09-864-636A-2487	Sequence
32.7	60	10	US-09-847-232-5	Sequence 53, Appl	c 665	11.2	50.9	23	10	US-09-864-636A-2491	Sequence
32.7	60	10	US-10-079-616-13	Sequence 13, Appl	c 666	11.2	50.9	23	11	US-09-864-426A-2487	Sequence
32.7	60	10	US-08-547-263-7	Sequence 7, Appl	c 667	11.2	50.9	23	11	US-09-864-426A-2491	Sequence
32.7	60	10	US-10-267-384-167	Sequence 167, App	c 668	11.2	50.9	23	12	US-10-349-557A-34	Sequence
32.7	60	10	US-09-780-533A-4284	Sequence 4284, Ap	c 669	11.2	50.9	23	14	US-10-267-411B-34	Sequence
32.7	60	10	US-09-263-959-170	Sequence 170, App	c 670	11.2	50.9	23	14	US-10-084-839-2487	Sequence
32.7	60	10	US-09-860-761-3	Sequence 3, Appl	c 671	11.2	50.9	23	14	US-10-084-839-2491	Sequence
32.7	60	10	US-10-284-084-45	Sequence 45, Appl	c 672	11.2	50.9	23	15	US-10-374-077-120	Sequence



50.9	24	9	US-09-378-295A-66	Sequence 66, Appl	746	11.2	50.9	24	15	US-10-313-963A-42	Sequence
50.9	24	9	US-09-378-697-66	Sequence 66, Appl	747	11.2	50.9	24	15	US-10-145-093A-66	Sequence
50.9	24	9	US-09-378-192A-66	Sequence 66, Appl	748	11.2	50.9	24	15	US-10-013-919A-66	Sequence
50.9	24	9	US-09-378-832A-66	Sequence 66, Appl	749	11.2	50.9	24	15	US-10-013-920A-66	Sequence
50.9	24	10	US-09-378-189-66	Sequence 66, Appl	750	11.2	50.9	24	15	US-10-198-447A-23	Sequence
50.9	24	10	US-09-378-608A-66	Sequence 66, Appl	751	11.2	50.9	24	15	US-10-215-112-7816	Sequence
50.9	24	10	US-09-378-585A-66	Sequence 66, Appl	c 751	11.2	50.9	25	14	US-10-215-112-7972	Sequence
50.9	24	10	US-09-378-191A-66	Sequence 66, Appl	c 753	11.2	50.9	25	14	US-10-098-263B-2560	Sequence
50.9	24	10	US-09-378-403A-66	Sequence 66, Appl	754	11.2	50.9	25	14	US-10-098-263B-4294	Sequence
50.9	24	10	US-09-378-564A-66	Sequence 66, Appl	c 755	11.2	50.9	25	14	US-10-098-263B-6808	Sequence
50.9	24	10	US-09-378-833A-66	Sequence 66, Appl	756	11.2	50.9	25	14	US-10-098-263B-8576	Sequence
50.9	24	10	US-09-381-915A-66	Sequence 66, Appl	c 757	11.2	50.9	25	14	US-10-098-263B-12152	Sequence
50.9	24	10	US-09-378-824-66	Sequence 66, Appl	758	11.2	50.9	25	14	US-10-098-263B-14191	Sequence
50.9	24	10	US-09-378-585A-66	Sequence 66, Appl	759	11.2	50.9	25	14	US-10-098-263B-14827	Sequence
50.9	24	10	US-09-378-423A-66	Sequence 66, Appl	760	11.2	50.9	25	14	US-10-098-263B-23901	Sequence
50.9	24	10	US-09-378-193A-66	Sequence 66, Appl	761	11.2	50.9	25	14	US-10-098-263B-25585	Sequence
50.9	24	10	US-09-378-830A-66	Sequence 66, Appl	762	11.2	50.9	25	14	US-10-098-263B-31738	Sequence
50.9	24	10	US-09-378-757A-66	Sequence 66, Appl	763	11.2	50.9	25	14	US-10-098-263B-33484	Sequence
50.9	24	10	US-09-378-185-3392	Sequence 3392, Ap	764	11.2	50.9	25	14	US-10-098-263B-34360	Sequence
50.9	24	10	US-09-378-185-3771	Sequence 3771, Ap	c 765	11.2	50.9	25	14	US-10-098-263B-35209	Sequence
50.9	24	10	US-09-378-187B-66	Sequence 66, Appl	766	11.2	50.9	25	14	US-10-098-263B-36751	Sequence
50.9	24	10	US-09-378-643A-66	Sequence 66, Appl	c 767	11.2	50.9	25	14	US-10-098-263B-39318	Sequence
50.9	24	10	US-09-378-375A-66	Sequence 66, Appl	768	11.2	50.9	25	14	US-10-098-263B-45311	Sequence
50.9	24	10	US-09-378-298A-66	Sequence 66, Appl	769	11.2	50.9	25	14	US-10-098-263B-55110	Sequence
50.9	24	10	US-09-378-188A-66	Sequence 66, Appl	770	11.2	50.9	25	14	US-10-098-263B-57687	Sequence
50.9	24	10	US-09-378-681A-66	Sequence 66, Appl	771	11.2	50.9	25	14	US-10-098-263B-58315	Sequence
50.9	24	10	US-09-378-194A-66	Sequence 66, Appl	772	11.2	50.9	25	14	US-10-098-263B-58576	Sequence
50.9	24	10	US-09-378-829A-66	Sequence 66, Appl	c 773	11.2	50.9	25	14	US-10-098-263B-60236	Sequence
50.9	24	10	US-09-378-299A-66	Sequence 66, Appl	774	11.2	50.9	25	14	US-10-098-263B-64931	Sequence
50.9	24	10	US-09-378-544A-66	Sequence 66, Appl	775	11.2	50.9	25	14	US-10-098-263B-64932	Sequence
50.9	24	10	US-09-378-665A-66	Sequence 66, Appl	776	11.2	50.9	25	14	US-10-098-263B-69584	Sequence
50.9	24	10	US-09-378-802A-66	Sequence 66, Appl	c 777	11.2	50.9	25	14	US-10-098-263B-76276	Sequence
50.9	24	12	US-10-164-749A-66	Sequence 66, Appl	c 778	11.2	50.9	25	14	US-10-098-263B-76785	Sequence
50.9	24	14	US-10-167-749-66	Sequence 66, Appl	c 779	11.2	50.9	25	14	US-10-098-263B-77686	Sequence
50.9	24	14	US-10-013-921A-66	Sequence 66, Appl	c 781	11.2	50.9	25	14	US-10-098-263B-84166	Sequence
50.9	24	14	US-10-016-177A-66	Sequence 66, Appl	c 782	11.2	50.9	25	14	US-10-098-263B-85587	Sequence
50.9	24	14	US-10-166-709A-66	Sequence 17, Appl	783	11.2	50.9	25	14	US-10-098-263B-86606	Sequence
50.9	24	14	US-10-143-031A-66	Sequence 66, Appl	784	11.2	50.9	25	14	US-10-098-263B-100401	Sequence
50.9	24	14	US-10-143-030A-66	Sequence 66, Appl	785	11.2	50.9	25	14	US-10-098-263B-104894	Sequence
50.9	24	14	US-10-143-030A-66	Sequence 66, Appl	c 786	11.2	50.9	25	14	US-10-098-263B-105209	Sequence
50.9	24	14	US-10-002-967A-66	Sequence 66, Appl	c 788	11.2	50.9	25	14	US-10-098-263B-105210	Sequence
50.9	24	14	US-10-017-083A-66	Sequence 66, Appl	c 789	11.2	50.9	25	14	US-10-098-263B-106375	Sequence
50.9	24	14	US-10-145-128A-66	Sequence 66, Appl	c 790	11.2	50.9	25	14	US-10-098-263B-108375	Sequence
50.9	24	14	US-10-017-191A-66	Sequence 66, Appl	c 791	11.2	50.9	25	14	US-10-098-263B-108620	Sequence
50.9	24	14	US-10-143-029A-66	Sequence 66, Appl	792	11.2	50.9	25	14	US-10-098-263B-116779	Sequence
50.9	24	14	US-10-145-089A-66	Sequence 66, Appl	793	11.2	50.9	25	14	US-10-098-263B-120180	Sequence
50.9	24	14	US-10-165-067A-66	Sequence 66, Appl	c 794	11.2	50.9	27	15	US-10-312-273-592	Sequence
50.9	24	14	US-10-145-017A-66	Sequence 66, Appl	c 795	11.2	50.9	28	14	US-10-234-432-82	Sequence
50.9	24	14	US-10-164-728A-66	Sequence 66, Appl	c 796	11.2	50.9	29	14	US-10-060-585-26	Sequence
50.9	24	14	US-10-013-926A-66	Sequence 66, Appl	c 797	11.2	50.9	29	14	US-10-336-638-870	Sequence
50.9	24	14	US-10-165-247A-66	Sequence 66, Appl	798	11.2	50.9	31	9	US-09-801-274-1056	Sequence
50.9	24	14	US-10-145-124A-66	Sequence 66, Appl	c 799	11.2	50.9	31	14	US-10-402-954-10	Sequence
50.9	24	14	US-10-160-502A-66	Sequence 66, Appl	c 800	11.2	50.9	32	14	US-10-207-655-26	Sequence
50.9	24	14	US-10-145-087A-66	Sequence 66, Appl	802	11.2	50.9	34	10	US-10-053-530-26	Sequence
50.9	24	14	US-10-017-086A-66	Sequence 66, Appl	c 803	11.2	50.9	34	15	US-09-884-465A-47	Sequence
50.9	24	14	US-10-164-829A-66	Sequence 66, Appl	c 804	11.2	50.9	35	9	US-09-150-811-5	Sequence
50.9	24	14	US-10-013-922A-66	Sequence 66, Appl	c 805	11.2	50.9	35	15	US-09-884-465A-174	Sequence
50.9	24	14	US-10-020-445A-66	Sequence 66, Appl	c 806	11.2	50.9	36	15	US-10-027-632-178323	Sequence
50.9	24	14	US-10-013-924A-66	Sequence 66, Appl	c 807	11.2	50.9	36	15	US-10-027-632-178338	Sequence
50.9	24	15	US-10-017-084A-66	Sequence 66, Appl	c 808	11.2	50.9	38	10	US-10-027-632-178353	Sequence
50.9	24	15	US-10-013-916A-66	Sequence 66, Appl	810	11.2	50.9	38	10	US-09-930-423-3247	Sequence
50.9	24	15	US-10-143-026B-66	Sequence 66, Appl	811	11.2	50.9	38	10	US-09-745-237A-3247	Sequence
50.9	24	15	US-10-013-918A-66	Sequence 66, Appl	c 812	11.2	50.9	38	14	US-10-402-954-32	Sequence
50.9	24	15	US-10-013-928A-66	Sequence 66, Appl	c 813	11.2	50.9	39	9	US-09-969-192-32	Sequence
50.9	24	15	US-10-162-522A-66	Sequence 66, Appl	c 814	11.2	50.9	41	10	US-09-846-797-4	Sequence
50.9	24	15	US-10-013-923A-66	Sequence 66, Appl	815	11.2	50.9	42	14	US-10-043-573-45	Sequence
50.9	24	15	US-10-013-925A-66	Sequence 66, Appl	c 816	11.2	50.9	42	14	US-10-225-938-71	Sequence
50.9	24	15	US-10-013-927A-66	Sequence 66, Appl	c 817	11.2	50.9	43	14	US-10-287-919-794	Sequence
50.9	24	15	US-10-013-927A-66	Sequence 66, Appl	818	11.2	50.9	43	14	US-10-032-585-1749	Sequence

00.9	44	9	US-09-934-706-12	Sequence 12, Appl	11	50.0	25	14	US-10-098-263B-68247	Sequence
00.9	45	9	US-09-969-192-30	Sequence 30, Appl	893	50.0	25	14	US-10-098-263B-78207	Sequence
00.9	46	14	US-10-218-567-45	Sequence 45, Appl	894	50.0	25	14	US-10-098-263B-78811	Sequence
00.9	47	15	US-10-349-143-815	Sequence 815, Appl	895	50.0	25	14	US-10-098-263B-82423	Sequence
00.9	50	14	US-10-218-567-46	Sequence 46, Appl	896	50.0	25	14	US-10-098-263B-83025	Sequence
00.9	50	15	US-10-131-827-2814	Sequence 2814, Ap	897	50.0	25	14	US-10-098-263B-86045	Sequence
00.9	50	15	US-10-131-827-3278	Sequence 3278, Ap	898	50.0	25	14	US-10-098-263B-86046	Sequence
00.9	50	15	US-10-131-827-3929	Sequence 3929, Ap	899	50.0	25	14	US-10-098-263B-87612	Sequence
00.9	50	15	US-10-131-827-5384	Sequence 5384, Ap	900	50.0	25	14	US-10-098-263B-91585	Sequence
00.9	50	15	US-10-131-827-5384	Sequence 5384, Ap	901	50.0	25	14	US-10-098-263B-93097	Sequence
00.9	50	15	US-10-131-827-6723	Sequence 7223, Ap	902	50.0	25	14	US-10-098-263B-93098	Sequence
00.9	50	15	US-10-131-827-7113	Sequence 7113, Ap	903	50.0	25	14	US-10-098-263B-94624	Sequence
00.9	50	15	US-10-131-827-7407	Sequence 7407, Ap	904	50.0	25	14	US-10-098-263B-98795	Sequence
00.9	50	15	US-10-131-827-7486	Sequence 7486, Ap	905	50.0	25	14	US-10-098-263B-98796	Sequence
00.9	54	15	US-10-349-858-12	Sequence 12, Appl	906	50.0	25	14	US-10-098-263B-99733	Sequence
00.9	59	10	US-09-935-1008-4	Sequence 4, Appl	907	50.0	25	14	US-10-098-263B-10007	Sequence
00.9	60	10	US-09-979-999-21	Sequence 21, Appl	908	50.0	25	14	US-10-098-263B-121337	Sequence
00.9	60	10	US-09-979-999-22	Sequence 22, Appl	909	50.0	26	10	US-09-468-147-65	Sequence
00.9	60	10	US-09-908-975-5878	Sequence 5878, Ap	910	50.0	26	12	US-10-451-892-4	Sequence
00.9	60	10	US-09-908-975-6590	Sequence 6590, Ap	911	50.0	26	14	US-10-084-839-3763	Sequence
00.9	60	10	US-09-908-975-7752	Sequence 7752, Ap	912	50.0	26	14	US-10-138-505-18	Sequence
00.9	60	10	US-09-908-975-8201	Sequence 8201, Ap	913	50.0	27	14	US-10-159-006-54	Sequence
00.9	60	10	US-09-908-975-8267	Sequence 8267, Ap	914	50.0	27	14	US-10-175-247-23	Sequence
00.9	60	10	US-09-908-975-9745	Sequence 9745, Ap	915	50.0	28	14	US-10-415-247-10	Sequence
00.9	60	10	US-09-908-975-10317	Sequence 10317, A	916	50.0	28	15	US-10-415-247-11	Sequence
00.9	60	10	US-09-908-975-11384	Sequence 11384, A	917	50.0	28	15	US-10-415-247-18	Sequence
00.9	60	10	US-09-908-975-11499	Sequence 11499, A	918	50.0	28	15	US-10-415-247-19	Sequence
00.9	60	10	US-09-908-975-11590	Sequence 11590, A	919	50.0	28	15	US-10-415-247-19	Sequence
00.9	60	10	US-09-908-975-14892	Sequence 14892, A	920	50.0	29	10	US-09-905-928-11	Sequence
00.9	60	10	US-09-908-975-15040	Sequence 15040, A	921	50.0	29	14	US-10-096-964-11	Sequence
00.9	60	10	US-09-908-975-15040	Sequence 15040, A	922	50.0	29	14	US-10-238-681-9	Sequence
00.9	60	10	US-09-908-975-15934	Sequence 15934, A	923	50.0	30	9	US-09-452-599-77	Sequence
00.9	60	10	US-09-908-975-16858	Sequence 16858, A	924	50.0	30	9	US-09-893-615-83	Sequence
00.9	60	10	US-09-908-975-17812	Sequence 17812, A	925	50.0	30	14	US-10-313-853-10	Sequence
00.9	60	10	US-09-908-975-18544	Sequence 18544, A	926	50.0	30	14	US-10-121-120-77	Sequence
00.9	60	10	US-09-908-975-19219	Sequence 19219, A	927	50.0	30	14	US-10-289-135A-99	Sequence
00.9	60	10	US-09-908-975-19647	Sequence 19647, A	928	50.0	30	15	US-10-601-171-83	Sequence
00.9	60	10	US-09-908-975-20251	Sequence 20251, A	929	50.0	31	9	US-09-801-274-199	Sequence
00.9	60	10	US-09-908-975-22972	Sequence 22972, A	930	50.0	31	9	US-09-801-274-687	Sequence
00.9	19	9	US-09-954-225-4	Sequence 4, Appl	931	50.0	31	10	US-09-874-141-43	Sequence
00.9	20	9	US-09-976-674-53	Sequence 53, Appl	932	50.0	31	10	US-09-912-263-311	Sequence
00.9	20	9	US-09-969-373-3060	Sequence 3060, Ap	933	50.0	31	14	US-10-283-349-53	Sequence
00.9	20	10	US-09-949-427-257	Sequence 257, Ap	934	50.0	32	9	US-09-933-497B-3	Sequence
00.9	20	14	US-10-222-334-70	Sequence 70, Appl	935	50.0	32	15	US-10-323-927-8	Sequence
00.9	20	14	US-10-006-430-67	Sequence 67, Appl	936	50.0	33	9	US-09-874-547-16	Sequence
00.9	20	15	US-10-380-931-87	Sequence 87, Appl	937	50.0	34	10	US-09-269-921-46	Sequence
00.9	21	9	US-09-765-081-323	Sequence 323, App	938	50.0	34	10	US-09-509-098-68	Sequence
00.9	21	13	US-10-060-301-98	Sequence 98, Appl	939	50.0	34	14	US-10-138-505-16	Sequence
00.9	21	13	US-10-060-301-100	Sequence 100, Appl	940	50.0	34	14	US-10-079-709-37	Sequence
00.9	23	10	US-09-860-761-26	Sequence 26, Appl	941	50.0	35	9	US-10-218-253-46	Sequence
00.9	24	10	US-09-989-420-59	Sequence 59, Appl	942	50.0	35	9	US-09-987-456-53	Sequence
00.9	24	10	US-09-927-121B-58	Sequence 58, Appl	943	50.0	35	14	US-10-195-752-29	Sequence
00.9	24	10	US-09-940-185-3448	Sequence 3448, Ap	944	50.0	35	14	US-10-168-809-20	Sequence
00.9	24	10	US-09-382-860-191	Sequence 191, App	945	50.0	37	9	US-09-987-456-84	Sequence
00.9	24	14	US-10-411-976-43	Sequence 43, Appl	946	50.0	37	14	US-10-052-942-106	Sequence
00.9	24	14	US-10-032-585-4727	Sequence 4727, Ap	947	50.0	38	14	US-10-313-853-8	Sequence
00.9	25	9	US-09-918-702-3	Sequence 3, Appl	948	50.0	39	9	US-09-794-927-37	Sequence
00.9	25	14	US-10-215-112-10003	Sequence 10003, A	949	50.0	39	9	US-09-794-927-38	Sequence
00.9	25	14	US-10-215-112-13718	Sequence 13718, A	950	50.0	39	9	US-09-795-847-37	Sequence
00.9	25	14	US-10-098-263B-3552	Sequence 3552, Ap	951	50.0	39	9	US-09-795-847-38	Sequence
00.9	25	14	US-10-098-263B-5001	Sequence 5001, Ap	952	50.0	39	9	US-09-794-743-37	Sequence
00.9	25	14	US-10-098-263B-8728	Sequence 8728, Ap	953	50.0	39	9	US-09-794-743-38	Sequence
00.9	25	14	US-10-098-263B-17749	Sequence 17749, A	954	50.0	39	9	US-09-794-748-37	Sequence
00.9	25	14	US-10-098-263B-21652	Sequence 21652, A	955	50.0	39	9	US-09-794-748-38	Sequence
00.9	25	14	US-10-098-263B-23500	Sequence 23500, A	956	50.0	39	9	US-09-794-925-37	Sequence
00.9	25	14	US-10-098-263B-30435	Sequence 30435, A	957	50.0	39	9	US-09-794-925-38	Sequence
00.9	25	14	US-10-098-263B-30436	Sequence 30436, A	958	50.0	39	9	US-09-681-442-37	Sequence
00.9	25	14	US-10-098-263B-39611	Sequence 39611, A	959	50.0	39	9	US-09-681-442-38	Sequence
00.9	25	14	US-10-098-263B-40852	Sequence 40852, A	960	50.0	39	10	US-09-263-959-220	Sequence
00.9	25	14	US-10-098-263B-47959	Sequence 47959, A	961	50.0	39	10	US-09-869-414-37	Sequence
00.9	25	14	US-10-098-263B-54424	Sequence 54424, A	962	50.0	39	10	US-09-869-414-38	Sequence
00.9	25	14	US-10-098-263B-55309	Sequence 55309, A	963	50.0	39	10	US-09-548-366-37	Sequence
00.9	25	14	US-10-098-263B-57831	Sequence 57831, A	964	50.0	39	10	US-09-548-366-38	Sequence
00.9	25	14	US-10-098-263B-58267	Sequence 58267, A						
00.9	25	14	US-10-098-263B-66895	Sequence 66895, A						

39 14 US-10-283-349-52  
 50.0 39 US-10-417-820A-109  
 50.0 40 US-09-995-973-29  
 50.0 40 US-09-995-484-29  
 50.0 42 9 US-09-874-547-17  
 50.0 43 14 US-10-156-604-4  
 50.0 46 14 US-10-062-809-65  
 50.0 47 14 US-10-076-802-67  
 50.0 47 14 US-10-010-729-54  
 50.0 47 15 US-10-367-169-67  
 50.0 47 15 US-10-349-143-1374  
 50.0 47 15 US-10-349-143-2638  
 50.0 47 15 US-10-349-143-3015  
 50.0 47 15 US-10-349-143-3089  
 50.0 47 15 US-10-349-143-3453  
 50.0 47 15 US-10-260-238-6029  
 50.0 49 14 US-10-078-337-44  
 50.0 50 15 US-10-131-827-2278  
 50.0 50 15 US-10-131-827-2550  
 50.0 50 15 US-10-131-827-3323  
 50.0 50 15 US-10-131-827-5584  
 50.0 50 15 US-10-131-827-6421  
 50.0 50 15 US-10-131-827-6811  
 50.0 50 15 US-10-131-827-7273  
 50.0 51 9 US-09-794-927-41  
 50.0 51 9 US-09-794-927-42  
 50.0 51 9 US-09-795-847-41  
 50.0 51 9 US-09-795-847-42  
 50.0 51 9 US-09-794-743-41  
 50.0 51 9 US-09-794-743-42  
 50.0 51 9 US-09-794-748-41  
 50.0 51 9 US-09-794-748-42  
 50.0 51 9 US-09-794-925-41  
 50.0 51 9 US-09-794-925-42  
 50.0 51 9 US-09-874-923-27  
 50.0 51 9 US-09-881-442-41

## ALIGNMENTS

/c  
 plication US/09931375A  
 US20030027151A1  
 TION:  
 MAN, Matthew L.  
 NG, Yacqin  
 SEN, Bjorn R.  
 WADI, Georges  
 MAN-ROMAN, Sergio  
 TION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY OF  
 TION: OSTEOPOROSIS  
 : 38464-0004  
 ATION NUMBER: US/09/931,375A  
 : DATE: 2001-08-17  
 'ION NUMBER: US 60/304,851  
 DATE: 2001-07-13  
 'ION NUMBER: US 60/234,337  
 DATE: 2000-09-22  
 'ION NUMBER: US 60/226,119  
 DATE: 2000-08-18  
 ID NOS: 89  
 ntIn version 3.0

Official Sequence  
 ATION: Primer

64.5%; Score 14.2; DB 10; Length 20;

Sequence 52, Appl  
 Sequence 109, Appl  
 Sequence 29, Appl  
 Sequence 29, Appl  
 Sequence 17, Appl  
 Sequence 4, Appl  
 Sequence 65, Appl  
 Sequence 67, Appl  
 Sequence 54, Appl  
 Sequence 67, Appl  
 Sequence 1374, Ap  
 Sequence 2638, Ap  
 Sequence 3015, Ap  
 Sequence 3089, Ap  
 Sequence 3453, Ap  
 Sequence 6029, Ap  
 Sequence 44, Appl  
 Sequence 2278, Ap  
 Sequence 2550, Ap  
 Sequence 3323, Ap  
 Sequence 5584, Ap  
 Sequence 6421, Ap  
 Sequence 6811, Ap  
 Sequence 7273, Ap  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 41, Appl  
 Sequence 42, Appl  
 Sequence 27, Appl  
 Sequence 41, Appl

Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 21  
 Db 20 AAAATCACAGTCTCTGCGG 2

## RESULT 2

US-09-908-975-15980/c  
 ; Sequence 15980, Application US/09908975  
 ; Publication No. US20030165843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHOSHAN, Avi  
 ; APPLICANT: WASSERMAN, Alon  
 ; APPLICANT: MINTZ, Eli  
 ; APPLICANT: MINTZ, Liat  
 ; APPLICANT: FAIGLER, Simchon  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN  
 ; FILE REFERENCE: 36688-0005  
 ; CURRENT APPLICATION NUMBER: US/09/908,975  
 ; CURRENT FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/287,724  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: US 60/221,607  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 32337  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 15980  
 ; LENGTH: 60  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-908-975-15980

Query Match 64.5%; Score 14.2; DB 10; Length 60;  
 Best Local Similarity 84.2%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCACAGTCTCTGC 19  
 Db 60 AGACAATCACAGTCTCTGC 42

## RESULT 3

US-10-098-263B-53982  
 ; Sequence 53982, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 53982  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-53982

Query Match 62.7%; Score 13.8; DB 14; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 2.1e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACAATCACAGTCTCTCT 17  
 Db 6 ATACAATCACAGTCTCTCT 22

09:38:24 2004

us-10-090-326-6.max.rnpb

```
/c
Application US/10215112
US20030082596A1
TION:
    hael Mittmann
    TION: Method of Genetic Analysis of Probes:
    TION: Test3
    : 3119
    ATION NUMBER: US/10/215,112
    DATE: 2002-08-08
    ID NOS: 14936
    SEQ for Windows Version 4.0

Official Sequence
TION: Synthetic Oligonucleotide
    }
        61.8%; Score 13.6; DB 14; Length 25;
        Larity 80.0%; Pred. No. 2.7e+03;
        Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCACAGTCTCTGCGGA 22
|||||
TTACCGGTCTACCGGA 4

4/c
Application US/10215112
US20030082596A1
TION:
    hael Mittmann
    TION: Method of Genetic Analysis of Probes:
    TION: Test3
    : 3119
    ATION NUMBER: US/10/215,112
    DATE: 2002-08-08
    ID NOS: 14936
    SEQ for Windows Version 4.0

Official Sequence
TION: Synthetic Oligonucleotide
    }
        61.8%; Score 13.6; DB 14; Length 25;
        Larity 80.0%; Pred. No. 2.7e+03;
        Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCACAGTCTCTGCGGA 22
|||||
TTACCGGTCTCTGCGG 4

700
Application US/10098263B
US20030104410A1
TION:
    tman, Michael
    TION: Human Microarray
    : 3118.1
    ATION NUMBER: US/10/098,263B
    DATE: 2003-01-08
    TION NUMBER: 60/276,759
    DATE: 2001-03-16
    ID NOS: 131066

/c
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-61700

Query Match
Best Local Similarity 61.8%; Score 13.6; DB 14; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21
Db 4 GACAACTCAGTGTCTCGG 23

RESULT 7
US-10-098-263B-126081/c
; Sequence 126081, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 126081
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-126081

Query Match
Best Local Similarity 61.8%; Score 13.6; DB 14; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCACAGTCTCTGCG 20
Db 20 AGACTCAGTGTCTCGAG 1

RESULT 8
US-10-298-796-41
; Sequence 41, Application US/10298796
; Publication No. US20030220490A1
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Shinichi
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: CELL MEMBRANE DIRECTED DRUGS
; FILE REFERENCE: 1110-253P
; CURRENT APPLICATION NUMBER: US/10/298,796
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/331,793
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Synthetic DNA Primers
US-10-298-796-41

Query Match
Best Local Similarity 61.8%; Score 13.6; DB 15; Length 37;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21
Db 9 GATCCTCAGAGTCTCTGCGG 28
```

1/c  
Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
TION NUMBER: US/09/908,975  
DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

no sapiens

11

61.8%; Score 13.6; DB 10; Length 60;  
ilarity 80.0%; Pred. No. 3e+03; 4; Indels 0; Gaps 0;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCACAGTCTCTGCGGA 22  
|||  
ATACCACTCTCTGGAA 7

366/c

Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
TION NUMBER: US/09/908,975  
DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

no sapiens

366

61.8%; Score 13.6; DB 10; Length 60;  
ilarity 80.0%; Pred. No. 3e+03; 4; Indels 0; Gaps 0;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCACAGTCTCTGCGG 21  
|||  
CAATCACTCTCTATACAG 37

RESULT 11  
US-09-908-975-14283/c  
; Sequence 14283, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14283  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-14283

Query Match 61.8%; Score 13.6; DB 10; Length 60;  
Best Local Similarity 80.0%; Pred. No. 3e+03; 4; Indels 0;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGGA 22  
|||  
Db 60 ACATTGACAGTCTCTGGCGA 41

RESULT 12

US-09-908-975-8908/c  
; Sequence 8908, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8908  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-8908

Query Match 60.9%; Score 13.4; DB 10; Length 60;  
Best Local Similarity 93.3%; Pred. No. 3.9e+03; 1; Indels 0;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 8 CACAGTCTCTGCGGA 22  
|||  
Db 16 CACAGTCTCTGAGGA 2

09:38:24 2004

us-10-090-326-6.max.rnpb

Publication US/10189256  
US20040005569A1  
TION: Antisense Oligonucleotide  
ada F. Baker  
san M. Freier  
meth W. Dobie  
TION: ANTISENSE MODULATION OF NF-KAPPA-B P50 SUBUNIT EXPRESSION  
PTS-0050  
TION NUMBER: US/10/189,256  
DATE: 2002-07-02  
ID NOS: 143

Official Sequence

TION: Antisense Oligonucleotide

60.0%; Score 13.2; DB 15; Length 20;  
larity 83.3%; Pred. No. 4.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATCAGAGTCTCTGCG 20  
|||||  
GTGACAGTCTCTGCG 3

Publication US/10190366  
US20040006031A1  
TION: Antisense Oligonucleotide  
holas M. Dean  
san M. Freier  
meth W. Dobie  
TION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION  
PTS-0023  
TION NUMBER: US/10/190,366  
DATE: 2002-07-02  
ID NOS: 409

Official Sequence

TION: Antisense Oligonucleotide

60.0%; Score 13.2; DB 15; Length 20;  
larity 83.3%; Pred. No. 4.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCACAGTCTCTGCGG 21  
|||||  
TCATAGCCTCTGTGG 20

Publication US/10190366  
US20040006031A1  
TION: Antisense Oligonucleotide  
holas M. Dean  
san M. Freier  
meth W. Dobie  
TION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION  
PTS-0023  
TION NUMBER: US/10/190,366  
DATE: 2002-07-02  
ID NOS: 409

SEQ ID NO 332  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-190-366-332

Query Match 60.0%; Score 13.2; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 4 CAATCAGAGTCTCTGCGG 21  
|||||  
DB 18 CAATCATAGCCTCTGTGG 1

RESULT 16

US-09-840-743-77/c  
Sequence 77, Application US/09840743  
Publication No. US20030135890A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Choi, Yeonhee  
APPLICANT: Hannon, Mike  
APPLICANT: Okamuro, Jack Kishiro  
APPLICANT: Tatarinova, Tatiana Valerievna  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Plant Development  
FILE REFERENCE: 023070-099910US  
CURRENT APPLICATION NUMBER: US/09/840,743  
CURRENT FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: US 09/553,690  
PRIOR FILING DATE: 2000-04-21  
NUMBER OF SEQ ID NOS: 119  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 77  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer SKB-  
US-09-840-743-77

Query Match 60.0%; Score 13.2; DB 10; Length 22;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 GACAATCAGAGTCTCTGC 19  
|||||  
DB 18 GACAATAACCGTCTCTCC 1

RESULT 17

US-10-098-263B-65769  
Sequence 65769, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 65769  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-65769

Query Match 60.0%; Score 13.2; DB 14; Length 25;

09:38:24 2004

us-10-090-326-6.max.rnpb

```
ilarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 3;
PCACAGTCTCTCGGA 22
|||||
TTATAGTCTCTCGGA 23

13912/c
2, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
NTION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
3 DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
12

no sapien
13912
60.0%; Score 13.2; DB 14; Length 25;
ilarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 3;
AATCAGTCTCTCGG 20
|||||
AACTCAGTCTCTCGG 1

15691
1, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
NTION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
3 DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
91

no sapien
15691
60.0%; Score 13.2; DB 14; Length 25;
ilarity 83.3%; Pred. No. 4.4e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 3;
ATCAGTCTCTCGG 21
|||||
ATCATATCTCTCGG 19

2312/c
2, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
NTION: Human Microarray
```

```
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 123312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-123312

Query Match 60.0%; Score 13.2; DB 14; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 ACAATCAGTCTCTCGG 20
|||||
Db 18 ACAACTCAGTCTCTCGG 1

RESULT 21
US-09-893-615-73/c
; Sequence 73, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Gerald W.
; Wong, Hing
; Stinson, Jeffrey L.
; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTE
; POSITIVE BACTERIA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/893,615
; FILING DATE: 29-Jun-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 04995.0041-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-893-615-73

Query Match 60.0%; Score 13.2; DB 9; Length 35;
Best Local Similarity 72.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0;
```

09:38:24 2004

us-10-090-326-6.max.rnpb

CAAGTCTCTGCGG 21  
|||||:|  
CAGTCTCTCYKAG 15

plication US/09215163  
US20030170248A1  
TION: HUMANIZED MONOCLONAL ANTIBODIES THAT PROTECT AGAINST  
TION: SHIGA TOXIN INDUCED DISEASE  
: 04995.0032-00000  
TION NUMBER: US/09/215,163  
DATE: 1998-12-18  
ID NOS: 44  
tIn Ver. 2.0

#### Official Sequence

TION: Description of Artificial Sequence: Synthetic  
TION: Oligonucleotide

60.0%; Score 13.2; DB 10; Length 35;  
larity 72.2%; Pred. No. 4.6e+03;  
Conservative 3; Mismatches 2; Indels 0; Gaps 0;

TCACAGTCTCTGCGG 21  
|||||:|  
TCACHGTCTCTCYKAG 15

plication US/10601171  
US20040013673A1  
MATION:  
T: Fischer, Gerald W.  
Schuman, Richard F.  
Wong, Hing  
Stinson, Jeffrey L.  
INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND  
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM  
POSITIVE BACTERIA

#### F SEQUENCES: 89

NDENCE ADDRESS:  
RESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP

EET: 1300 I Street, NW  
Y: Washington

NTY: DC

: 20005-3315

#### READABLE FORM:

IUM TYPE: Floppy disk  
PUTER: IBM PC compatible  
ATING SYSTEM: PC-DOS/MS-DOS  
WARE: PatentIn Release #1.0, Version #1.30  
APPLICATION DATA:  
PLICATION NUMBER: US/10/601,171  
ING DATE: 23-Jun-2003  
/AGENT INFORMATION:  
E: Einaudi, Carol P.  
ISTRATION NUMBER: 32,220  
ERENCE/DOCKET NUMBER: 04995.0041-00000

#### TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-10-601-171-73

Query Match 60.0%; Score 13.2; DB 15; Length 35;  
Best Local Similarity 72.2%; Pred. No. 4.6e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCACAGTCTCTGCGG 21  
|||||:|  
Db 32 CASTCACHGTCTCTCYKAG 15

#### RESULT 24

US-10-349-143-1473

; Sequence 1473, Application US/10349143  
; Publication No. US2004000584A1

#### GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilyia  
; TITLE OF INVENTION: Biallelic markers for use in constructing a hi  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,85  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,73  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,61  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1473

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 24

OTHER INFORMATION: 99-25379-389 : polymorphic base C or T

US-10-349-143-1473

Query Match 60.0%; Score 13.2; DB 15; Length 47;  
Best Local Similarity 75.0%; Pred. No. 4.8e+03;  
Matches 15; Conservative 1; Mismatches 4; Indels 0;

QY 2 GACATCACAGTCTCTGCGG 21  
|||||:|  
Db 19 GAGCAYCACACTCTGCGG 38

#### RESULT 25

US-10-131-827-852/c

; Sequence 852, Application US/10131827  
; Publication No. US20040009479A1

#### GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MC



09:38:24 2004

us-10-090-326-6.max.rnpb

```

TION: CHRONIC INFLAMMATORY DISEASES
: 506612000120
ATION NUMBER: US/10/131,827
DATE: 2002-09-06
ION NUMBER: US 10/006,290
ATE: 2001-10-22
ION NUMBER: US 60/296,764
ATE: 2001-06-08
ID NOS: 9090
ntIn version 3.1

to sapiens
50.0%; Score 13.2; DB 15; Length 50;
larity 83.3%; Pred. No. 4.8e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CACAGTCTCTGCGGA 22
|||||
CATAGTCTCTGGGTA 4

46/c
Application US/09908975
US20030165843A1
ATION:
SHAN, Avi
SSERMAN, Alon
NTZ, Eli
NTZ, Liat
LIGIER, Simchon
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
: 36688-0005
ATION NUMBER: US/09/908,975
DATE: 2001-07-20
ION NUMBER: US 60/287,724
DATE: 2001-05-02
ION NUMBER: US 60/221,607
DATE: 2000-07-28
ID NOS: 32337
ntIn version 3.0

to sapiens
146
60.0%; Score 13.2; DB 10; Length 60;
larity 83.3%; Pred. No. 4.9e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATCAGTCTCTGCGG 21
|||||
ATCATAGTCTCTGCTG 24

3781/c
Application US/10098263B
US20030104410A1
ATION:
ttman, Michael
TION: Human Microarray
3: 3118.1
ATION NUMBER: US/10/098,263B
DATE: 2003-01-08
ION NUMBER: 60/276,759
DATE: 2001-03-16

```

```

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 65781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-65781

Query Match 59.1%; Score 13; DB 14; Length 25;
Best Local Similarity 76.2%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21
DB 25 AGAGCCTCAGAGTCTCTGTGG 5

RESULT 28
US-10-098-263B-113313/c
; Sequence 113313, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 113313
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-113313

Query Match 59.1%; Score 13; DB 14; Length 25;
Best Local Similarity 76.2%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21
DB 22 AGACTCTCGAGTCACTGCGG 2

RESULT 29
US-10-098-263B-113314/c
; Sequence 113314, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 113314
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-113314

Query Match 59.1%; Score 13; DB 14; Length 25;
Best Local Similarity 76.2%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21
DB 22 AGACTCTCGTAGTCACTGCGG 2

```

```
RESULT 32
US-09-795-006A-40/c
; Sequence 40, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: oligonucleotide sequence derived from multiple
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-40

Query Match          59.1%; Score 13; DB 9; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGGA 22
   ||||| ||||| |||||
Db 54 GCCAATCACACTTCTCTCGGA 34

RESULT 33
US-09-908-975-19195
; Sequence 19195, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19195
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19195

Query Match          59.1%; Score 13; DB 10; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGGA 22
   ||||| ||||| |||||
Db 10 GCCCATGACTGTCTCTCGGA 30

RESULT 34
US-09-908-975-19195
; Sequence 19195, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19195
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19195

Query Match          59.1%; Score 13; DB 15; Length 50;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGG 21
   ||||| ||||| |||||
Db 15 GACCAATGACTGTCTCAGG 4
```

108/c  
 ; Application US/09908975  
 ; Publication No. US20030165843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHOSHAN, AVI  
 ; APPLICANT: WASSERMAN, ALON  
 ; APPLICANT: MINTZ, ELI  
 ; APPLICANT: FAIGLER, SIMCHON  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
 ; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
 ; FILE REFERENCE: 36688-0005  
 ; CURRENT APPLICATION NUMBER: US/09/908,975  
 ; CURRENT FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/287,724  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: US 60/221,607  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 32337  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 32337  
 ; LENGTH: 60  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

no sapiens  
 108

59.1%; Score 13; DB 10; Length 60;  
 ilarity 76.2%; Pred. No. 6.2e+03;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGAGTCTCTCGGG 21  
 ||||| ||||| ||||| ||||| |||||  
 CAATCAGAGTCTCTCGGG 26

372/c

; Application US/09908975  
 ; Publication No. US20030165843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHOSHAN, AVI  
 ; APPLICANT: WASSERMAN, ALON  
 ; APPLICANT: MINTZ, ELI  
 ; APPLICANT: FAIGLER, SIMCHON  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
 ; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
 ; FILE REFERENCE: 36688-0005  
 ; CURRENT APPLICATION NUMBER: US/09/908,975  
 ; CURRENT FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/287,724  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: US 60/221,607  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 32337  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 32337  
 ; LENGTH: 60  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens

no sapiens  
 172

59.1%; Score 13; DB 10; Length 60;  
 ilarity 76.2%; Pred. No. 6.2e+03;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

AAATCAGAGTCTCTCGGG 22  
 ||||| ||||| ||||| ||||| |||||  
 AAGTACCATCTCTCTGGA 8

253

; Sequence 23253, Application US/09908975  
 ; Publication No. US20030165843A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHOSHAN, AVI  
 ; APPLICANT: WASSERMAN, ALON  
 ; APPLICANT: MINTZ, ELI  
 ; APPLICANT: FAIGLER, SIMCHON  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA  
 ; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
 ; FILE REFERENCE: 36688-0005  
 ; CURRENT APPLICATION NUMBER: US/09/908,975  
 ; CURRENT FILING DATE: 2001-07-20  
 ; PRIOR APPLICATION NUMBER: US 60/287,724  
 ; PRIOR FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: US 60/221,607  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 32337  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 23253  
 ; LENGTH: 60  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

Query Match 59.1%; Score 13; DB 10; Length 60;  
 Best Local Similarity 76.2%; Pred. No. 6.2e+03;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGAATCAGAGTCTCTCGGG 21  
 ||||| ||||| ||||| ||||| |||||  
 Db 14 ACATTCAGAGTCTCTCGGG 34

RESULT 37

US-10-156-306-4767  
 ; Sequence 4767, Application US/10156306  
 ; Publication No. US20030119017A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases  
 ; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
 ; FILE REFERENCE: MEH01-664-A (400/050)  
 ; CURRENT APPLICATION NUMBER: US/10/156,306  
 ; CURRENT FILING DATE: 2002-05-28  
 ; NUMBER OF SEQ ID NOS: 8013  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4767  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens

Query Match 58.2%; Score 12.8; DB 14; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 6.7e+03;  
 Matches 10; Conservative 4; Mismatches 2; Indels 0;

QY 4 CAATCAGAGTCTCTGC 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 2 CAUCCAGAGUCUCUC 17

RESULT 38

US-10-156-306-5763  
 ; Sequence 5763, Application US/10156306  
 ; Publication No. US20030119017A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases  
 ; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
 ; FILE REFERENCE: MEH01-664-A (400/050)

09:38:24 2004

us-10-090-326-6.max.rnpb

ATION NUMBER: US/10/156,306  
DATE: 2002-05-28  
ID NOS: 8013  
ntin version 3.0

o sapiens  
3

58.2%; Score 12.8; DB 14; Length 17;  
larity 62.5%; Pred. No. 6.7e+03;  
Conservative 4; Mismatches 2; Indels 0; Gaps 0;

TCACAGTCTCTGC 19  
: |||||:|:  
UCCAGUCUCUUC 16

Publication US/09833067  
02005488A1

TION:

ANLEY, PETER

NICH, KENNETH

TION: DISSOCIATED PILI, THEIR PRODUCTION AND USE

: 050939/0102

ATION NUMBER: US/09/833,067

DATE: 2001-04-12

ION NUMBER: 60/196,493

ATE: 2000-04-12

ID NOS: 26

ntin Ver. 2.1

ificial Sequence

TION: Description of Artificial Sequence: Primer

58.2%; Score 12.8; DB 9; Length 20;  
larity 87.5%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CAATCAGCTCTC 16  
: |||||:  
3AATCGCAGCTCTC 3

Publication US/09833079  
020142008A1

TION:

ANLEY, PETER

NICH, KENNETH

AMIDT, M. ALEXANDER

TION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR

TION: PRODUCTION AND USE

: 050939/0104

ATION NUMBER: US/09/833,079

DATE: 2001-04-12

ID NOS: 39

ntin Ver. 2.1

ificial Sequence

TION: Description of Artificial Sequence: Primer

Query Match 58.2%; Score 12.8; DB 9; Length 20;  
Best Local Similarity 87.5%; Pred. No. 6.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACAATCAGCTCTC 16  
DB 18 AGAGAATCGCAGCTCTC 3

RESULT 41

US-09-797-207-16

; Sequence 16, Application US/09797207

; Patent No. US20020098563A1

; GENERAL INFORMATION:

; APPLICANT: KORCZAK, BOZENA

; TITLE OF INVENTION: NOVEL CORE 2 BETA-1, 6-N-ACETYLGLYCOSAMINYLTRE

; FILE REFERENCE: GLYCO-7P1

; CURRENT APPLICATION NUMBER: US/09/797,207

; CURRENT FILING DATE: 2001-03-02

; EARLIER APPLICATION NUMBER: 09/495,913

; EARLIER FILING DATE: 2000-02-02

; EARLIER APPLICATION NUMBER: 60/118,674

; EARLIER FILING DATE: 1999-02-03

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-797-207-16

Query Match 58.2%; Score 12.8; DB 9; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 7 TCACAGTCTCTGCGGA 22  
DB 2 TCACAGTCTCTGTTGA 17

RESULT 42

US-10-445-318-16

; Sequence 16, Application US/10445318

; Publication No. US20040033521A1

; GENERAL INFORMATION:

; APPLICANT: KORCZAK, BOZENA

; TITLE OF INVENTION: NOVEL CORE 2 BETA-1, 6-N-ACETYLGLYCOSAMINYLTRE

; FILE REFERENCE: GLYCO-7P1

; CURRENT APPLICATION NUMBER: US/10/445,318

; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/797,207

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 09/495,913

; PRIOR FILING DATE: 2000-02-02

; PRIOR APPLICATION NUMBER: 60/118,674

; PRIOR FILING DATE: 1999-02-03

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-445-318-16

Query Match 58.2%; Score 12.8; DB 12; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7e+03;

09:38:24 2004

us-10-090-326-6.max.rnpb

Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
ACAGTCTCTGGCGA 22  
|||||  
ACAGTCTCTGGTGA 17

2151/c  
Application US/10098263B  
US20030104410A1  
tman, Michael  
TION: Human Microarray  
3: 3118.1  
ATION NUMBER: US/10/098,263B  
3 DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
array Probe Sequence Listing Generator V 1.1

to sapien  
2151

58.2%; Score 12.8; DB 14; Length 25;  
larity 87.5%; Pred. No. 7.1e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TAATCACAGTCTCT 17  
|||||  
TAATCAGGTCTACT 1

1483  
Application US/10098263B  
US20030104410A1  
tman, Michael  
TION: Human Microarray  
3: 3118.1  
ATION NUMBER: US/10/098,263B  
3 DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
array Probe Sequence Listing Generator V 1.1

to sapien  
1483

58.2%; Score 12.8; DB 14; Length 25;  
larity 87.5%; Pred. No. 7.1e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ACAGTCTCTGGCGA 22  
|||||  
ACAGTCTCTGGGAA 21

1605  
Application US/10098263B  
US20030104410A1  
tman, Michael  
TION: Human Microarray  
3: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 86605  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-86605  
  
Query Match 58.2%; Score 12.8; DB 14; Length 25;  
Best Local Similarity 87.5%; Pred. No. 7.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
  
QY 2 GACAATCACAGTCTCT 17  
|||||  
Db 8 GACAATCACAGTCTCT 23  
  
Search completed: February 29, 2004, 13:42:33  
Job time : 149.143 secs

09:38:25 2004

us-10-090-326-6.max.rst

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1651.43 Seconds  
(without alignments)  
397.818 Million cell updates/sec

JS-10-090-326-6

22  
1 agacaatcacagtctctgogga 22

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

bits satisfying chosen parameters: 203984

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

EST:\*

1: em estba:\*

2: em esthum:\*

3: em estin:\*

4: em estnu:\*

5: em estov:\*

6: em estpl:\*

7: em estro:\*

8: em htc:\*

9: gb est1:\*

10: gb est2:\*

11: gb htc:\*

12: gb est3:\*

13: gb est4:\*

14: gb est5:\*

15: em estfun:\*

16: em estom:\*

17: em gss hum:\*

18: em gss inv:\*

19: em gss pln:\*

20: em gss vrt:\*

21: em gss fun:\*

22: em gss nam:\*

23: em gss mus:\*

24: em gss pro:\*

25: em gss rod:\*

26: em gss phg:\*

27: em gss vrl:\*

28: gb gss1:\*

29: gb gss2:\*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

# SUMMARIES

* entry	at	ch	Length	DB	ID	Description
67.3	39	9	AV954296			AV954296 AV954296
64.5	41	28	AZ612511			AZ612511 IM0439006
63.6	59	28	AZ345576			AZ345576 IM0080K16
61.8	58	9	AA211707			AA211707 zq84fl1.r

51.8	20	AZ412898	1M0186F07	11	50.0	47	14	T25588	T25588		
51.8	29	CF861062	psZ0003iH	11	50.0	48	28	BH840707	BH840707		
51.8	30	CF860995	psZ0003iA	11	50.0	50	9	AI127829	AI127829		
51.8	31	AA863835	vx09e08.r	11	50.0	50	9	AUI02391	AUI02391		
51.8	31	AZ4317063	1M0225C07	11	50.0	50	9	AUI02935	AUI02935		
51.8	31	BH851766	BH851766 SALK_0734	11	50.0	50	29	TA208F04Q	TA208F04Q		
51.8	31	BZ353562	SALK_1204	11	50.0	51	10	AW461289	AW461289		
51.8	34	AZ785142	2M0028L17	11	50.0	51	28	B04190	B04190		
51.8	37	AA444863	ve75f02.r	11	50.0	51	29	CG802231	CG802231		
51.8	39	BJ075771	BJ075771	11	50.0	52	9	AA967363	AA967363		
51.8	45	AZ502422	1M0341N12	11	50.0	52	9	AI214100	AI214100		
51.8	46	AA607492	vm61n02.r	11	50.0	52	14	CA795142	CA795142		
51.8	47	AI2643	CHR90163	11	50.0	52	14	CB221476	CB221476		
51.8	48	AZ603153	1M0422K14	11	50.0	52	28	AZ773269	AZ773269		
51.8	49	AZ768953	1M0569M11	11	50.0	52	28	BH862019	BH862019		
51.8	50	AUI06551	AUI06551	11	50.0	53	28	B05229	B05229		
51.8	50	AUI06829	AUI06829	11	50.0	53	28	BH850069	BH850069		
51.8	50	AUI06909	AUI06909	11	50.0	55	29	AB081958	AB081958		
51.8	50	AUI08071	AUI08071	11	50.0	56	28	AZ630437	AZ630437		
51.8	50	AI940148	Arabidops	11	50.0	57	9	AA790616	AA790616		
51.8	52	BF641940	NF011F091	11	50.0	57	14	CB913876	CB913876		
51.8	52	14	CF300173	7LEAF--04	11	50.0	57	28	BH909214	BH909214	
51.8	53	14	CF291012	14ROOT--0	11	50.0	58	10	BE057307	BE057307	
51.8	54	CG326783	RR1222 Ba	11	50.0	58	28	BH912876	BH912876		
51.8	57	AZ482281	1M0307B22	11	50.0	58	28	AZ790062	AZ790062		
51.8	58	CB548541	MMP10003	11	50.0	58	28	AZ861517	AZ861517		
51.8	60	AL850332	AL850332	11	50.0	59	28	CC053444	CC053444		
50.9	29	AZ424753	1M0204F04	11	50.0	60	28	BZ378400	BZ378400		
50.9	31	10	BF666946	602121169	11	50.0	60	28	BZ378520	BZ378520	
50.9	31	28	AZ810463	2M0076D02	181	10.8	49.1	22	28	AZ790062	AZ790062
50.9	36	28	AZ800134	2M0058C04	182	10.8	49.1	22	28	AZ790062	AZ790062
50.9	37	28	AZ827785	2M0104J23	183	10.8	49.1	29	28	BZ592652	BZ592652
50.9	37	29	DR32K10S	Danio rer	184	10.8	49.1	30	28	AZ837449	AZ837449
50.9	42	28	AZ511989	1M0357I13	185	10.8	49.1	31	13	BQ587774	BQ587774
50.9	43	14	H41669	yo06808.s1	186	10.8	49.1	31	13	BQ587775	BQ587775
50.9	43	28	AZ793373	2M0049M03	187	10.8	49.1	31	29	TA274B11Q	TA274B11Q
50.9	47	28	BH633020	1007058D0	188	10.8	49.1	31	29	TA83D06Q	TA83D06Q
50.9	49	9	AA693305	vr62h02.s	189	10.8	49.1	34	9	AA108667	AA108667
50.9	50	9	AUI03545	AUI03545	190	10.8	49.1	34	12	B1832750	B1832750
50.9	50	9	AUI07254	AUI07254	191	10.8	49.1	34	28	AZ658401	AZ658401
50.9	51	14	N99012	za67a06.r1	192	10.8	49.1	34	29	TA23A05Q	TA23A05Q
50.9	53	14	CB922548	VVD08EA06	193	10.8	49.1	35	29	TA19B03Q	TA19B03Q
50.9	53	14	CD029923	mgmk004xB	194	10.8	49.1	36	29	TA164B05Q	TA164B05Q
50.9	54	28	BZ382315	SALK_1181	195	10.8	49.1	37	29	TA96H07P	TA96H07P
50.9	55	9	AI625660	ty58f05.x	196	10.8	49.1	38	28	AZ806846	AZ806846
50.9	55	9	AI941388	sc12f12.y	197	10.8	49.1	40	29	TA369C08Q	TA369C08Q
50.9	55	10	BE374434	601227409	198	10.8	49.1	41	28	AZ324505	AZ324505
50.9	55	28	BH861943	SALK_0883	199	10.8	49.1	41	28	BH846254	BH846254
50.9	56	10	BF013330	rk23f01.y	200	10.8	49.1	41	28	BH909818	BH909818
50.9	56	12	BJ058421	BJ058421	201	10.8	49.1	41	29	AG218427	AG218427
50.9	56	28	AZ603330	1M0422C14	202	10.8	49.1	42	29	BX187126	BX187126
50.9	57	12	BG152248	naq74g01.r	203	10.8	49.1	42	28	AZ771653	AZ771653
50.9	58	9	AI963579	wr65b03.x	204	10.8	49.1	42	28	BH810095	BH810095
50.9	58	9	AUI09179	AUI09179	205	10.8	49.1	42	28	BH909806	BH909806
50.9	58	28	AZ818314	2M0088GL6	206	10.8	49.1	42	29	TA348G01Q	TA348G01Q
50.9	60	9	AU257207	AU257207	207	10.8	49.1	43	9	AA763910	AA763910
50.9	60	28	CC456672	SALK_0998	208	10.8	49.1	43	14	R93342	R93342
50.9	25	28	BZ352906	BZ352906 SALK_1194	209	10.8	49.1	43	28	BH863323	BH863323
50.0	28	9	AA138008	mq29g07.r	210	10.8	49.1	43	29	TA53C02Q	TA53C02Q
50.0	29	28	AZ6589502	AZ6589502 1M0535M12	211	10.8	49.1	44	14	H21630	H21630
50.0	34	9	AA116347	AA116347 mq70g12.x	212	10.8	49.1	44	28	AZ833880	AZ833880
50.0	34	13	CO1088	CO1088 HUMG000774	213	10.8	49.1	44	29	AB082470	AB082470
50.0	34	29	AL943585	AL943585 Arabidops	214	10.8	49.1	45	29	AB081995	AB081995
50.0	37	28	AZ662395	AZ662395 1M0541P21	215	10.8	49.1	46	29	AZ769815	AZ769815
50.0	38	28	AZ410352	AZ410352 1M0182D12	216	10.8	49.1	48	29	BX203428	BX203428
50.0	42	14	D67715	D67715 CELK076H4F	217	10.8	49.1	48	9	AA402658	AA402658
50.0	42	28	AZ579512	AZ579512 1M0367F06	218	10.8	49.1	48	28	AZ634499	AZ634499
50.0	44	28	AZ825920	AZ825920 2M0101C23	219	10.8	49.1	49	9	AUI093925	AUI093925
50.0	44	29	CG892045	CG892045 01S0561-0	220	10.8	49.1	49	28	AZ659694	AZ659694
50.0	44	29	AB082470	AB082470 Drosophil	221	10.8	49.1	49	28	AZ807976	AZ807976
50.0	45	28	AZ439466	AZ439466 1M0230E12	222	10.8	49.1	50	9	AL787018	AL787018
50.0	45	28	BZ357956	BZ357956 SALK_1316	223	10.8	49.1	50	9	AUI03208	AUI03208

49.1	50	9	AU105007	AU105007	AU105007	10.6	48.2	52	10	BE321854	BE321854
49.1	50	9	AU105007	AU105007	AU105007	10.6	48.2	52	14	CB226148	CB226148
49.1	50	9	AU105008	AU105008	AU105008	10.6	48.2	52	28	BZ768479	BZ768479
49.1	50	9	AU105008	AU105008	AU105008	10.6	48.2	53	29	CC516008	CC516008
49.1	50	9	AU105010	AU105010	AU105010	10.6	48.2	53	29	CG892142	CG892142
49.1	50	9	AU105010	AU105010	AU105010	10.6	48.2	54	9	AV669957	AV669957
49.1	50	14	CF291606	CF291606	14ROOT--0	10.6	48.2	54	12	BJ062424	BJ062424
49.1	50	28	AZ351661	AZ351661	IM0089MI7	10.6	48.2	54	28	AZ776469	AZ776469
49.1	50	29	TAJ30E01Q	TAJ30E01Q	T. brucei	10.6	48.2	55	9	AA886912	AA886912
49.1	51	13	BQ548575	BQ548575	rd33e09.y	10.6	48.2	55	9	AV619150	AV619150
49.1	51	52	AA903054	AA903054	ok51e07.s	10.6	48.2	55	10	BE057857	BE057857
49.1	52	9	AI431224	AI431224	sa22c10.y	10.6	48.2	55	14	CB357612	CB357612
49.1	52	14	CB056129	CB056129	NISC_jj13	10.6	48.2	55	28	BZ377638	BZ377638
49.1	52	29	BX555460	BX555460	ArabiDops	10.6	48.2	55	29	CG719978	CG719978
49.1	54	9	AA916665	AA916665	oh85g02.s	10.6	48.2	55	29	TA373B02Q	TA373B02Q
49.1	54	9	AI926524	AI926524	wo46a08.x	10.6	48.2	56	9	AA654695	AA654695
49.1	54	28	BH811867	BH811867	SALK_0602	10.6	48.2	56	9	AA487913	AA487913
49.1	54	28	BZ594263	BZ594263	SALK_0837	10.6	48.2	56	9	AI582069	AI582069
49.1	54	29	AL938861	AL938861	ArabiDops	10.6	48.2	57	9	CF864827	CF864827
49.1	55	9	AI091130	AI091130	qa46e02.s	10.6	48.2	57	14	CF864827	CF864827
49.1	55	9	AI241482	AI241482	q69c04.x	10.6	48.2	57	28	CC060282	CC060282
49.1	55	14	H84389	H84389	yv85g10.r1	10.6	48.2	57	29	BX661466	BX661466
49.1	55	28	AZ325145	AZ325145	IM0047J23	10.6	48.2	58	9	AA711331	AA711331
49.1	55	28	CC035254	CC035254	3591.1.74	10.6	48.2	58	12	BJ035240	BJ035240
49.1	57	10	BF507211	BF507211	359P-24a	10.6	48.2	58	28	AZ371514	AZ371514
49.1	57	13	BQ625664	BQ625664	ph9h05.y	10.6	48.2	59	28	AZ402760	AZ402760
49.1	57	28	AZ481308	AZ481308	IM0303P24	10.6	48.2	59	28	AZ848297	AZ848297
49.1	57	29	AL938862	AL938862	ArabiDops	10.6	48.2	59	29	BX894663	BX894663
49.1	57	29	BX547649	BX547649	ArabiDops	10.6	48.2	60	10	BE023743	BE023743
49.1	57	29	AA769106	AA769106	oa74g08.s	10.6	48.2	60	12	BG315430	BG315430
49.1	58	9	AI324804	AI324804	mc33c06.x	10.6	48.2	60	28	AZ758212	AZ758212
49.1	58	9	AA260418	AA260418	vb06a04.r	10.6	48.2	60	28	BH789942	BH789942
49.1	58	29	BX57531	BX57531	ArabiDops	10.6	48.2	60	29	CNS06E2T	AL394587
49.1	58	29	AZ371127	AZ371127	IM0122L06	10.6	48.2	60	29	DME545946	AJ545946
49.1	59	28	AZ774911	AZ774911	2M0004F13	10.4	47.3	21	9	AB088506	AB088506
49.1	60	28	AZ774911	AZ774911	2M0004F13	10.4	47.3	27	28	AZ780337	AZ780337
49.1	60	28	AZ419130	AZ419130	IM0195D03	10.4	47.3	27	28	AZ812632	AZ812632
49.1	62	28	AZ419130	AZ419130	IM0195D03	10.4	47.3	28	28	AZ310671	AZ310671
48.2	25	28	AZ604981	AZ604981	IM0425M22	10.4	47.3	29	14	CF317180	CF317180
48.2	30	28	BH861186	BH861186	SALK_0346	10.4	47.3	31	9	AU257331	AU257331
48.2	31	29	BX533801	BX533801	ArabiDops	10.4	47.3	31	12	BI768049	BI768049
48.2	32	28	AZ780813	AZ780813	2M0018I20	10.4	47.3	31	28	AZ657691	AZ657691
48.2	34	9	AA108667	AA108667	mp30h11.r	10.4	47.3	32	28	AZ635323	AZ635323
48.2	35	9	AU244000	AU244000	AU244000	10.4	47.3	32	29	BX894321	BX894321
48.2	37	29	BX285618	BX285618	ArabiDops	10.4	47.3	32	29	AZ828702	AZ828702
48.2	38	14	D45802	D45802	HUMGS03019	10.4	47.3	33	28	AA101200	AA101200
48.2	38	29	AL753738	AL753738	ArabiDops	10.4	47.3	34	9	AA101200	AA101200
48.2	39	10	BE388093	BE388093	601284409	10.4	47.3	35	28	AZ664145	AZ664145
48.2	39	29	TA13501Q	TA13501Q	T. brucei	10.4	47.3	35	29	TA83D02P	TA83D02P
48.2	39	29	TA150B10P	TA150B10P	T. brucei	10.4	47.3	36	28	AZ307723	AZ307723
48.2	40	9	AA226145	AA226145	nc09f09.r	10.4	47.3	37	28	AZ596892	AZ596892
48.2	40	28	AZ422365	AZ422365	IM0201H03	10.4	47.3	37	29	CC798598	CC798598
48.2	40	28	AZ591528	AZ591528	IM0401K11	10.4	47.3	37	29	CG712147	CG712147
48.2	40	29	AL949623	AL949623	ArabiDops	10.4	47.3	37	29	CC798599	CC798599
48.2	41	28	AZ776402	AZ776402	2M0010B05	10.4	47.3	37	29	TA130F10P	TA130F10P
48.2	41	28	BZ595938	BZ595938	SALK_0904	10.4	47.3	38	28	AZ597945	AZ597945
48.2	43	29	CC940781	CC940781	01S0591-0	10.4	47.3	38	29	BX660257	BX660257
48.2	43	29	CL002012	CL002012	01S0614-0	10.4	47.3	38	29	AA938064	AA938064
48.2	45	28	AZ320120	AZ320120	IM040F02	10.4	47.3	40	9	BH011355	BH011355
48.2	46	9	AI242223	AI242223	qb87d04.x	10.4	47.3	42	29	TA115G05P	TA115G05P
48.2	46	29	AL764340	AL764340	ArabiDops	10.4	47.3	42	29	TA232A04Q	TA232A04Q
48.2	47	29	BX002665	BX002665	ArabiDops	10.4	47.3	43	9	AI079098	AI079098
48.2	47	29	BZ763638	BZ763638	SALK_1200	10.4	47.3	43	14	W95731	W95731
48.2	50	9	AL661103	AL661103	AL661103	10.4	47.3	43	28	BH810212	BH810212
48.2	50	9	AI03880	AI03880	AI03880	10.4	47.3	44	9	AI153789	AI153789
48.2	50	9	AI03931	AI03931	AI03931	10.4	47.3	45	28	AZ809363	AZ809363
48.2	50	9	AI05229	AI05229	AI05229	10.4	47.3	46	28	AZ501490	AZ501490
48.2	50	9	AI06245	AI06245	AI06245	10.4	47.3	47	28	AZ795054	AZ795054
48.2	50	9	AI06829	AI06829	AI06829	10.4	47.3	47	28	BH904732	BH904732
48.2	50	14	CD028816	CD028816	mgc5010x0	10.4	47.3	47	29	BX201354	BX201354
48.2	50	28	AZ841710	AZ841710	2M0139C22	10.4	47.3	48	14	CF298019	CF298019
48.2	50	29	CG800335	CG800335	1118010B1	10.4	47.3	49	9	AV960480	AV960480
48.2	51	9	AV838411	AV838411	AV838411	10.4	47.3	49	28	BH608677	BH608677
48.2	52	10	BF631987	BF631987	NF025C05D	10.4	47.3	49	28	BZ384969	BZ384969
48.2	52	10	BF631987	BF631987	NF025C05D	10.4	47.3	49	29	BX531144	BX531144



47.3	50	9	AU105499	AU105499	AU105499	C 443	10.2	46.4	38	28	AZ439902
47.3	50	9	AU105500	AU105500	AU105500	444	10.2	46.4	38	28	AZ791447
47.3	50	9	AU105501	AU105501	AU105501	445	10.2	46.4	38	29	AG239701
47.3	50	9	AU105502	AU105502	AU105502	446	10.2	46.4	39	29	CG719218
47.3	50	9	AU105503	AU105503	AU105503	447	10.2	46.4	40	14	H43763
47.3	50	9	AU105504	AU105504	AU105504	448	10.2	46.4	40	14	R50450
47.3	50	9	AU105505	AU105505	AU105505	449	10.2	46.4	40	28	BH893295
47.3	50	9	AU105506	AU105506	AU105506	450	10.2	46.4	41	28	BH893295
47.3	50	9	AU105507	AU105507	AU105507	451	10.2	46.4	41	29	CG708849
47.3	50	9	AU105508	AU105508	AU105508	452	10.2	46.4	44	14	H21630
47.3	50	9	AU105509	AU105509	AU105509	453	10.2	46.4	44	28	CC457233
47.3	50	9	AU105510	AU105510	AU105510	454	10.2	46.4	45	12	BG118003
47.3	50	9	AU105511	AU105511	AU105511	455	10.2	46.4	45	28	BH811345
47.3	50	9	AU105512	AU105512	AU105512	456	10.2	46.4	45	29	BX167809
47.3	50	9	AU105513	AU105513	AU105513	457	10.2	46.4	45	29	BX662880
47.3	50	9	AU105514	AU105514	AU105514	458	10.2	46.4	46	9	AI153463
47.3	50	9	AU105515	AU105515	AU105515	459	10.2	46.4	48	9	AI006951
47.3	50	9	AU105516	AU105516	AU105516	460	10.2	46.4	48	14	CB210335
47.3	50	9	AU105517	AU105517	AU105517	461	10.2	46.4	48	28	AZ843479
47.3	50	9	AU105518	AU105518	AU105518	462	10.2	46.4	48	28	BH864584
47.3	50	9	AU105519	AU105519	AU105519	463	10.2	46.4	49	9	AA878633
47.3	50	9	AU105520	AU105520	AU105520	464	10.2	46.4	49	9	AA154640
47.3	50	9	AU105521	AU105521	AU105521	465	10.2	46.4	49	10	BF722018
47.3	50	9	AU105522	AU105522	AU105522	466	10.2	46.4	49	28	AZ425231
47.3	50	9	AU105523	AU105523	AU105523	467	10.2	46.4	49	28	AZ487167
47.3	50	9	AU105524	AU105524	AU105524	468	10.2	46.4	50	9	AI581704
47.3	50	9	AU105525	AU105525	AU105525	469	10.2	46.4	50	9	AU105252
47.3	50	9	AU105526	AU105526	AU105526	470	10.2	46.4	50	9	AU105214
47.3	50	9	AU105527	AU105527	AU105527	471	10.2	46.4	50	9	AU105215
47.3	50	9	AU105528	AU105528	AU105528	472	10.2	46.4	50	9	AU105216
47.3	50	9	AU105529	AU105529	AU105529	473	10.2	46.4	50	9	AU105219
47.3	50	9	AU105530	AU105530	AU105530	474	10.2	46.4	50	9	AU105221
47.3	50	9	AU105531	AU105531	AU105531	475	10.2	46.4	50	9	AU105222
47.3	50	9	AU105532	AU105532	AU105532	476	10.2	46.4	50	9	AU105223
47.3	50	9	AU105533	AU105533	AU105533	477	10.2	46.4	50	9	AU105224
47.3	50	9	AU105534	AU105534	AU105534	478	10.2	46.4	50	9	AU105225
47.3	50	9	AU105535	AU105535	AU105535	479	10.2	46.4	50	9	AU105226
47.3	50	9	AU105536	AU105536	AU105536	480	10.2	46.4	50	9	AU105228
47.3	50	9	AU105537	AU105537	AU105537	481	10.2	46.4	50	9	AU105230
47.3	50	9	AU105538	AU105538	AU105538	482	10.2	46.4	50	9	AU105743
47.3	50	9	AU105539	AU105539	AU105539	483	10.2	46.4	50	9	AU107042
47.3	50	9	AU105540	AU105540	AU105540	484	10.2	46.4	50	10	AW248365
47.3	50	9	AU105541	AU105541	AU105541	485	10.2	46.4	50	29	BX205056
47.3	50	9	AU105542	AU105542	AU105542	486	10.2	46.4	50	29	TA211F06Q
47.3	50	9	AU105543	AU105543	AU105543	487	10.2	46.4	51	9	AU257216
47.3	50	9	AU105544	AU105544	AU105544	488	10.2	46.4	51	13	C01618
47.3	50	9	AU105545	AU105545	AU105545	489	10.2	46.4	51	28	AZ592190
47.3	50	9	AU105546	AU105546	AU105546	490	10.2	46.4	51	28	CC326366
47.3	50	9	AU105547	AU105547	AU105547	491	10.2	46.4	51	29	BX288220
47.3	50	9	AU105548	AU105548	AU105548	492	10.2	46.4	51	29	DME547569
47.3	50	9	AU105549	AU105549	AU105549	493	10.2	46.4	52	9	AA657950
47.3	50	9	AU105550	AU105550	AU105550	494	10.2	46.4	52	9	AA659205
47.3	50	9	AU105551	AU105551	AU105551	495	10.2	46.4	52	9	AA711175
47.3	50	9	AU105552	AU105552	AU105552	496	10.2	46.4	52	9	AA170022
47.3	50	9	AU105553	AU105553	AU105553	497	10.2	46.4	52	10	AW692215
47.3	50	9	AU105554	AU105554	AU105554	498	10.2	46.4	52	28	AZ817029
47.3	50	9	AU105555	AU105555	AU105555	499	10.2	46.4	53	9	AA507333
47.3	50	9	AU105556	AU105556	AU105556	500	10.2	46.4	53	28	AQ025275
47.3	50	9	AU105557	AU105557	AU105557	501	10.2	46.4	53	28	BH865135
47.3	50	9	AU105558	AU105558	AU105558	502	10.2	46.4	53	28	BH865135
47.3	50	9	AU105559	AU105559	AU105559	503	10.2	46.4	54	13	BQ567415
47.3	50	9	AU105560	AU105560	AU105560	504	10.2	46.4	54	28	AZ771621
47.3	50	9	AU105561	AU105561	AU105561	505	10.2	46.4	54	28	BX380151
47.3	50	9	AU105562	AU105562	AU105562	506	10.2	46.4	54	29	BX896725
47.3	50	9	AU105563	AU105563	AU105563	507	10.2	46.4	55	9	AI244233
47.3	50	9	AU105564	AU105564	AU105564	508	10.2	46.4	55	12	BU036839
47.3	50	9	AU105565	AU105565	AU105565	509	10.2	46.4	55	14	CD777492
47.3	50	9	AU105566	AU105566	AU105566	510	10.2	46.4	55	28	AZ784245
47.3	50	9	AU105567	AU105567	AU105567	511	10.2	46.4	55	28	BH865520
47.3	50	9	AU105568	AU105568	AU105568	512	10.2	46.4	56	10	BF461399
47.3	50	9	AU105569	AU105569	AU105569	513	10.2	46.4	56	28	AZ655711
47.3	50	9	AU105570	AU105570	AU105570	514	10.2	46.4	56	28	AZ954049
47.3	50	9	AU105571	AU105571	AU105571	515	10.2	46.4	56	28	CC025391

46.4	57	28	AZ606962	1M0423I08	C 589	10	45.5	49	9	AA588107	AA588107
46.4	57	28	AZ799654	2M0057C14	590	10	45.5	49	12	BJ034094	BJ034094
46.4	57	28	BZ770470	SALK 1434	C 591	10	45.5	49	28	AZ788840	AZ788840
46.4	58	9	AL887120	AL887120	592	10	45.5	49	28	AZ852964	AZ852964
46.4	58	13	BX622133	BX622133	593	10	45.5	50	9	AU102591	AU102591
46.4	58	14	CF117521	fp620_21	C 594	10	45.5	50	9	AU103250	AU103250
46.4	58	28	AZ820315	2M0092K22	C 595	10	45.5	50	9	AU103496	AU103496
46.4	58	28	BH911876	BH911876 SALK_0726	C 596	10	45.5	50	9	AU103942	AU103942
46.4	58	28	BZ664694	SALK 1099	C 597	10	45.5	50	9	AU103944	AU103944
46.4	59	9	A1246105	A1246105 Q128G05.x	598	10	45.5	50	9	AU104460	AU104460
46.4	59	9	A1902424	CM-BT006-	599	10	45.5	50	9	AU104460	AU104460
46.4	59	28	AZ799451	2M0056N19	600	10	45.5	50	9	AU104751	AU104751
46.4	59	28	BH790579	BH790579 SALK_0573	601	10	45.5	50	9	AU104921	AU104921
46.4	59	28	BZ53776	BZ53776 SALK_1221	602	10	45.5	50	9	AU104999	AU104999
46.4	60	9	AZ55711	AZ55711 AU255711	603	10	45.5	50	9	AU105100	AU105100
46.4	60	10	BF638152	BF638152 NF032F02P	604	10	45.5	50	9	AU105503	AU105503
46.4	60	14	CD963913	SDY 213 G	605	10	45.5	50	9	AU106131	AU106131
46.4	60	29	AL752218	Arabidops	606	10	45.5	50	9	AU106243	AU106243
46.4	60	29	AL752219	Arabidops	607	10	45.5	50	9	AU106245	AU106245
46.4	60	29	AL752219	Arabidops	608	10	45.5	50	9	AU108034	AU108034
46.4	60	29	AL752219	Arabidops	609	10	45.5	50	14	T11356	T11356
46.4	60	29	AL752219	Arabidops	610	10	45.5	51	9	AA989603	AA989603
46.4	60	29	AL752219	Arabidops	611	10	45.5	51	9	AL887036	AL887036
46.4	60	29	AL752219	Arabidops	612	10	45.5	51	28	AZ768265	AZ768265
46.4	60	29	AL752219	Arabidops	613	10	45.5	51	28	AZ917839	AZ917839
46.4	60	29	AL752219	Arabidops	614	10	45.5	51	28	AZ917868	AZ917868
46.4	60	29	AL752219	Arabidops	615	10	45.5	51	28	AZ990935	AZ990935
46.4	60	29	AL752219	Arabidops	616	10	45.5	51	28	BZ766946	BZ766946
46.4	60	29	AL752219	Arabidops	617	10	45.5	51	28	CC040051	CC040051
46.4	60	29	AL752219	Arabidops	618	10	45.5	52	9	AA068274	AA068274
46.4	60	29	AL752219	Arabidops	619	10	45.5	52	9	AA627779	AA627779
46.4	60	29	AL752219	Arabidops	620	10	45.5	52	12	AW697135	AW697135
46.4	60	29	AL752219	Arabidops	621	10	45.5	52	12	BI858951	BI858951
46.4	60	29	AL752219	Arabidops	622	10	45.5	52	12	BM076700	BM076700
46.4	60	29	AL752219	Arabidops	623	10	45.5	52	14	H28465	H28465
46.4	60	29	AL752219	Arabidops	624	10	45.5	52	14	UI7529	UI7529
46.4	60	29	AL752219	Arabidops	625	10	45.5	52	28	AZ356499	AZ356499
46.4	60	29	AL752219	Arabidops	626	10	45.5	52	28	B03518	B03518
46.4	60	29	AL752219	Arabidops	627	10	45.5	52	28	B33728	B33728
46.4	60	29	AL752219	Arabidops	628	10	45.5	52	28	BZ769458	BZ769458
46.4	60	29	AL752219	Arabidops	629	10	45.5	53	9	AA716037	AA716037
46.4	60	29	AL752219	Arabidops	630	10	45.5	53	29	AL946415	AL946415
46.4	60	29	AL752219	Arabidops	631	10	45.5	53	29	TA300807P	TA300807P
46.4	60	29	AL752219	Arabidops	632	10	45.5	54	12	B0001183	B0001183
46.4	60	29	AL752219	Arabidops	633	10	45.5	54	14	CA898530	CA898530
46.4	60	29	AL752219	Arabidops	634	10	45.5	54	28	CC033971	CC033971
46.4	60	29	AL752219	Arabidops	635	10	45.5	54	29	CG426277	CG426277
46.4	60	29	AL752219	Arabidops	636	10	45.5	55	9	AA673303	AA673303
46.4	60	29	AL752219	Arabidops	637	10	45.5	55	9	AA736635	AA736635
46.4	60	29	AL752219	Arabidops	638	10	45.5	55	9	AA513533	AA513533
46.4	60	29	AL752219	Arabidops	639	10	45.5	55	14	CA868924	CA868924
46.4	60	29	AL752219	Arabidops	640	10	45.5	55	14	CA905572	CA905572
46.4	60	29	AL752219	Arabidops	641	10	45.5	55	28	AZ933821	AZ933821
46.4	60	29	AL752219	Arabidops	642	10	45.5	55	28	BH790250	BH790250
46.4	60	29	AL752219	Arabidops	643	10	45.5	55	29	TA381A03P	TA381A03P
46.4	60	29	AL752219	Arabidops	644	10	45.5	56	9	AI920126	AI920126
46.4	60	29	AL752219	Arabidops	645	10	45.5	56	9	AW100567	AW100567
46.4	60	29	AL752219	Arabidops	646	10	45.5	56	14	CB275121	CB275121
46.4	60	29	AL752219	Arabidops	647	10	45.5	56	14	D21636	D21636
46.4	60	29	AL752219	Arabidops	648	10	45.5	56	28	AZ232243	AZ232243
46.4	60	29	AL752219	Arabidops	649	10	45.5	56	28	BH641779	BH641779
46.4	60	29	AL752219	Arabidops	650	10	45.5	56	29	CC882862	CC882862
46.4	60	29	AL752219	Arabidops	651	10	45.5	56	29	CG710793	CG710793
46.4	60	29	AL752219	Arabidops	652	10	45.5	56	29	CG785744	CG785744
46.4	60	29	AL752219	Arabidops	653	10	45.5	56	29	BX203710	BX203710
46.4	60	29	AL752219	Arabidops	654	10	45.5	57	28	AZ378584	AZ378584
46.4	60	29	AL752219	Arabidops	655	10	45.5	57	28	AZ591159	AZ591159
46.4	60	29	AL752219	Arabidops	656	10	45.5	57	28	AZ629479	AZ629479
46.4	60	29	AL752219	Arabidops	657	10	45.5	57	28	BH849364	BH849364
46.4	60	29	AL752219	Arabidops	658	10	45.5	57	28	BH850801	BH850801
46.4	60	29	AL752219	Arabidops	659	10	45.5	57	29	CC940871	CC940871
46.4	60	29	AL752219	Arabidops	660	10	45.5	57	29	CC940927	CC940927
46.4	60	29	AL752219	Arabidops	661	10	45.5	57	29	CG427634	CG427634
46.4	60	29	AL752219	Arabidops	661	10	45.5	57	29	BX659862	BX659862

45.5	57	29	TA32A09P	AL454444 T. brucei	735	9.8	44.5	40	28	BH792128	BH792121
45.5	58	13	BQ626004	BQ626004 ph8a04.y	c 736	9.8	44.5	40	28	BH905777	BH90577
45.5	58	14	R29183	R29183 F1-29D2 22	c 737	9.8	44.5	40	28	BZ662351	BZ66235
45.5	58	14	AZ797403	AZ797403 2M0053C12	c 738	9.8	44.5	41	14	CF329037	CF32903
45.5	58	28	BH635408	BH635408 1008004F0	c 739	9.8	44.5	41	28	AZ598104	AZ59810
45.5	58	28	BZ291526	BZ291526 SALK 1208	c 740	9.8	44.5	41	28	BZ353306	BZ35330
45.5	58	28	BZ766732	BZ766732 SALK 1377	c 741	9.8	44.5	41	29	BX229919	BX22991
45.5	58	28	BZ766894	BZ766894 SALK 1380	c 742	9.8	44.5	41	29	BX290940	BX29094
45.5	58	29	CG732759	CG732759 111915OH0	c 743	9.8	44.5	41	29	BX659231	BX65923
45.5	59	9	AW059770	AW059770 LE4e07.YG	c 744	9.8	44.5	42	9	AJ878619	AJ878619
45.5	59	12	BP134619	BP134619 BP134619	c 745	9.8	44.5	42	28	AZ388234	AZ38823
45.5	59	14	CB356900	CB356900 2F001-F00	c 746	9.8	44.5	42	28	AZ785487	AZ78548
45.5	59	14	RI2254	RI2254 YF33FI2.r1	c 747	9.8	44.5	42	28	AZ988113	AZ98811
45.5	59	28	AZ810237	AZ810237 2M0074I08	c 748	9.8	44.5	42	29	BX004505	BX00450
45.5	59	28	AZ962219	AZ962219 2M0230P19	c 749	9.8	44.5	42	29	BX157375	BX15737
45.5	59	28	AZ997591	AZ997591 2M0284L07	c 750	9.8	44.5	42	29	BX246612	BX24661
45.5	59	28	BH791228	BH791228 SALK 0592	c 751	9.8	44.5	42	29	TA275B04Q	TA275B04
45.5	59	29	CG986132	CG986132 CH240.156	c 752	9.8	44.5	43	28	AZ444259	AZ44425
45.5	60	12	BG742961	BG742961 602632063	c 753	9.8	44.5	43	28	AZ647300	AZ64730
45.5	60	13	BQ565015	BQ565015 gi29a01.Y	c 754	9.8	44.5	43	29	CC886686	CC88668
45.5	60	14	CD954417	CD954417 SBO 245 G	c 755	9.8	44.5	43	29	CG726304	CG72630
45.5	60	14	H55216	H55216 CHR220155 C	c 756	9.8	44.5	44	9	AJ509940	AJ50994
45.5	60	28	BH866641	BH866641 SALK 1012	c 757	9.8	44.5	44	14	CF301381	CF30138
45.5	60	28	CC179537	CC179537 SALK_0708	c 758	9.8	44.5	44	28	AZ502054	AZ50205
45.5	60	29	CA933318	CA933318 CH240.327	c 759	9.8	44.5	44	28	AZ509981	AZ50998
45.5	60	29	CG715527	CG715527 1119042B0	c 760	9.8	44.5	44	28	AZ661695	AZ66169
45.5	60	29	BX893293	BX893293 Arabidops	c 761	9.8	44.5	45	9	AV958176	AV95817
44.5	19	9	AA912825	AA912825 ol143d11.s	c 762	9.8	44.5	45	10	BE267956	BE26795
44.5	22	29	TA147E06Q	TA147E06Q T. brucei	c 763	9.8	44.5	45	10	BE513871	BE51387
44.5	22	29	TA20A05P	TA20A05P T. brucei	c 764	9.8	44.5	45	10	BE560611	BE56061
44.5	23	9	AU256868	AU256868 AU256868	c 765	9.8	44.5	45	28	AZ590180	AZ59018
44.5	23	28	AZ389515	AZ389515 1M0150110	c 766	9.8	44.5	45	28	BH847646	BH84764
44.5	24	12	BM397400	BM397400 5009-0-32	c 767	9.8	44.5	45	29	EX133661	EX13366
44.5	26	28	AZ579595	AZ579595 1M0367012	c 768	9.8	44.5	46	9	AA780164	AA78016
44.5	28	14	CF319548	CF319548 HD--10-B1	c 769	9.8	44.5	46	10	BE267872	BE26787
44.5	28	28	AZ781011	AZ781011 2M0018D21	c 770	9.8	44.5	46	28	AZ437798	AZ43779
44.5	29	28	AZ441837	AZ441837 1M0234007	c 771	9.8	44.5	46	28	AZ833146	AZ83314
44.5	29	28	AZ654172	AZ654172 1M0528007	c 772	9.8	44.5	46	28	CC455214	CC45521
44.5	29	28	BH609778	BH609778 HIV09D10	c 773	9.8	44.5	47	10	BE267896	BE26789
44.5	31	12	BI768049	BI768049 603056352	c 774	9.8	44.5	47	10	BE270087	BE27008
44.5	32	10	BF120744	BF120744 601758133	c 775	9.8	44.5	47	10	BE295974	BE29597
44.5	32	28	AZ579540	AZ579540 1M0367107	c 776	9.8	44.5	47	10	BE513247	BE51324
44.5	32	28	AZ607412	AZ607412 1M0429A24	c 777	9.8	44.5	47	10	BE561502	BE56150
44.5	34	28	AZ647310	AZ647310 1M0513D15	c 778	9.8	44.5	47	28	AZ760561	AZ76056
44.5	35	28	AZ345535	AZ345535 1M0080005	c 779	9.8	44.5	47	28	AZ760561	AZ76056
44.5	35	28	AZ598147	AZ598147 1M0412J16	c 780	9.8	44.5	47	29	DR46K23S	DR46K23
44.5	35	28	AZ950698	AZ950698 2M0214F19	c 781	9.8	44.5	48	9	AI008951	AI00895
44.5	36	9	AZ990339	AZ990339 2M0274G01	c 782	9.8	44.5	48	12	BG430009	BG43000
44.5	36	28	AU258458	AU258458 AU258458	c 783	9.8	44.5	48	28	BH914173	BH91417
44.5	36	28	AZ335390	AZ335390 1M0065M16	c 784	9.8	44.5	48	28	BZ763133	BZ76313
44.5	36	28	AZ454226	AZ454226 1M0256P04	c 785	9.8	44.5	49	9	AA872957	AA87295
44.5	36	28	AZ465655	AZ465655 1M0275A10	c 786	9.8	44.5	49	9	AA935229	AA93522
44.5	36	28	BH850482	BH850482 SALK 0713	c 787	9.8	44.5	49	9	AI019278	AI01927
44.5	36	29	BX653401	BX653401 Arabidops	c 788	9.8	44.5	49	9	AJ587540	AJ58754
44.5	36	29	BX895439	BX895439 Arabidops	c 789	9.8	44.5	49	10	BE397307	BE39730
44.5	37	9	AA657467	AA657467 rt66c03.s	c 790	9.8	44.5	49	14	W65956	W65956
44.5	37	9	AA994662	AA994662 ou46g09.s	c 791	9.8	44.5	49	28	AZ802864	AZ80286
44.5	37	9	AI138690	AI138690 qc23a11.x	c 792	9.8	44.5	49	29	AL7523367	AL75233
44.5	37	14	H28311	H28311 Y160d11.s1	c 793	9.8	44.5	50	9	AI013551	AI01355
44.5	37	28	AZ430297	AZ430297 1M0214A15	c 794	9.8	44.5	50	9	AI013911	AI01391
44.5	37	28	BH855008	BH855008 SALK_0867	c 795	9.8	44.5	50	9	AI040414	AI04041
44.5	37	29	TA28AE05P	TA28AE05P T. brucei	c 796	9.8	44.5	50	9	AI045523	AI04552
44.5	38	9	AL643708	AL643708 AL643708	c 797	9.8	44.5	50	9	AI045524	AI04552
44.5	38	28	AQ025540	AQ025540 EP(X)1614	c 798	9.8	44.5	50	9	AI045526	AI04552
44.5	38	29	TA241B11Q	TA241B11Q T. brucei	c 799	9.8	44.5	50	9	AI045528	AI04552
44.5	39	10	BE512831	BE512831 601171854	c 800	9.8	44.5	50	9	AI045529	AI04552
44.5	39	10	BE544028	BE544028 601069976	c 801	9.8	44.5	50	9	AI045530	AI04553
44.5	40	9	AI154170	AI154170 ud78h11.r	c 802	9.8	44.5	50	9	AI045531	AI04553
44.5	40	9	AI424339	AI424339 te95e12.x	c 803	9.8	44.5	50	9	AI045532	AI04553
44.5	40	9	AA437989	AA437989 vd21b08.s	c 804	9.8	44.5	50	9	AI045534	AI04553
44.5	40	14	H43763	H43763 YP21b05.r1	c 805	9.8	44.5	50	9	AI045535	AI04553
44.5	40	28	AZ322671	AZ322671 1M0043N11	c 806	9.8	44.5	50	9	AI045536	AI04553
44.5	40	28	BH642154	BH642154 1008058G1	c 807	9.8	44.5	50	9	AI045537	AI04553

44.5	50	9	AUI04542	AUI04542	AUI04542	881	9.8	44.5	54	29	CC796046	CC796046
44.5	50	9	AUI04545	AUI04545	AUI04545	882	9.8	44.5	54	29	AL758438	AL758438
44.5	50	9	AUI04546	AUI04546	AUI04546	C 883	9.8	44.5	54	29	BX893257	BX893257
44.5	50	9	AUI04548	AUI04548	AUI04548	C 884	9.8	44.5	54	29	TA358C03P	TA358C03P
44.5	50	9	AUI04551	AUI04551	AUI04551	885	9.8	44.5	55	9	AA058459	AA058459
44.5	50	9	AUI04561	AUI04561	AUI04561	886	9.8	44.5	55	9	AA711965	AA711965
44.5	50	9	AUI04565	AUI04565	AUI04565	887	9.8	44.5	55	9	AA922594	AA922594
44.5	50	9	AUI04568	AUI04568	AUI04568	C 888	9.8	44.5	55	9	AI021508	AI021508
44.5	50	9	AUI04569	AUI04569	AUI04569	C 889	9.8	44.5	55	9	AA627357	AA627357
44.5	50	9	AUI04570	AUI04570	AUI04570	C 890	9.8	44.5	55	14	CB369327	CB369327
44.5	50	9	AUI04576	AUI04576	AUI04576	891	9.8	44.5	55	14	CF327435	CF327435
44.5	50	9	AUI04577	AUI04577	AUI04577	892	9.8	44.5	55	28	AZ309353	AZ309353
44.5	50	9	AUI04578	AUI04578	AUI04578	C 893	9.8	44.5	55	28	AZ958077	AZ958077
44.5	50	9	AUI04581	AUI04581	AUI04581	C 894	9.8	44.5	55	29	DME546724	DME546724
44.5	50	9	AUI04583	AUI04583	AUI04583	C 895	9.8	44.5	56	9	AA650287	AA650287
44.5	50	9	AUI04873	AUI04873	AUI04873	C 896	9.8	44.5	56	12	BG315269	BG315269
44.5	50	9	AUI04880	AUI04880	AUI04880	C 897	9.8	44.5	56	12	BG694574	BG694574
44.5	50	9	AUI04886	AUI04886	AUI04886	C 898	9.8	44.5	56	14	CF300304	CF300304
44.5	50	9	AUI04904	AUI04904	AUI04904	899	9.8	44.5	56	28	AZ419420	AZ419420
44.5	50	9	AUI04916	AUI04916	AUI04916	900	9.8	44.5	56	28	BH849530	BH849530
44.5	50	9	AUI05371	AUI05371	AUI05371	C 901	9.8	44.5	56	28	BH849530	BH849530
44.5	50	9	AUI05594	AUI05594	AUI05594	C 902	9.8	44.5	56	29	AL761721	AL761721
44.5	50	9	AUI06515	AUI06515	AUI06515	903	9.8	44.5	57	9	AA894441	AA894441
44.5	50	10	BE373543	BE373543	BE373543	904	9.8	44.5	57	10	BF636979	BF636979
44.5	50	12	B1331898	B1331898	B1331898	905	9.8	44.5	57	10	BF643402	BF643402
44.5	50	14	CB369340	CB369340	CB369340	C 906	9.8	44.5	57	14	CA794226	CA794226
44.5	50	14	CB753410	CB753410	CB753410	C 907	9.8	44.5	57	28	AZ311594	AZ311594
44.5	50	14	D19973	D19973	D19973	C 908	9.8	44.5	57	28	AZ311594	AZ311594
44.5	50	14	H55222	H55222	H55222	C 909	9.8	44.5	57	28	AZ508051	AZ508051
44.5	50	14	CS565133	CS565133	CS565133	910	9.8	44.5	57	28	AZ792680	AZ792680
44.5	50	29	EX651733	EX651733	EX651733	C 911	9.8	44.5	57	28	BH900967	BH900967
44.5	51	10	AW213478	AW213478	AW213478	C 912	9.8	44.5	57	28	CC248731	CC248731
44.5	51	10	AW247867	AW247867	AW247867	C 913	9.8	44.5	57	29	DRIM24T	DRIM24T
44.5	51	14	CA911579	CA911579	CA911579	C 914	9.8	44.5	58	9	AA669819	AA669819
44.5	51	14	CB368388	CB368388	CB368388	C 915	9.8	44.5	58	9	AI960912	AI960912
44.5	51	14	CB369278	CB369278	CB369278	916	9.8	44.5	58	9	AA260418	AA260418
44.5	51	14	CB383647	CB383647	CB383647	917	9.8	44.5	58	9	AA527714	AA527714
44.5	51	14	R87253	R87253	R87253	918	9.8	44.5	58	9	AA595844	AA595844
44.5	51	28	AZ592484	AZ592484	AZ592484	C 919	9.8	44.5	58	12	BI327689	BI327689
44.5	51	28	AZ830258	AZ830258	AZ830258	C 920	9.8	44.5	58	12	BI903269	BI903269
44.5	51	28	BH792413	BH792413	BH792413	C 921	9.8	44.5	58	12	BI903329	BI903329
44.5	51	29	CL002800	CL002800	CL002800	C 922	9.8	44.5	58	12	BI966898	BI966898
44.5	52	9	AL961397	AL961397	AL961397	C 923	9.8	44.5	58	14	CB752435	CB752435
44.5	52	9	AA545281	AA545281	AA545281	C 924	9.8	44.5	58	14	R60614	R60614
44.5	52	10	AW781349	AW781349	AW781349	C 925	9.8	44.5	58	14	W84003	W84003
44.5	52	10	BE248274	BE248274	BE248274	C 926	9.8	44.5	58	28	AZ784257	AZ784257
44.5	52	12	BI418262	BI418262	BI418262	C 927	9.8	44.5	58	28	AZ785541	AZ785541
44.5	52	12	Bj035097	Bj035097	Bj035097	C 928	9.8	44.5	58	28	BH863476	BH863476
44.5	52	14	CF327377	CF327377	CF327377	C 929	9.8	44.5	58	28	BZ596071	BZ596071
44.5	52	28	AZ784267	AZ784267	AZ784267	C 930	9.8	44.5	58	29	CG777339	CG777339
44.5	52	28	B02129	B02129	B02129	C 931	9.8	44.5	58	29	CG777339	CG777339
44.5	52	28	CC042729	CC042729	CC042729	C 932	9.8	44.5	59	9	AA207740	AA207740
44.5	52	29	CG784934	CG784934	CG784934	933	9.8	44.5	59	10	AW516149	AW516149
44.5	53	9	AI865237	AI865237	AI865237	934	9.8	44.5	59	14	CB373617	CB373617
44.5	53	9	AU076690	AU076690	AU076690	C 935	9.8	44.5	59	14	CB751654	CB751654
44.5	53	10	BE386052	BE386052	BE386052	936	9.8	44.5	59	14	D21021	D21021
44.5	53	12	BI735167	BI735167	BI735167	C 937	9.8	44.5	59	28	AZ800944	AZ800944
44.5	53	14	CF290833	CF290833	CF290833	938	9.8	44.5	59	28	AZ812360	AZ812360
44.5	53	14	CF291470	CF291470	CF291470	C 939	9.8	44.5	59	28	BZ384935	BZ384935
44.5	53	14	CF291480	CF291480	CF291480	C 940	9.8	44.5	60	9	AI202808	AI202808
44.5	53	14	CF300766	CF300766	CF300766	941	9.8	44.5	60	9	AV949826	AV949826
44.5	53	14	CF319067	CF319067	CF319067	942	9.8	44.5	60	12	BM176063	BM176063
44.5	53	28	AZ806537	AZ806537	AZ806537	C 943	9.8	44.5	60	14	CB006939	CB006939
44.5	53	28	AZ806855	AZ806855	AZ806855	944	9.8	44.5	60	14	CB019945	CB019945
44.5	53	28	B46648	B46648	B46648	945	9.8	44.5	60	14	CD288877	CD288877
44.5	53	28	BH852213	BH852213	BH852213	C 946	9.8	44.5	60	14	CD711104	CD711104
44.5	53	29	TA254C04Q	TA254C04Q	TA254C04Q	947	9.8	44.5	60	14	H55414	H55414
44.5	53	29	TA278G01Q	TA278G01Q	TA278G01Q	C 948	9.8	44.5	60	28	AZ389209	AZ389209
44.5	54	13	BQ835161	BQ835161	BQ835161	949	9.8	44.5	60	28	AZ433302	AZ433302
44.5	54	14	CF291727	CF291727	CF291727	C 950	9.8	44.5	60	28	BH797925	BH797925
44.5	54	14	CF310715	CF310715	CF310715	C 951	9.8	44.5	60	28	BH865646	BH865646
44.5	54	14	CF328491	CF328491	CF328491	952	9.8	44.5	60	28	BZ661548	BZ661548
44.5	54	14	D38714	D38714	D38714	953	9.8	44.5	60	29	BX293141	BX293141

43.6 22 29 TXA13C09P  
 43.6 22 29 TXA4R06P  
 43.6 24 28 A2480758  
 43.6 24 28 A2612609  
 43.6 25 28 A2368070  
 43.6 25 28 A2368070  
 43.6 27 29 A2348F09Q  
 43.6 28 28 A2633750  
 43.6 28 28 A2381403  
 43.6 28 28 A2650845  
 43.6 29 28 A2306174  
 43.6 29 28 A2391934  
 43.6 29 28 A2493781  
 43.6 29 28 A2514176  
 43.6 29 28 A2618807  
 43.6 29 28 A2458567  
 43.6 30 28 A2458683  
 43.6 30 28 A2471850  
 43.6 30 28 A2179D12P  
 43.6 31 28 A2587885  
 43.6 31 28 BH848251  
 43.6 32 28 BH903706  
 43.6 32 28 BH903708  
 43.6 32 28 BH903709  
 43.6 32 28 CC456593  
 43.6 32 29 AG217358  
 43.6 33 9 AV957181  
 43.6 33 9 AW059779  
 43.6 33 28 A2796922  
 43.6 33 28 A2867886  
 43.6 34 9 A259780  
 43.6 34 9 AV955108  
 43.6 34 10 BE257894  
 43.6 34 28 A2589160  
 43.6 35 9 AV950287  
 43.6 35 28 B2382809  
 43.6 36 13 C21469  
 43.6 36 28 BH856945  
 43.6 36 28 BH856991  
 43.6 36 28 B2382634  
 43.6 36 28 B2383354  
 43.6 37 9 AA931624  
 43.6 37 9 AA933761  
 43.6 37 9 AI720133  
 43.6 37 14 T52826  
 43.6 37 28 A2304994  
 43.6 37 28 A2815710  
 43.6 37 28 B2382743

## ALIGNMENTS

\*4296 39 bp mRNA linear EST 14-MAR-2002  
 \*4296 Nori Satoh unpublished cDNA library, cleavage stage embryo  
 \*4296 intestinalis cDNA clone c106b12 5', mRNA sequence.

\*4296.1 GI:19442595

intestinalis  
 intestinalis  
 uryzoa; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 bobranchia; Clonidae; Ciona.  
 (bases 1 to 39)  
 h.N., Satou,Y., Kohara,Y. and Shin-i,T.  
 ressed genes in Ciona intestinalis  
 ublished (2000)  
 .act: Nori Satoh  
 irtment of Zoology  
 o University  
 o-Ku, Kyoto, Kyoto 606-8502, Japan  
 81-75-753-4081

AL490298 T. brucei  
 AL455010 T. brucei  
 A2480758 IM0302604  
 A2612609 IM0439P23  
 A2368070 IM0118A01  
 AL496196 T. brucei  
 A2633750 IM0489I09  
 A2381403 IM0138A04  
 A2650845 IM0521B13  
 A2306174 IM0070G07  
 A2391934 IM0154N14  
 A2493781 IM0328F09  
 A2514176 IM0360K14  
 A2618807 IM0450N11  
 CC458567 SALK\_1197  
 A2471850 IM0286M08  
 AL474655 T. brucei  
 A2587885 IM0395C23  
 BH848251 SALK\_0677  
 BH903706 SALK\_1031  
 BH903708 SALK\_1031  
 BH903709 SALK\_1031  
 CC456593 SALK\_0994  
 AG217358 Drosophila  
 AV957181 AV957181  
 AW059779 LE5602.Y9  
 A2796922 2M0052D21  
 A2867886 2M017RH22  
 A259780 Y87b10.r  
 AV955108 AV955108  
 BE257894 601109491  
 A2589160 IM0397O21  
 AV950287 AV950287  
 B2382809 SALK\_1189  
 C21469 HUMG001046  
 BH856945 SALK\_0775  
 BH856991 SALK\_0774  
 B2382634 SALK\_1185  
 B2383354 SALK\_1338  
 AA931624 o035b08.s  
 AA933761 om59g06.s  
 AI720133 as78a11.x  
 T52826 Y8a1b02.s1  
 A2304994 IM0005E09  
 A2815710 2M0084E16  
 B2382743 SALK\_1187

## ORIGIN

Query Match 67.3%; Score 14.8; DB 9; Length 39;  
 Best Local Similarity 72.7%; Pred. No. 8.5e+03;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0;

QY 1 AGACAATCACAGTCTCTCGGA 22  
 38 ANANNATCCAGTCCTCGGA 17  
 |||||  
 |||||

## RESULT 2

AZ612511/c 41 bp DNA linear GSS  
 LOCUS IM0439006R Mouse 10kb plasmid UUGC1M library Mus musculi  
 DEFINITION clone UUGC1M0439006 R, genomic survey sequence.

ACCESSION AZ612511

VERSION AZ612511.1 GI:11734797

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu

## REFERENCE

1 (bases 1 to 41)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Han  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,J  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads fr  
 plasmid inserts

## JOURNAL

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0439 row: 0 column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

## FEATURES

Location/Qualifiers

1..41

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0439006"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resista  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA fr  
 musculus C57BL/6J (male) was obtained from the  
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/  
 was hydrodynamically sheared by repeated passag  
 0.005 inch orifice at constant velocity. The st  
 was blunt end-repaired with T4 DNA polymerase a

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

## FEATURES

source

1..39

/organism="Ciona intestinalis"

/mol\_type="mRNA"

/db\_xref="taxon:7719"

/clone="c106b12"

/tissue\_type="whole animal"

/dev\_stage="cleavage stage embryo"

/clone\_lib="Nori Satoh unpublished cDNA library"

stage embryo"

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

64.5%; Score 14.2; DB 28; Length 41;  
 Similarity 84.2%; Pred. No. 1.7e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ACAATCAGTCTCTGC 19  
 ||||| ||||| |||||  
 ACAATCTCAGTCACTGC 22

3576 59 bp DNA linear GSS 29-SEP-2000  
 10K16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 3 UUGC1M0080K16 F, genomic survey sequence.

3576.1 GI:10424813

musculus (house mouse)  
 musculus  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 to 59)  
 D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Y.H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Y.M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Hauser, A. and Wright, D., Weiss, R.  
 whole genome scaffolding with paired end reads from 10kb  
 mid inserts  
 lished (2000)  
 ct: Robert B. Weiss  
 rsity of Utah Genome Center  
 rsity of Utah  
 08, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 , USA  
 801 585 5606  
 801 585 7177  
 : ddunn@genetics.utah.edu  
 t Length: 10000 Std Error: 0.00  
 : 0080 row: K column: 16  
 primer: CGTTGTAAACGACGCCAGT  
 : plasmid ends  
 quality sequence stop: 59.  
 Location/Qualifiers  
 1. .59  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0080K16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: pWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4

# ORIGIN

Query Match 63.6%; Score 14; DB 28; Length 59;  
 Best Local Similarity 77.3%; Pred. No. 2.4e+04;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCAGTCTCTCGGGA 22  
 ||||| ||||| |||||  
 Db 37 AGAAATCAGCTCTCAGGA 16

## RESULT 4

AA211707 58 bp mRNA linear EST  
 LOCUS 2984F11.r1 Stratagene hNT neuron (#937233) Homo sapiens  
 DEFINITION IMAGE:648333 5' similar to TR:G1322042 G1322042 GOK ; m  
 3576 sequence.

ACCESSION AA211707  
 VERSION AA211707.1 GI:1810511  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 58)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, J.,  
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson,  
 WashU-NCI human EST Project  
 UNPUBLISHED (1997)  
 TITLE Unpublished (1997)  
 JOURNAL  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; cont  
 IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further infor  
 Trace considered overall poor quality  
 Possible reversed clone: Similarity on wrong strand  
 Insert Length: 1561 Std Error: 0.00  
 Seq primer: -28m3 rev1 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. .58  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5277996"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:648333"  
 /dev\_stage="hNT neurons"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene hNT neuron (#937233)"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; S  
 XhoI; Cloned unidirectionally. Primer: Oligo d  
 Differentiated, post mitotic hNT neurons. Avera  
 size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor seq  
 GAATTCGACGACGAG 3' -3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3'

## FEATURES

source  
 1. .58  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:5277996"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:648333"  
 /dev\_stage="hNT neurons"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene hNT neuron (#937233)"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; S  
 XhoI; Cloned unidirectionally. Primer: Oligo d  
 Differentiated, post mitotic hNT neurons. Avera  
 size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor seq  
 GAATTCGACGACGAG 3' -3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3'

## ORIGIN

AA93361.1 GI:3089879  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo  
1 (bases 1 to 49)  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., NCI  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Cloning Distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: [www.biol.llnl.gov/bbrp/image/image.html](http://www.biol.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m3 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1474030"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Co8"  
/note="Organ: colon; Vector: pTT73D-Pac (Pharmacia) modified polylinker; 1st strand cDNA was prepared with oligo(dT) primer. Double-stranded cDNA was ligated into the Not I and Eco RI sites of the modified vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
ORIGIN  
Query Match 60.0%; Score 13.2; DB 9; Length 49;  
Best Local Similarity 83.3%; Pred. No. 5.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 5 AATCACAGTCTCTCGCGA 22  
DB 30 AATTTCAGTCTCTCGAGA 13  
BM307546 49 bp mRNA linear EST  
saks30f06 Y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLON  
Gm-cl075-4500 5', mRNA sequence.  
ACCESSION BM307546  
VERSION BM307546.1 GI:18039252  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Fabales; Fabaceae; Papilionoideae; Fabaceae  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, K., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Ma, Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Bowers, J., Person, B., Swallier, T., Gibbons, M., Pape, D., F. Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Carl McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project

AA93361.1 GI:3089879  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo  
1 (bases 1 to 49)  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., NCI  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Cloning Distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: [www.biol.llnl.gov/bbrp/image/image.html](http://www.biol.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m3 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1474030"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Co8"  
/note="Organ: colon; Vector: pTT73D-Pac (Pharmacia) modified polylinker; 1st strand cDNA was prepared with oligo(dT) primer. Double-stranded cDNA was ligated into the Not I and Eco RI sites of the modified vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
ORIGIN  
Query Match 60.0%; Score 13.2; DB 9; Length 49;  
Best Local Similarity 83.3%; Pred. No. 5.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 5 AATCACAGTCTCTCGCGA 22  
DB 30 AATTTCAGTCTCTCGAGA 13  
BM307546 49 bp mRNA linear EST  
saks30f06 Y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLON  
Gm-cl075-4500 5', mRNA sequence.  
ACCESSION BM307546  
VERSION BM307546.1 GI:18039252  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Fabales; Fabaceae; Papilionoideae; Fabaceae  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, K., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Ma, Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Bowers, J., Person, B., Swallier, T., Gibbons, M., Pape, D., F. Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Carl McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project

AA93361.1 GI:3089879  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo  
1 (bases 1 to 49)  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., NCI  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Cloning Distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: [www.biol.llnl.gov/bbrp/image/image.html](http://www.biol.llnl.gov/bbrp/image/image.html)  
Seq primer: -40m3 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1474030"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Co8"  
/note="Organ: colon; Vector: pTT73D-Pac (Pharmacia) modified polylinker; 1st strand cDNA was prepared with oligo(dT) primer. Double-stranded cDNA was ligated into the Not I and Eco RI sites of the modified vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."  
ORIGIN  
Query Match 60.0%; Score 13.2; DB 9; Length 49;  
Best Local Similarity 83.3%; Pred. No. 5.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 5 AATCACAGTCTCTCGCGA 22  
DB 30 AATTTCAGTCTCTCGAGA 13  
BM307546 49 bp mRNA linear EST  
saks30f06 Y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLON  
Gm-cl075-4500 5', mRNA sequence.  
ACCESSION BM307546  
VERSION BM307546.1 GI:18039252  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids I; Fabales; Fabaceae; Papilionoideae; Fabaceae  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, K., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Ma, Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Bowers, J., Person, B., Swallier, T., Gibbons, M., Pape, D., F. Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Carl McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project

published (1999)  
 tact: Shoemaker R/Public Soybean EST Project  
 ilic Soybean EST Project  
 ington University School of Medicine  
 4 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 : 314 286 1800  
 : 314 286 1810  
 il: est@watson.wustl.edu  
 s clone is available through: ResGen, Invitrogen Corp. 2130  
 th Memorial Parkway Huntsville, AL 35801 For further information  
 1: (800)-533-4363 or contact: ccu@resgen.com web site:  
 .resgen.com

ative full length read  
 tor to vector length is 50  
 primer: -40RP from Gibco.  
 Location/Qualifiers  
 1..49  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl075-4500"  
 /tissue\_type="differentiating somatic embryos cultured on  
 MSM6AC"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl075"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; The cDNA library was constructed from mRNA isolated  
 from differentiating somatic embryos cultured on MSM6AC.  
 The library was prepared using the Stratagene pBluescript  
 II SK(+) library construction kit. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a  
 poly(dT) sequence with an XhoI restriction site. EcoRI  
 adaptors were ligated to the blunt-ended cDNA fragments  
 followed by XhoI digestion. The cDNA fragments were  
 directionally cloned into the EcoRI-XhoI restriction site  
 of the pBluescript vector. The ligated cDNA fragments  
 were transformed into E. coli Electromax DH10B host cells.  
 Tissue culture and library construction were performed by  
 Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,  
 University of Illinois)."

60.0%; Score 13.2; DB 12; Length 49;  
 milarity 83.3%; Pred. No. 5.3e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GACAATCACAGTCTCTG 18  
 |||||  
 GACAATCATAGTATTG 2

48549 52 bp mRNA linear EST 01-APR-2002  
 025D03 59719 An expressed sequence tag database for the  
 olerant green alga, Dunaliella salina Dunaliella salina cDNA  
 ne DSA025D03 5, mRNA sequence.

48549  
 48549.1 GI:19854121

aliella salina  
 aliella salina  
 ayoria; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 aliellaceae; Dunaliella.  
 (bases 1 to 52)  
 hman,J.C.  
 expressed sequence tag database for the halotolerant green alga,  
 aliella salina  
 ublished (2002)  
 tact: Cushman JC  
 artment of Biochemistry  
 versity of Nevada  
 00, Reno, NV 89557-0014, USA

Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer  
 Plate: 025 row: D column: 03  
 Seq primer: T3 20mer  
 High quality sequence stop: 52.  
 Location/Qualifiers  
 1..52  
 /organism="Dunaliella salina"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3046"  
 /clone="DSA025D03"  
 /tissue\_type="Cells, which was adapted in 2.5M  
 incremental series from 1.7 to 2.0 to 2.25 to  
 were exposed to 3.4 M NaCl for 5 hours"  
 /cell\_type="Green"  
 /clone\_lib="An expressed sequence tag database  
 halotolerant green alga, Dunaliella salina"  
 /note="Vector: Lambda Uni-Zap XR, Bluescript I  
 EcoRI; Site 2: XhoI; Library construction was  
 according to Stratagene's recommended protocol  
 Lambda UniZapXR vector and cDNA synthesis kit.

Query Match 60.0%; Score 13.2; DB 12; Length 52;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GACAATCACAGTCTCTGC 19  
 |||||  
 Db 18 GAAAGTCACAGTCTTGC 1

RESULT 9  
 BG527761/c  
 LOCUS  
 DEFINITION  
 BG527761 59 bp mRNA linear EST  
 602556705F1 NIH\_MGC\_59 Homo sapiens cDNA clone IMAGE:46  
 mRNA sequence.

ACCESSION  
 VERSION  
 BG527761.1 GI:13519298  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hc  
 1 (bases 1 to 59)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collectio  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: ARCC  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLCMI495 row: i column: 02  
 High quality sequence stop: 59.  
 Location/Qualifiers  
 1..59  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4685641"  
 /tissue\_type="mucoepidermoid carcinoma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_59"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech

FEATURES  
 source



SfilI (ggcgctcgcc); Site 2: SfilI (ggccattatggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGCGCGCAGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

60.0%; Score 13.2; DB 12; Length 59;  
similarity 83.3%; Pred. No. 5.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
ATCACAGTCTCTGCGGA 22  
|||||  
ATCCCGTCTCTGCGGA 39  
|||||

8468 60 bp mRNA linear EST 16-OCT-2001  
8468 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5218207 5',  
a sequence.

8468.1 GI:16171424

sapiens (human)  
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
bases 1 to 60  
MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
published (1999)  
Contact: Robert Strausberg, Ph.D.  
E-mail: cgabs@mail.nih.gov  
Library Preparation: Life Technologies, Inc.  
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Sequencing by: Incyte Genomics, Inc.  
Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
e: L16M11548 row: g column: 08  
quality sequence stop: 60.  
Location/Qualifiers

1. 60  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5218207"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_118"  
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source: leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."

60.0%; Score 13.2; DB 12; Length 60;  
similarity 83.3%; Pred. No. 5.8e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGACAATCACACTCTCTG 18  
|||  
Db 38 AGGAATCACACTCTCAG 55  
|||  
|||

RESULT 11  
AZ313241/c

LOCUS  
DEFINITION  
AZ313241 35 bp DNA linear GSS  
clone UGCLM0029H13 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
bases 1 to 35

REFERENCE  
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, R., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0029 row: H column: 13  
Seq primer: CACACGAGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 35.  
Location/Qualifiers

JOURNAL  
COMMENT

FEATURES  
source

1. 35  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCLM0029H13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant"  
/clone\_lib="Mouse 10kb plasmid UGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/)  
was hydrodynamically sheared by repeated passage of 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and polynucleotide kinase. Adaptor oligonucleotides ligated to the blunt ends in high molar excess. Adaptor DNA was purified and size-selected for 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a clone of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector with adaptors complementary to the insert adaptor was purified. The sheared, adaptor mouse DNA was adapted to the vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

ORIGIN

Query Match 59.1%; Score 13; DB 28; Length 35;  
Best Local Similarity 76.2%; Pred. No. 5.7e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

ACAATCACAGTCTCTGCGG 21  
|||||  
ACTATCACAGGCAGTGTGG 3

6366 40 bp DNA linear GSS 14-NOV-2003  
044 pig genomic DNA Sus scrofa genomic, genomic survey  
ence.

6366  
6366.1 GI:38323955

scrofa (pig)  
scrofa  
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
bases 1 to 40)  
itakis,E.T., Raymond,A., Scamuffa,N., Ucla,C., Kirkness,E.,  
ier,C. and Antonarakis,S.E.  
utionary discrimination of mammalian conserved non-genic  
ences (CNGs)  
nce 302 (5647), 1033-1035 (2003)  
.7884

act: Dermitzakis ET  
sion of Medical Genetics  
ersity of Geneva Medical School  
e Michel Servet, 1211 Geneva, Switzerland  
0041 22 3795719  
0041 22 3795706  
l: emanouil.dermitzakis@medecine.unige.ch  
is: PCR product.

Location/Qualifiers  
1..40  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9823"  
/clone\_lib="pig genomic DNA"  
/note="direct sequencing of PCR product; sequences  
orthologous to human chromosome 21 conserved sequences or  
non-coding RNAs from the whole genome"

59.1%; Score 13; DB 29; Length 40;  
ilarity 76.2%; Pred. No. 6e+04;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACAATCACAGTCTCTGCGG 21  
|||||  
CAATTCACAGTCTCAGCTG 18

2233 58 bp mRNA linear EST 11-APR-2003  
TZYH81g11.y1 TgME49 3 day invitro bradyzoite Toxoplasma gondii  
\ Clone TgESTyh81g11.y1 5', mRNA sequence.

2233.1 GI:29819525

plasma gondii  
plasma gondii  
aryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
ocystidae; Toxoplasma.  
(bases 1 to 58)  
J.K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,  
ton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,  
ier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,  
er E., Bennett,J., Franklin,C., Tsagarelshvili,R., Ronko,I.,  
edy,S., Maguire,L., Waterston,R. and Wilson,R.  
plasma EST Project  
blished (2001)  
act: Clifton, S.

Toxoplasma EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: toxo@watson.wustl.edu  
Contact David Sibley (toxoes@borcim.wustl.edu) for fur  
information relating to organism, libraries, or clone a  
Seq primer: -40RP from Gibco.

Location/Qualifiers  
source  
1..58

/organism="Toxoplasma gondii"  
/mol\_type="mRNA"  
/db\_xref="taxon:5811"  
/clone="TgESTyh81g11.y1"  
/dev\_stage="3 day"  
/lab\_host="ElectronTen Blue cells"  
/clone\_lib="TgME49 3 day invitro bradyzoite"  
/note="Vector: pBluescript SK; Site 1: NotI; S;  
cDNA was reverse transcribed using Superscript  
anchored (7wobble') oligo dt primer, containing  
restriction site, according to standard proto  
second strand cDNA was digested with NOTI rest:  
endonuclease, purified and size fractionated w  
SizeSep 400 spun column (Amersham) and directl  
cloned into the SmaI and NotI sites of pBluesc  
Following electroporation into ElectronTen Blu  
(Stratagene), 5 x 106 primary CFU were bottle  
semisolid culture media [2xLB+15% SeaPrep agar  
After 48 hrs at 30 degrees Celcius, cells were  
pooled and stored in 2xLB + 15% glycerol."

## ORIGIN

Query Match 59.1%; Score 13; DB 14; Length 58;  
Best Local Similarity 76.2%; Pred. No. 7.1e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
|||||  
Db 45 AGAAAAACAGAGGCTCCGCGG 25

RESULT 14  
AG255919/c  
LOCUS  
DEFINITION  
Lotus corniculatus var. japonicus DNA, clone:LjT40i08\_s;  
survey sequence.

ACCESSION AG255919  
VERSION AG255919.1 GI:26655756  
KEYWORDS  
SOURCE  
ORGANISM  
Lotus corniculatus var. japonicus (Lotus japonicus)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; L  
Lotus.

REFERENCE  
1  
AUTHORS Sato,S., Nakamura,Y. and Tabata,S.  
TITLE Lotus japonicus TAC End sequences  
JOURNAL Published Only in Database (2002)  
REFERENCE 2 (bases 1 to 36)  
AUTHORS Sato,S.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Researc  
The First Laboratory for Plant Gene Research; 2-6-7  
Kazusa-kamatori, Kisarazu, Chiba 292-0818, Japan  
(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/  
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)

## FEATURES

source  
1..36  
/organism="Lotus corniculatus var. japonicus"  
/mol\_type="genomic DNA"  
/strain="Miyakojima MG-20"

```

/variety="japonicus"
/db_xref="taxon:34305"
/clone="LJ740108.sfi"
/clone_lib="genomic TAC library"
/note="VECTOR:pYLFACT-synonym: Lotus japonicus"

58.2%; Score 12.8; DB 29; Length 36;
ilarity 87.5%; Pred. No. 7.2e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATCACAGTCTCTGC 19
|||||
ATCAAGTCTCTGC 18

4053 44 bp DNA linear GSS 13-JUN-2002
078674.42.00.x Arabidopsis thaliana TDNA insertion lines
idopsis thaliana genomic clone SALK_078674.42.00.x, genomic
ey sequence.
4053
4053.1 GI:21424924

idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 44)
iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
n,P., Zimmerman,J. and Ecker,J.R.
quence-Indexed Library of Insertion Mutations in the
idopsis Genome
ublished (2001)
act: Joseph R. Ecker
stitute Genomic Analysis Laboratory (SIGNAL)
alk Institute for Biological Studies
0 N. Torrey Pines Road, La Jolla, CA 92037, USA
: 858 453 4100 x1752
: 858 558 6379
l: ecker@alk.edu
is single pass sequence recovered from the left border of
A. This sequence lies within 300 bases of the 5' end of
28715.
ss: TDNA tagged.
Location/Qualifiers
1..44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_078674.42.00.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

58.2%; Score 12.8; DB 28; Length 44;
milarity 87.5%; Pred. No. 7.8e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATCACAGTCTCTGC 19
|||||
GATCACATCTCTGC 17

```

```

RESULT 16
BH861326/c
LOCUS
DEFINITION
SALK_067995 Arabidopsis thaliana TDNA insertion lines Ar
thaliana genomic clone SALK_067995, genomic survey seque
ACCESSION
BH861326
VERSION
BH861326.1 GI:22096652
SOURCE
GSS.
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi
1 (bases 1 to 45)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., I
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bo
TDNA. This sequence lies within an annotated exon of At:
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_067995"
/clone_lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thalia
each of which contains one or more TDNA inser
elements. The resultant fragment for each lin
directly sequenced to determine the genomic se
the site of insertion. Details of the protoc
be found at http://signal.salk.edu/tdna_protoc

Query Match 58.2%; Score 12.8; DB 28; Length 45;
Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CAATCACAGTCTCTGC 19
|||||
Db 18 CAATCACAGCTCTCTAC 3

RESULT 17
BF643352/c
LOCUS
DEFINITION
NF004A05EC1F1034 Elicited cell culture Medicago truncat
clone NF004A05EC 5', mRNA sequence.
ACCESSION
BF643352
VERSION
BF643352.1 GI:11908477
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Medicago.
1 (bases 1 to 52)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A.
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble F

```

09:38:25 2004

us-10-090-326-6.max.rst

pr for Medicago Genomics Research  
lished (2000)  
ct: Dixon RA  
: Biology Division  
Samuel Roberts Noble Foundation  
Sam Noble Parkway, Ardmore, OK 73402, USA  
580 221 7302  
580 221 7380  
l: radixon@noble.org  
t length: 52 Std Error: 0.00  
3: 004 row: A column: 05  
primer: TCACACAGGAACACGCTATGAC.  
Location/Qualifiers  
1. .52  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF004A05EC"  
/tissue type="Cell cultures derived from root tissues"  
/dev stage="Cell suspensions were subcultured every 14  
days. Cells were induced six days after subculture"  
/clone\_lib="Elicited cell culture"  
/note="vector: Lambda Zap; Cells were induced with yeast  
cell wall extracts equivalent to 50ug/ml glucose in the  
final concentration. Samples were taken at 0.5, 1, 12 and  
24 hours after induction. Equal amounts of RNA from each  
time point were pooled and used for mRNA isolation."

58.2%; Score 12.8; DB 10; Length 52;  
ilarity 87.5%; Pred. NO. 8.4e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CAATCAGCTCTCT 17  
|||||  
CAACACACTCTCT 29

3382 60 bp DNA linear GSS 05-AUG-2002  
093779 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
iana genomic clone SALK\_093779, genomic survey sequence.  
3382  
3382.1 GI:22098936  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 60)  
so,J.M., Leisse,T.J.; Barajas,P.; Chen,H.; Cheuk,R.;  
inab,C.; Jeske,A.; Karnes,M.; Kim,C.J.; Parker,H.; Prednis,L.;  
n.P.; Zimmerman,J. and Ecker,J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)  
act: Joseph R. Ecker  
: Institute Genomic Analysis Laboratory (SIGAL)  
Salk Institute for Biological Studies  
O.N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 558 6379  
l: ecker@salk.edu  
is single pass sequence recovered from the left border of  
A. This sequence lies within 300 bases of the 5' end of  
#28715.  
3s: TDNA tagged.  
Location/Qualifiers  
1. .60  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_093779"  
/note="PCR was performed on Arabidopsis thaliana TDNA insertion  
each of which contains one or more TDNA insert  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protocol](http://signal.salk.edu/tdna_protocol)

Query Match 58.2%; Score 12.8; DB 28; Length 60;  
Best Local Similarity 87.5%; Pred. NO. 8.9e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
QY 4 CAATCAGCTCTCTGC 19  
|||||  
Db 23 CGATCAATCTCTGC 38  
|||||

RESULT 19  
AI958680  
LOCUS  
DEFINITION  
IC95B01.y1 Zebrafish WashU WPMG EST Danio rerio cDNA cl  
IMAGE:3729097.5, similar to SW:PUS1\_MOUSE P50580  
PROLIFERATION-ASSOCIATED PROTEIN 1 ; mRNA sequence.  
AI958680  
ACCESSION  
VERSION AI958680.1 GI:5751393  
KEYWORDS  
EST  
SOURCE  
ORGANISM  
Danio rerio (zebrafish)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 34)  
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra  
Bddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyll  
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,  
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., S  
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mc  
Waterston,R. and Wilson,R.  
WashU Zebrafish EST Project 1998  
Unpublished (1998)  
Other ESTs: fc95b01.x1  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zbrfish@wustl.wustl.edu  
cDNA Library Preparation: Matthew Clark. cDNA Library Ar  
Matthew Clark. DNA Sequencing by: Washington University  
Sequencing Center Clone Distribution: Genome Systems, St  
Missouri (web address: [www.genomesystems.com](http://www.genomesystems.com)) (email cor  
info@genomesystems.com) and Research Genetics, Huntsville  
(web address: [www.resgen.com](http://www.resgen.com)) (email contact: info@resge  
ResourcenzentrumPrimarDatenbank, Berlin, Germany (web e  
[www.rzpd.de](http://www.rzpd.de))  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: T3 Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .34  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3729097"  
/sex="mixed"  
/tissue type="26 somite embryos, adult livers,  
stage embryos"  
/lab\_host="XLI-blue MRF"

FEATURES  
source

/clone lib="Zebrafish WashU MPIMG EST"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st  
 strand cDNA was primed with a Not I - oligo(dT)15 primer  
 [5'-pGACTAGTCTACGCGGCGCGCGCCCTTTTCTTTT3'];  
 double-stranded cDNA was ligated to Sal I adaptors (BRL),  
 digested with Not I and cloned into the Not I and Sal I  
 sites of the pSPORT1 vector (BRL). Library was constructed  
 by Matthew Clark (Lehrach lab; ICRF, London and Max Planck  
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
 analysis were selected following oligonucleotide  
 hybridization fingerprinting of arrayed clones from  
 zebrafish late somitogenesis (26 ss), adult liver or  
 embryonic shield stage (5.6 h) libraries. Fingerprint  
 data were used to computationally cluster cDNAs, and a  
 single cDNA from each cluster was chosen for sequencing.  
 In some cases multiple members of the same cluster were  
 sequenced to assess clustering parameters, or single clones  
 were sequenced additional times to assess quality  
 control."

57.3%; Score 12.6; DB 9; Length 34;  
 ilarity 78.9%; Pred. No. 8.7e+04; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 4;

HACATACAGTCTCTGC 19

TCATAACTGTCCTGC 28

7818 37 bp mRNA linear EST 15-FEB-1999  
 g12.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:1980166 3'  
 lar to TR\_001943\_Q01943 EXTENSIN; contains element TAR1  
 titive element ; mRNA sequence.

7818 GI:4109439

sapiens (human)

sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 nalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 37)

-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

or Gene Index

ublished (1997)

tact: Robert Strausberg, Ph.D.

il: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

sue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

ert-Buck, M.D., Ph.D.

NA Library Preparation: Life Technologies, Inc.

NA Library Arrayed by: Greg Lennon, Ph.D.

A Sequencing by: Washington University Genome Sequencing Center

one distribution: NCI-CGAP clone distribution information can be

nd through the I.M.A.G.E. Consortium/LLNL at:

-bio.llnl.gov/bbrp/image/image.html

ce considered overall poor quality

ert length: 1039 Std Error: 0.00

primer: -40up from Gibco

h quality sequence stop: 1.

Location/Qualifiers

1. .37

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1980166"

/tissue type="poorly differentiated adenocarcinoma with

signed ring cell features"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Gas4"

# ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 9e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 21

DB 19 ACAATGAAGACTGCGCGG 37

## RESULT 21

AZ782132

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .37

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0022D08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resist

/clone\_lib="Mouse 10Kb plasmid UUGCLM library"

/note="Vector: PWB42nv; Purified genomic DNA f

musculus C57BL/6J (male) was obtained from th

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares>

was hydrodynamically sheared by repeated passa

0.005 inch orifice at constant velocity. The s

was blunt end-repaired with T4 DNA polymerase

polynucleotide kinase. Adaptor oligonucleotide

ligated to the blunt ends in high molar exces

adapted DNA was purified and size-selected f

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from

of PWB42 (GI4732114|gb|AF129072.1), a copy-nu

inducible derivative of plasmid R1. The vector

with adaptors complementary to the insert adap

/note="Organ: stomach; Vector: PCMV-SPORT6; Sit  
 Site 2: NotI; Cloned unidirectionally. Primer:  
 Average insert size 1.69 kb. Life Technologies  
 11549-011"

AZ782132 37 bp DNA linear GSS  
 2M0022D08F Mouse 10Kb plasmid UUGCLM library Mus musculi  
 clone UUGC2M0022D08 F, genomic survey sequence.

AZ782132

AZ782132.1 GI:12915518

GSS

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus

1 (bases 1 to 37)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hai

Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, J.

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niedermaier, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fr

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert length: 10000 Std Error: 0.00

Plate: 0022 row: D column: 08

Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

1. .37

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0022D08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Ti-resist

/clone\_lib="Mouse 10Kb plasmid UUGCLM library"

/note="Vector: PWB42nv; Purified genomic DNA f

musculus C57BL/6J (male) was obtained from th

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares>

was hydrodynamically sheared by repeated passa

0.005 inch orifice at constant velocity. The s

was blunt end-repaired with T4 DNA polymerase

polynucleotide kinase. Adaptor oligonucleotide

ligated to the blunt ends in high molar exces

adapted DNA was purified and size-selected f

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from

of PWB42 (GI4732114|gb|AF129072.1), a copy-nu

inducible derivative of plasmid R1. The vector

with adaptors complementary to the insert adap

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

57.3%; Score 12.6; DB 28; Length 37;  
ilarity 78.9%; Pred. No. 9e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCAGTCTCTGC 19  
|||||  
CTAACTAGTCTCTGC 33

3640 43 bp DNA linear GSS 20-FEB-2001  
15B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
e UUGC2M0115B23 R, genomic survey sequence.

3640  
3640.1 GI:13003548

musculus (house mouse)

musculus  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 43)

D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
m, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
ly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
erhauser, A. and Wright, D., Weiss, R.

e whole genome scaffolding with paired end reads from 10kb  
mid inserts

blished (2000)

act: Robert B. Weiss

ersity of Utah Genome Center

308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
2, USA

801 585 5606  
801 585 7177

l: ddunn@genetics.utah.edu

rt Length: 10000 Std Error: 0.00

e: 0115 row: B column: 23

primer: CACACAGGAAACAGCTATGACC

s: plasmid ends

quality sequence stop: 43.

Location/Qualifiers

1. .43

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0115B23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/).

The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 57.3%; Score 12.6; DB 28; Length 43;  
Best Local Similarity 78.9%; Pred. No. 9.6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

Qy 1 AGACAATCAGTCTCTGC 19  
|||||  
Db 24 AGACACAGCGTCTCTTC 6

# RESULT 23

AZ955701/c

LOCUS

DEFINITION 2M0221H21R Mouse 10kb plasmid UUGC2M library Mus musculus  
clone UUGC2M0221H21 R, genomic survey sequence.

ACCESSION AZ955701

VERSION AZ955701.1 GI:13826928

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
1 (bases 1 to 45)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fro  
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0221 row: H column: 21

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0221H21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, Tl-resistant

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA fr

musculus C57BL/6J (female) was obtained from t

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/

was hydrodynamically sheared by repeated passag

0.005 inch orifice at constant velocity. The sh

was blunt end-repaired with T4 DNA polymerase a

polynucleotide kinase. Adaptor oligonucleotides

ligated to the blunt ends in high molar excess

adapted DNA was purified and size-selected fo

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a

of PWD42 (gi|4732114|gb|AF129072.1), a copy-num

inducible derivative of plasmid R1. The vector

with adaptors complementary to the insert adapt

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

57.3%; Score 12.6; DB 28; Length 45;  
Similarity 78.9%; Pred. No. 9.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GACAAATCACAGTCTCTGC 19  
|||||  
GACACTCACAGTTTCTCC 24

35957 50 bp mRNA linear EST 30-AUG-2001  
35957 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
35957 mRNA sequence.

35957.1 GI:13555478

Source  
sapiens (human)  
sapiens  
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
(bases 1 to 50)

1. 50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="Sugano Homo sapiens cDNA library"  
Location/Qualifiers

Query Match 57.3%; Score 12.6; DB 9; Length 50;  
Best Local Similarity 78.9%; Pred. No. 1e+05; Indels 0;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;  
QY 1 AGCAATCACAGTCTCTGC 19  
|||||  
DB 38 AGCGACACAGCCTGTGC 20

RESULT 26  
AUI05959/c  
LOCUS  
AUI05959 Sugano Homo sapiens cDNA library Homo sapiens  
DEFINITION  
INCE0044, mRNA sequence.  
ACCESSION  
AUI05959  
VERSION  
AUI05959.1 GI:13555480  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho  
1 (bases 1 to 50)  
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Ok  
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
Diverse transcriptional initiation revealed by fine, la  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929

GACAAATCACAGTCTCTGC 19  
|||||  
GACGACACAGCCTGTGC 26

05958 50 bp mRNA linear EST 30-AUG-2001  
05958 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
05753, mRNA sequence.

05958.1 GI:13555479

Source  
sapiens (human)  
sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho  
1 (bases 1 to 50)  
Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., S  
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Ok  
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
Diverse transcriptional initiation revealed by fine, la  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929

Contact: Yutaka Suzuki

Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A  
Sugano.S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gen  
149-156 (1997).

Location/Qualifiers

Source

1. 50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HS105753"  
/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 50;  
Best Local Similarity 78.9%; Pred. No. 1e+05; Indels 0;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;  
QY 1 AGCAATCACAGTCTCTGC 19  
|||||  
DB 38 AGCGACACAGCCTGTGC 20

RESULT 26  
AUI05959/c  
LOCUS  
AUI05959 Sugano Homo sapiens cDNA library Homo sapiens  
DEFINITION  
INCE0044, mRNA sequence.  
ACCESSION  
AUI05959  
VERSION  
AUI05959.1 GI:13555480  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho  
1 (bases 1 to 50)  
Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Ok  
Sakaki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
Diverse transcriptional initiation revealed by fine, la  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A  
Sugano.S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gen  
149-156 (1997).

Location/Qualifiers

Source

1. 50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

```

/clone="INEC0044"
/clone_lib="Sugano Homo sapiens cDNA library"

    57.3%; Score 12.6; DB 9; Length 50;
    78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTGTC 19
|||||
CGACCACAGCCTGTC 26

1754          51 bp mRNA linear EST 09-OCT-1997
005.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
3:976641 5', mRNA sequence.
1754
1754.1 GI:2523630
musculus (house mouse)
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
bases 1 to 51)
t,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
l,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
lenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
ing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
ston,R.
YashU-HMI Mouse EST Project
lished (1996)
J-HMI Mouse EST Project
ington University School of MedicineP
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
l: mouseest@watson.wustl.edu
clone is available royalty-free through LLNL ; contact the
3 Consortium (info@image.llnl.gov) for further information.
357369.

    Location/Qualifiers
      1..51
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J x DBA/2J F1"
        /db_xref="taxon:10090"
        /clone="IMAGE:976641"
        /tissue_type="embryo"
        /dev_stage="2-cell"
        /lab_host="DH10B"
        /clone_lib="Knowles Solter mouse 2 cell"
        /note="Organ: embryo; Vector: pBluescribe (modified);
      Site 1: Mu1; Site 2: Sal1; Cloned unidirectionally from
      mRNA prepared from 13,500 2-cell stage embryos. Primer:
      Sal1(dT): 5'-CGGTGACCGTCGACCGTTTGTGTTT-3'. cDNAs
      were cloned into the Mu1/Sal1 sites of a modified
      pBluescribe vector using commercial linkers (NEB).
      Average insert size: 1.2 kb."

    57.3%; Score 12.6; DB 9; Length 51;
    78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTGTC 19
|||||
TCATCCACAGCCTGTC 21

```

```

CK225144/c
LOCUS
DEFINITION
mRNA sequence.
51 bp mRNA linear EST
700324494H1 RAHINOT01 Rattus norvegicus cDNA clone 70032
mRNA sequence.
CK225144
VERSION
CK225144.1 GI:39631248
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
Rattus.
1 (bases 1 to 51)
Vitt,U., Gietzen,D., Stevens,K., Wingrove,J., Becha,S.,
Burill,J., Chawla,N., Chien,J., Crawford,M., Ison,C., K
Kwong,M., Park,J., Policky,J., Weiler,M., White,R., Xu,Y
Daniels,S., Jacob,H., Jensen-Seaman,M.I., Lazar,J., Stuv
Schmidt,J.
Identification of candidate disease genes by EST alignme
synteny and expression and verification of Ensembl genes
chromosome 1q43-54
Genome Res. (2004) In press
Contact: Vitt U
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 849 8840
Fax: 650 845 5495
Email: uvitt@incyte.com.
    Location/Qualifiers
      1..51
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /db_xref="taxon:10116"
        /clone="700324484"
        /tissue_type="Hippocampus"
        /clone_lib="RAHINOT01"
        /note="Rat, Hippocampus, SD, M, Pool"

ORIGIN
Query Match 57.3%; Score 12.6; DB 14; Length 51;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

Qy 3 ACAATCACAGTCTGTCGG 21
|||||
Db 25 ACACCTACAGGCTCTCGG 7

RESULT 29
BG386881/c
LOCUS
DEFINITION
mRNA sequence.
57 bp mRNA linear EST
602454676F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:458
mRNA sequence.
BG386881
VERSION
BG386881.1 GI:13280430
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1 (bases 1 to 57)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: sgapb-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```



```

e: LNCM1306 row: 9 column: 19
quality sequence stop: 57.
Location/Qualifiers
1. 57
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4583082"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MSC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
57.3%; Score 12.6; DB 12; Length 57;
ularity 78.9%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;
ATCACAGTCTCTGCGGA 22
|||||
ACTCACAGTCATCGCGGA 9

37
c12.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone
E:76150 5', mRNA sequence.
37
37.1 GI:661574
sapiens (human)
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 58)
ier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
soe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
ins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
is, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
fing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
askis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
Maria, M.
ration and analysis of 280,000 human expressed sequence tags
me Res. 6 (9), 807-828 (1996)
4478
549
act: Wilson RK
ington University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
l: est@watson.wustl.edu
rt Size: 126
ce: IMAGE Consortium, LNL This clone is available royalty-free
ugh LNL; contact the IMAGE Consortium (info@image.llnl.gov)
further information.
rt Length: 126 Std Error: 0.00
primer: M13RPI
quality sequence stop: 282.
Location/Qualifiers
1. 58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:76150"
/dev_stage="49 year old"
/lab_host="SOLR cells (Kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1:
XhoI; Site 2: XhoI; Cloned unidirectionally. Primer
Total ovary tissue, normal, caucasian. Average
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor s:
GAATTCGGCAGCAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTCCTTTTTCCTTTT 3'"

ORIGIN
Query Match 57.3%; Score 12.6; DB 14; Length 58;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACATCACAGTCTCTGCGG 21
|||||
DB 46 ACAAGTCAGTCTCTGCGG 28

RESULT 31
AA111557/c
LOCUS
DEFINITION
mp33e05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone 1
5' similar to TR:G688443 G688443 ALL-1 PROTEIN ;, mRNA
ACCESSION
AA111557
VERSION
AA111557.1 GI:1663509
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (bases 1 to 43)
REFERENCE
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R.,
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 3-4 286 1800
Fax: 3-4 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; cont
IMAGE Consortium (info@image.llnl.gov) for further infor
MGI:347608
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:572960"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: p7T3D-Pac (Pharmacia) with a mc
polylinker; Site 1: Not I; Site 2: Eco RI; 1st
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCGCTTTTTCCTTTTTCCTTTT
3']; double-stranded cDNA was ligated to Eco RI

```

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Donaldo."

ilarity 56.4%; Score 12.4; DB 9; Length 43;

Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ACATCAGCTCTCTCGGA 22

|||||  
ATCCCACTGCTCTGTGA 5

2203 43 bp DNA linear GSS 04-SEP-2002  
091457.21.55.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_091457.21.55.x, genomic  
ev sequence.

2203.1 GI:22713084

idopsis thaliana (thale cress)

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 43)

so, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
n, P., Zimmermann, J. and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the

idopsis Genome

blished (2001)

act: Joseph R. Ecker

Institute Genomic Analysis Laboratory (SIGnAL)

Salk Institute for Biological Studies

0 N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

l: ecker@salk.edu

is single pass sequence recovered from the left border of  
. This sequence lies within an annotated exon of At4g37610.

s: TDNA tagged.

Location/Qualifiers

1. .43

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_091457.21.55.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ilarity 56.4%; Score 12.4; DB 28; Length 43;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ATCAGCTCTCT 17

|||||

ATCAGCTCTCT 18

CC886732/c  
LOCUS

DEFINITION SALK\_148961.18.00.n Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_148961.18.00.n,  
survey sequence.

ACCESSION

VERSION CC886732.1 GI:33363088

KEYWORDS GSS.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidof  
1 (bases 1 to 51)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., E  
Shinn, P., Zimmermann, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bor

TDNA. This sequence lies within an annotated exon of At1

Class: TDNA tagged.

Location/Qualifiers

1. .51

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_148961.18.00.n"

/clone\_lib="Arabidopsis thaliana TDNA insertion  
note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA insert  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

Query Match 56.4%; Score 12.4; DB 29; Length 51;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 1 AGACAATCACAGTC 14

|||||

Db 26 AGACAATCACAGTC 13

RESULT 34

AZ849766/c

LOCUS

DEFINITION 2M0151P13F Mouse 10kb plasmid UGCLM library Mus musculus  
clone UUC2M0151P13 F, genomic survey sequence.

ACCESSION

VERSION AZ849766.1 GI:13034106

KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
1 (bases 1 to 55)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads fro

mid inserts  
 blished (2000)  
 act: Robert B. Weiss  
 ersity of Utah Genome Center  
 ersity of Utah  
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 2, USA  
 801 585 5606  
 801 585 7177  
 l: ddunne@genetics.utah.edu  
 rt Length: 10000 Std Error: 0.00  
 e: 0151 row: P column: 13  
 primer: CCGTGTAAACAGCGCCAGT  
 s: plasmid ends  
 quality sequence stop: 55.  
 Location/Qualifiers  
 1..55  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0151P13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10Kb plasmid UUGC1M library"  
 /note="Vector: PWB42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

56.4%; Score 12.4; DB 28; Length 55;  
 ilarity 72.7%; Pred. No. 1.3e+05;  
 Conservativity 0; Mismatches 6; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGCGGA 22  
 |||||  
 ACAGGCCAAGGCTCTGCAGA 14

8163 57 bp DNA linear GSS 13-JUN-2002  
 067586.49.45.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_067586.49.45.x, genomic  
 ey sequence.  
 8163  
 8163.1 GI:21419034

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 (bases 1 to 57)  
 iso J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 zinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 nt, P., Zimmerman, J. and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bot  
 TDNA. This sequence lies within an annotated exon of ACT  
 Class: TDNA tagged.  
 FEATURES  
 Location/Qualifiers  
 1..57  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_067586.49.45.x"  
 /note="Arabidopsis thaliana TDNA insertion  
 /clone\_lib="Arabidopsis thaliana TDNA insert  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic sec  
 the site of insertion. Details of the protocol  
 be found at http://signal.salk.edu/tdna\_protoc

ORIGIN  
 Query Match 56.4%; Score 12.4; DB 28; Length 57;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 5 AATCACAGTCTCTG 18  
 |||||  
 Db 10 AATCATAGTCTCTG 23  
 |||||

RESULT 36  
 AW059588/c  
 LOCUS AW059588 60 bp mRNA linear EST  
 DEFINITION HuH.best.dncl5.final.cluster\_78\_(3) DNCL5 Homo sapiens  
 similar to glutathione peroxidase, mRNA sequence.  
 ACCESSION AW059588  
 VERSION AW059588.1 GI:6651910  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
 1 (bases 1 to 60)  
 Brenner, S., Williams, S.R., Verma, E.H., Storch, T., Moor  
 McCollum, C., Mao, J.I., Kirchner, J.J., Eiler, S., DuBridge  
 Burcham, T. and Albrecht, G.  
 In vitro cloning of complex mixtures of DNA on microbeac  
 separation of differentially expressed cDNAs  
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 20144098  
 10677516  
 Contact: Burcham TS  
 LYNX Therapeutics, Inc.  
 25861 Industrial Blvd., Hayward, CA 94545, USA  
 Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: timb@lynxgen.com  
 Sequence obtained from LYNX Therapeutics Megasort techn  
 Collected from the down-regulated gate. Consensus sequen  
 sequences in cluster.  
 High quality sequence stop: 60.  
 Location/Qualifiers  
 1..60  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

```

/db xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"
/notes="Vector: PCR2.1; Cloning of PCR products from
micro-beads carrying 3' end of down-regulated cDNA. THP-1
cells non-induced (treated with DMSO only). "
```

56.4%; Score 12.4; DB 9; Length 60;  
 ilarity 92.9%; Pred. No. 1.4e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TACAGTCTCTGC 19  
 |||||  
 TCCAGTCTCTGC 46

3761 60 bp mRNA linear EST 23-AUG-2000  
 3761 YG DNC15 Homo sapiens cDNA similar to GLUTATHIONE  
 KIDASE, mRNA sequence.  
 3761  
 3761.1 GI:6652083

sapiens (human)  
 sapiens  
 cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 bases 1 to 60)  
 her,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,  
 llum,C., Mao,J.I., Kirchner,J.J., Electr,S., DuBridge,R.B.,  
 am,T. and Albrecht,G.  
 itro cloning of complex mixtures of DNA on microbeads: Physical  
 ration of differentially expressed cDNAs  
 . Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 1098  
 7516  
 act: Burcham TS  
 Therapeutics, Inc.  
 . Industrial Blvd., Hayward, CA 94545, USA  
 510 670 9338  
 510 670 9302  
 t: timbelynxgen.com  
 nce obtained from LYNX Therapeutics Megasort technology.  
 acted from the down-regulated gate.  
 quality sequence stop: 60.  
 Location/Qualifiers  
 1. .60  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /notes="Vector: PCR2.1; Cloning of PCR products from  
 micro-beads carrying 3' end of down-regulated cDNA. THP-1  
 cells non-induced (treated with DMSO only). "

56.4%; Score 12.4; DB 9; Length 60;  
 ilarity 92.9%; Pred. No. 1.4e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TACAGTCTCTGC 19  
 |||||  
 TCCAGTCTCTGC 46

33 37 bp mRNA linear EST 30-JUL-1996

DEFINITION HUMG901659 Human promyelocyte Homo sapiens cDNA clone pm  
 mRNA sequence.

ACCESSION D20683  
 VERSION D20683.1 GI:501779  
 KEYWORDS Est.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)  
 AUTHORS Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 TITLE Gene expression of human promyelocytic cell line HL60 be  
 after induction of differentiation. A new application of  
 cDNA sequencing  
 JOURNAL Unpublished (1993)  
 COMMENT Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T.,  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 3-1 Yamada-oka,Suita,Osaka 565,Japan.

FEATURES  
 source Location/Qualifiers  
 1. .37  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="pm2073"  
 /clone\_lib="Human promyelocyte"  
 /notes="Female, adult, cell\_line = HL60, cell\_ty  
 promyelocyte. "

ORIGIN  
 Query Match 55.5%; Score 12.2; DB 14; Length 37;  
 Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 6 ATCACAGTCTCTCGGA 22  
 |||||  
 2 ATCCAGTCTCTGAAGA 18

Db

RESULT 39  
 BX289471/c  
 LOCUS BX289471 47 bp DNA linear GSS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-426G01-0  
 genomic survey sequence.

ACCESSION BX289471  
 VERSION BX289471.1 GI:28888467  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., S.  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of F  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

REFERENCE 2  
 AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We  
 A new Arabidopsis thaliana T-DNA mutagenised population  
 for flanking sequence tag based reverse genetics  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 47)  
 AUTHORS Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion within the locus defined by clone

ences are generated at the MPI for Plant Breeding Research in context of the GABI-Kat project. GABI-Kat is part of the German Genomics program designated 'GABI'. Information on line availability can be found at:  
 p://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1. .47  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="CK-426G01-018075"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (Tri) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

55.5%; Score 12.2; DB 29; Length 47;  
 Similarity 82.4%; Pred. No. 1.5e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACATCATCAGTCTCT 17  
 |||||  
 ACATCATAGCCTCT 8

18085 53 bp mRNA linear EST 18-AUG-2003  
 -08-M20\_b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 ary (JMT) Oryza sativa cDNA clone JMT--08-M20, mRNA sequence.  
 18085  
 18085.1 GI:33824545

sa sativa  
 sa sativa  
 rycoya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 tarioideae; Oryzeae; Oryza.  
 bases 1 to 53)  
 J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 I.S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 re-scale Sequencing Analysis of Rice ESTs  
 ublished (2003)  
 act: Nahm B.H.  
 mics and Genetics Institute, GreenGene Biotech Inc.; Division  
 ioscience and Bioinformatics, Myongji University  
 in, Kyeonggi, Korea  
 82 31 330 6193  
 82 31 321 6355  
 1: bhnamg@bio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. .53  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT--08-M20"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jasmonate Carboxyl

methytransferase overexpression line."

ORIGIN  
 Query Match 55.5%; Score 12.2; DB 14; Length 53;  
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCACAGTCTCT 17  
 |||||  
 Db 36 AGAAATTCACAGTCTCT 52

RESULT 41  
 AZ463714/c  
 LOCUS  
 DEFINITION  
 1M0272C15R Mouse 10kb plasmid UUGC1M library Mus musculi  
 clone JUGC1M0272C15 R, genomic survey sequence.

ACCESSION  
 AZ463714  
 VERSION  
 AZ463714.1 GI:10621839  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu;  
 1 (bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha;  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niedernausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads fr

Plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
 Plate: 0272 row: C column: 15  
 Seq primer: CACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1. .28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0272C15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resiste  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA fr  
 musculus C57BL/6J (male) was obtained from the  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/  
 was hydrodynamically sheared by repeated passag  
 0.005 inch orifice at constant velocity. The si  
 was blunt end-repaired with T4 DNA polymerase a  
 polynucleotide kinase. Adaptor oligonucleotides  
 ligated to the blunt ends in high molar excess  
 adapted DNA was purified and size-selected fr  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-num  
 inducible derivative of plasmid R1. The vector  
 with adaptors complementary to the insert adapt  
 purified. The sheared, adapted mouse DNA was  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Strata

FEATURES  
 source

and selected for ampicillin resistance."

54.5%; Score 12; DB 28; Length 28;  
 larity 100.0%; Pred. No. 1.5e+05;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATCACAGTCT 15  
 |||||  
 ATCACAGTCT 14

1793 36 bp DNA linear GSS 13-DEC-2000  
 70E18R Mouse 10kb plasmid UGCM library Mus musculus genomic  
 3 UGCM1M0370E18 R, genomic survey sequence.

1793.1 GI:11697160

musculus (house mouse)  
 musculus  
 cyota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 bases 1 to 36)  
 .D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 ly, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 3 M., Rose, R., Stokes, R., Tingey, A., von  
 3 rhausen, A. and Wright, D., Weiss, R.  
 3 a whole genome scaffolding with paired end reads from 10kb  
 mid inserts  
 3 lished (2000)

3 ct: Robert B. Weiss  
 3 rsity of Utah Genome Center  
 3 rsity of Utah  
 3 08. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 3 , USA  
 3 801 585 5606  
 3 801 585 7177  
 3 : ddunn@genetics.utah.edu  
 3 t Length: 10000 Std Error: 0.00  
 3 : 0370 row: E column: 18  
 3 rimer: CACACGGAACACCTAIGACC  
 3 : plasmid ends  
 3 quality sequence stop: 36.

Location/Qualifiers  
 1. 36  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCM1M0370E18"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCM library"  
 /notes="Vector: FWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWB42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells

# ORIGIN

Query Match 54.5%; Score 12; DB 28; Length 36;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCG 20  
 |||||  
 15 AGCCATTACAGTGTCTGTG 34

RESULT 43  
 AL947932/c  
 LOCUS 41 bp DNA linear GSS  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-308D12-0  
 genomic survey sequence.

ACCESSION AL947932  
 VERSION AL947932.1 GI:24404554  
 SOURCE GSS.

ORGANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1

REFERENCE Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S.  
 and Weisshaar, B.  
 A pipeline for automated high-throughput generation of F.  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

JOURNAL 2  
 REFERENCE 2  
 AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and We  
 A new Arabidopsis thaliana T-DNA mutagenesis population  
 for flanking sequence tag based reverse genetics

JOURNAL 3 (bases 1 to 41)  
 REFERENCE 3  
 AUTHORS Rosso, M., Strizhov, N., Li, Y. and Weisshaar, B.  
 Direct Submission

JOURNAL Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion within the locus defined by clone  
 The sequences are generated at the MPI for Plant Breeding  
 in the context of the GABI-Kat project. GABI-Kat is part  
 German Plant Genomics program designated 'GABI'. Informa  
 line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. 41  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-308D12-015815"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion  
 /note="PCR was performed on DNA from Arabidopsis  
 vector pAC161. The lines contain one or more T-D  
 plant (T1) which were transformed with the T-D  
 insertions. The DNA fragment(s) resulting from t  
 were directly sequenced to determine the genomic  
 flanking the insertion. Sequences displaying sig  
 similarity to the A. thaliana nuclear genome seq  
 processed for submission. T-DNA derived sequence  
 removed"

# ORIGIN

Query Match 54.5%; Score 12; DB 29; Length 41;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 3 ACAATCACAGTCTCTGCGGA 22

||||| ||| |||  
AGTCACAGATCTCTCGGA 1

4299 45 bp mRNA linear EST 08-SEP-1999  
56940 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis  
iana cDNA clone 701556940, mRNA sequence.  
4299  
4299.1 GI:5951328

idopsis thaliana (thale cress)

idopsis thaliana  
xyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

bases 1 to 45)  
, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,  
, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
one, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,  
R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,  
io, T., Policky, J., Suzuki, G., Argentine, C., Shah, S.,  
iga, A., Murry, L., Turner, C., Krikorian, S., Elder, D. and  
on, D.

idopsis thaliana Gene Expression MicroArray

ublished (1999)

act: David Smoller, Ph.D.

me Systems, Inc., a wholly owned subsidiary of Incyte

macuticals, Inc.

. World Parkway Circle, St. Louis, MO 63134, USA

877-577-2733

314-427-3324

1: service@genomesystems.com.

Location/Qualifiers

1. .45

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/cultivar="Columbia Col-0"

/db\_xref="taxon:3702"

/clone="701556940"

/tissue\_type="rosette"

/dev\_stage="4 - 7 weeks"

/clone\_lib="A. thaliana, Columbia Col-0, rosette-3"

/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cDNA

library was derived from untreated rosette tissue from

Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.

Plants were grown in 1:1:1 peat moss/vermiculite/perlite

soil at 22 deg. C +/- 3 deg. C under constant light, and

watered with fertilizer. cDNA synthesis was initiated

using a NotI-oligo(dT) primer. Double-stranded cDNA was

blunted, ligated to SalI adaptors, digested with NotI,

size-selected, and cloned into the NotI and SalI sites of

the pSPORT vector."

54.5%; Score 12; DB 9; Length 45;

ilarity 75.0%; Pred. No. 1.9e+05;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TATCAGATCTCTCTCGGA 22

|||||

TACACACTCTCTCTCGGA 38

57345 50 bp DNA linear GSS 18-JUN-2002  
idopsis thaliana T-DNA flanking sequence GK-218E10-014201,  
omic survey sequence.

57345

57345.1 GI:21520464

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidop

REFERENCE 1  
AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S  
and Weisshaar, B.  
TITLE A pipeline for automated high-throughput generation of F  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines

JOURNAL 2  
AUTHORS Unpublished

REFERENCE 2  
AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and We  
TITLE A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 50)  
AUTHORS Li, Y., Rosso, M., Strizhov, N. and Weisshaar, B.  
TITLE Direct Submission

JOURNAL Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institu  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829  
This sequence is recovered from the left border of the T  
indicates an insertion within the locus defined by clone

COMMENT The sequences are generated at the MPI for Plant Breedin  
in the context of the GABI-Kat project. GABI-Kat is part  
German Plant Genomics program designated 'GABI'. Informa  
line availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES Location/Qualifiers

source

1. .50

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-218E10-014201"

/clone\_lib="Arabidopsis thaliana T-DNA insertic

/note="PCR was performed on DNA from Arabidopsi

plants (T1) which were transformed with the T-I

vector pAC161. The lines contain one or more T-

insertions. The DNA fragment(s) resulting from

were directly sequenced to determine the genom

flanking the insertion. Sequences displaying si

similarity to the A. thaliana nuclear genome se

processed for submission. T-DNA derived sequen

removed"

ORIGIN

Query Match 54.5%; Score 12; DB 29; Length 50;

Best Local Similarity 75.0%; Pred. No. 2e+05; Indels 0;

Matches 15; Conservative 0; Mismatches 5;

QY 2 GACATCAGTCTCTCTCGGG 21

|||||

Db 23 GACAGCCCATCTCTCTCGG 4

Search completed: February 29, 2004, 11:20:00

Job time : 1706.43 secs

09:38:25 2004

us-10-090-326-7.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 08:42:24 ; Search time 624.416 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

IS-10-090-326-7

atccctgtctccacgggtt 20

IDENTITY NUC

hapop 10.0 , Gapext 1.0

470272 seqs, 2167516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl.\*

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.ov.\*  
5: gb.pat.\*  
6: gb.ph.\*  
7: gb.pl.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: em.ba.\*  
15: em.fun.\*  
16: em.hum.\*  
17: em.in.\*  
18: em.mu.\*  
19: em.om.\*  
20: em.or.\*  
21: em.ov.\*  
22: em.pat.\*  
23: em.ph.\*  
24: em.pl.\*  
25: em.ro.\*  
26: em.sts.\*  
27: em.un.\*  
28: em.vi.\*  
29: em.htg.hum.\*  
30: em.htg.in.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.man.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being p  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	75.0	17	6	AX723803	AX723803
2	14.8	74.0	20	6	BD268717	BD268717
3	14.8	74.0	20	6	BD268720	BD268720
4	14.8	74.0	20	6	AR229114	AR229114
5	14.8	74.0	20	6	AR229117	AR229117
6	14.8	74.0	20	6	AR281377	AR281377
7	14.8	74.0	20	6	AR281380	AR281380
8	14.8	74.0	20	6	AR304586	AR304586
9	14.8	74.0	20	6	AR304589	AR304589
10	14.8	74.0	20	6	AR337582	AR337582
11	14.8	74.0	20	6	AR337585	AR337585
12	14.8	74.0	20	6	AX696154	AX696154
13	14.4	72.0	38	6	AR216216	AR216216
14	14	70.0	33	6	I11490	I11490 Sec
15	13.6	68.0	24	6	BD234781	BD234781
16	13.6	68.0	24	6	AX011544	AX011544
17	13.6	68.0	32	6	AX899510	AX899510
18	13.4	67.0	20	6	AX601037	AX601037
19	13.4	67.0	29	6	AR176562	AR176562
20	13.4	67.0	29	6	AR176564	AR176564
21	13.4	67.0	29	6	AR342701	AR342701
22	13.4	67.0	29	6	AR342703	AR342703
23	13.4	67.0	41	6	AX517020	AX517020
24	13.4	67.0	41	6	AX519531	AX519531
25	13.2	66.0	20	6	AX167919	AX167919
26	13.2	66.0	30	6	AR095317	AR095317
27	13.2	66.0	30	6	AR172127	AR172127
28	13.2	66.0	30	6	AR173470	AR173470
29	13.2	66.0	32	6	I69389	I69389 Sec
30	13.2	66.0	47	6	AR289265	AR289265
31	13.2	66.0	54	9	HUMC1A201	M22817 Hur
32	13.2	66.0	55	6	AR422169	AR422169
33	13.2	66.0	55	6	BD117722	BD117722
34	13	65.0	31	6	AX248870	AX248870
35	13	65.0	55	8	AJ594698	AJ594698
36	12.8	64.0	17	6	AX674525	AX674525
37	12.8	64.0	21	6	BD226165	BD226165
38	12.8	64.0	22	6	AX663735	AX663735
39	12.8	64.0	22	6	BD133427	BD133427
40	12.8	64.0	24	6	AX289046	AX289046
41	12.8	64.0	28	6	AR090871	AR090871
42	12.8	64.0	28	6	AR197906	AR197906
43	12.8	64.0	28	6	AR260060	AR260060
44	12.8	64.0	37	8	AJ590113	AJ590113
45	12.8	64.0	41	6	AX516800	AX516800
46	12.8	64.0	41	6	AX518956	AX518956
47	12.8	64.0	45	6	AR009531	AR009531
48	12.8	64.0	45	6	AR172143	AR172143
49	12.8	64.0	45	6	I66205	I66205 Sec
50	12.8	64.0	45	6	I66218	I66218 Sec
51	12.8	64.0	45	6	BD165783	BD165783
52	12.8	64.0	47	6	E13358	E13358 Pr
53	12.8	64.0	57	6	AR248873	AR248873
54	12.8	64.0	60	14	AF466414	AF466414
55	12.8	64.0	60	14	AF466415	AF466415
56	12.8	64.0	60	14	AF466416	AF466416
57	12.8	64.0	60	14	AF466417	AF466417
58	12.8	64.0	60	14	AF466418	AF466418
59	12.8	64.0	60	14	AF466419	AF466419
60	12.8	64.0	60	14	AF466420	AF466420
61	12.8	64.0	60	14	AF466421	AF466421
62	12.8	64.0	60	14	AF466422	AF466422
63	12.8	64.0	60	14	AF466423	AF466423
64	12.8	64.0	60	14	AF466424	AF466424
65	12.8	64.0	60	14	AF466425	AF466425



64.0	60	14	AF466426	AF466426 Hepatitis	139	12.4	62.0	14	6	A89288	A89288 Se
64.0	60	14	AF466427	AF466427 Hepatitis	140	12.4	62.0	14	6	A89988	A89988 Se
64.0	60	14	AF466428	AF466428 Hepatitis	141	12.4	62.0	14	6	BD065534	BD065534
64.0	60	14	AF466429	AF466429 Hepatitis	142	12.4	62.0	14	6	BD066801	BD066801
64.0	60	14	AF466430	AF466430 Hepatitis	143	12.4	62.0	14	6	A89289	A89289 Se
64.0	60	14	AF466431	AF466431 Hepatitis	144	12.4	62.0	14	6	BD066802	BD066802
64.0	60	14	AF466432	AF466432 Hepatitis	145	12.4	62.0	14	6	AX728183	AX728183
64.0	60	14	AF466433	AF466433 Hepatitis	146	12.4	62.0	36	6	AX410186	AX410186
64.0	60	14	AF466434	AF466434 Hepatitis	147	12.4	62.0	36	6	AX576979	AX576979
64.0	60	14	AF466435	AF466435 Hepatitis	148	12.4	62.0	47	6	AX378320	AX378320
64.0	60	14	AF466436	AF466436 Hepatitis	149	12.4	62.0	54	10	AB043126S2	AB043126
64.0	60	14	AF466437	AF466437 Hepatitis	150	12.4	62.0	60	14	AF466482	AF466482
64.0	60	14	AF466438	AF466438 Hepatitis	151	12.4	62.0	60	14	AF466463	AF466463
64.0	60	14	AF466439	AF466439 Hepatitis	152	12.4	62.0	60	14	AF466464	AF466464
64.0	60	14	AF466440	AF466440 Hepatitis	153	12.4	62.0	60	14	AF466465	AF466465
64.0	60	14	AF466441	AF466441 Hepatitis	154	12.4	62.0	60	14	AF466466	AF466466
64.0	60	14	AF466442	AF466442 Hepatitis	155	12.4	62.0	60	14	AF466467	AF466467
64.0	60	14	AF466443	AF466443 Hepatitis	156	12.4	62.0	60	14	AF466468	AF466468
64.0	60	14	AF466444	AF466444 Hepatitis	157	12.4	62.0	60	14	AF466469	AF466469
64.0	60	14	AF466445	AF466445 Hepatitis	158	12.4	62.0	60	14	AF466470	AF466470
64.0	60	14	AF466446	AF466446 Hepatitis	159	12.4	62.0	60	14	AF466471	AF466471
64.0	60	14	AF466447	AF466447 Hepatitis	160	12.4	62.0	60	14	AF466472	AF466472
64.0	60	14	AF466448	AF466448 Hepatitis	161	12.4	62.0	60	14	AF466473	AF466473
64.0	60	14	AF466449	AF466449 Hepatitis	162	12.4	62.0	60	14	AF466474	AF466474
64.0	60	14	AF466450	AF466450 Hepatitis	163	12.4	62.0	60	14	AF466475	AF466475
64.0	60	14	AF466451	AF466451 Hepatitis	164	12.4	62.0	60	14	AF466476	AF466476
64.0	60	14	AF466452	AF466452 Hepatitis	165	12.4	62.0	60	14	AF466477	AF466477
64.0	60	14	AF466453	AF466453 Hepatitis	166	12.4	62.0	60	14	AF466478	AF466478
64.0	60	14	AF466454	AF466454 Hepatitis	167	12.4	62.0	60	14	AF466479	AF466479
64.0	60	14	AF466455	AF466455 Hepatitis	168	12.4	62.0	60	14	AF466480	AF466480
64.0	60	14	AF466456	AF466456 Hepatitis	169	12.4	62.0	60	14	AF466481	AF466481
64.0	60	14	AF466457	AF466457 Hepatitis	170	12.4	62.0	60	14	AF466482	AF466482
64.0	60	14	AF466458	AF466458 Hepatitis	171	12.4	62.0	60	14	AF466483	AF466483
64.0	60	14	AF466459	AF466459 Hepatitis	172	12.4	62.0	60	14	AF466484	AF466484
64.0	60	14	AF466460	AF466460 Hepatitis	173	12.4	62.0	60	14	AF466485	AF466485
64.0	60	14	AF466461	AF466461 Hepatitis	174	12.4	62.0	60	14	AF466486	AF466486
64.0	60	14	AF466489	AF466489 Hepatitis	175	12.4	62.0	60	14	AF466487	AF466487
64.0	60	14	AF466490	AF466490 Hepatitis	176	12.4	62.0	60	14	AF466488	AF466488
64.0	60	14	AF466491	AF466491 Hepatitis	177	12.4	62.0	60	14	AF466493	AF466493
64.0	60	14	AF466494	AF466494 Hepatitis	178	12.2	61.0	17	6	AX531573	AX531573
64.0	60	14	AF466495	AF466495 Hepatitis	179	12.2	61.0	20	6	AX294106	AX294106
64.0	60	14	AF466496	AF466496 Hepatitis	180	12.2	61.0	21	6	AR183211	AR183211
64.0	60	14	AF466497	AF466497 Hepatitis	181	12.2	61.0	24	6	AX289473	AX289473
64.0	60	14	AF466498	AF466498 Hepatitis	182	12.2	61.0	24	6	AX348066	AX348066
64.0	60	14	AF466499	AF466499 Hepatitis	183	12.2	61.0	24	6	AX540331	AX540331
64.0	60	14	AF466500	AF466500 Hepatitis	184	12.2	61.0	25	6	AX533635	AX533635
64.0	60	14	AF466501	AF466501 Hepatitis	185	12.2	61.0	25	6	AX533636	AX533636
64.0	60	14	AF466502	AF466502 Hepatitis	186	12.2	61.0	25	6	AX533637	AX533637
64.0	60	14	AF466503	AF466503 Hepatitis	187	12.2	61.0	25	6	AX533638	AX533638
64.0	60	14	AF466504	AF466504 Hepatitis	188	12.2	61.0	25	6	AX533639	AX533639
64.0	60	14	AF466505	AF466505 Hepatitis	189	12.2	61.0	25	6	AX533640	AX533640
64.0	60	14	AF466506	AF466506 Hepatitis	190	12.2	61.0	25	6	AX533641	AX533641
64.0	60	14	AF466508	AF466508 Hepatitis	191	12.2	61.0	25	6	AX533642	AX533642
64.0	60	14	AF466509	AF466509 Hepatitis	192	12.2	61.0	25	6	AX533643	AX533643
63.0	20	6	AX743539	AX743539 Sequence	193	12.2	61.0	29	6	AX010778	AX010778
63.0	20	6	AX774462	AX774462 Sequence	194	12.2	61.0	29	6	BD211699	BD211699
63.0	25	6	ES3850	ES3850 LUNX gene a	195	12.2	61.0	31	6	AR043929	AR043929
63.0	27	6	AR040348	AR040348 Sequence	196	12.2	61.0	31	6	AR073462	AR073462
63.0	31	6	AX326596	AX326596 Sequence	197	12.2	61.0	31	6	193333	193333 Se
63.0	34	6	AX235755	AX235755 Sequence	198	12.2	61.0	31	6	AX022056	AX022056
63.0	41	6	A74298	A74298 Sequence 10	199	12.2	61.0	31	6	BD080633	BD080633
63.0	41	6	AR038839	AR038839 Sequence	200	12.2	61.0	31	6	BD087579	BD087579
63.0	41	6	BD232071	BD232071 Remedy re	201	12.2	61.0	32	6	189374	189374 Se
63.0	41	6	AX014733	AX014733 Sequence	202	12.2	61.0	32	6	E09062	E09062 DN
63.0	43	6	AX287618	AX287618 Sequence	203	12.2	61.0	33	6	E09066	E09066
63.0	43	6	AX739903	AX739903 Sequence	204	12.2	61.0	33	6	AX163908	AX163908
63.0	45	6	AR007987	AR007987 Sequence	205	12.2	61.0	33	6	AX472710	AX472710
63.0	45	6	AR433004	AR433004 Sequence	206	12.2	61.0	36	6	132360	132360 Se
63.0	51	6	AX204414	AX204414 Sequence	207	12.2	61.0	37	6	AX809438	AX809438
63.0	52	6	AR086666	AR086666 Sequence	208	12.2	61.0	39	6	AX722230	AX722230
63.0	55	6	A10481	A10481 oligonucleo	209	12.2	61.0	39	6	AX722231	AX722231
63.0	55	6	A13639	A13639 oligonucleo	210	12.2	61.0	39	6	AR050513	AR050513
62.0	14	6	A88021	A88021 Sequence 16	211	12.2	61.0	45	6		

09:38:25 2004

us-10-090-326-7.max.rge

61.0 45 6 AR124641 Sequence  
61.0 45 6 AX697100 Sequence  
61.0 48 6 AR160227 Sequence  
61.0 51 6 AR231224 Sequence  
61.0 51 6 AR308005 Sequence  
61.0 51 6 AR525468 Sequence  
61.0 54 6 BD245074 Regions o  
61.0 56 6 AR086650 Sequence  
61.0 59 6 AX756512 Sequence  
61.0 60 9 HUMSAU3A03  
61.0 60 9 HUMSAU3A12  
61.0 60 9 HUMSAU3A37  
61.0 60 9 HUMSAU3A39  
61.0 17 6 BD104906  
60.0 24 6 AR077870 Sequence  
60.0 24 6 AR111452 Sequence  
60.0 24 6 AR159861 Sequence  
60.0 24 6 I19889 Sequence 14  
60.0 24 6 I44680 Sequence 15  
60.0 24 6 I60457 Sequence 15  
60.0 24 6 I79555 Sequence 14  
60.0 24 6 AR213260 Sequence  
60.0 24 6 AR216146 Sequence  
60.0 24 6 AX343407 Sequence  
60.0 27 6 AR109762 Sequence  
60.0 28 6 A44445 Sequence 8  
60.0 28 6 AR009690 Sequence  
60.0 28 6 I68088 Sequence 8  
60.0 28 6 AR241823 Sequence  
60.0 29 6 AX696197 Sequence  
60.0 30 6 A42577 Sequence 94  
60.0 30 6 A88766 Sequence 91  
60.0 30 6 AX037170 Sequence  
60.0 30 6 AX037186 Sequence  
60.0 30 6 BD066279 Sequence  
60.0 38 6 A86831 Sequence 15  
60.0 38 6 A86835 Sequence 19  
60.0 38 6 AR316941 Sequence  
60.0 38 6 AR316945 Sequence  
60.0 38 6 BD070407 Factor X  
60.0 38 6 BD070411 Factor X  
60.0 41 6 BD224821 Novel pla  
60.0 56 8 AY199115 Arabidops  
60.0 57 6 AR381796 Sequence  
60.0 57 6 AR381820 Sequence  
60.0 57 6 BD107773 Opsonic a  
60.0 57 6 BD107797 Opsonic a  
59.0 17 6 AX725064 Sequence  
59.0 18 6 AX785461 Sequence  
59.0 20 6 AR107754 Sequence  
59.0 20 6 AR199735 Sequence  
59.0 20 6 AR373464 Sequence  
59.0 20 6 AX060355 Sequence  
59.0 22 6 AX241169 Sequence  
59.0 22 6 AX486753 Sequence  
59.0 24 6 A57530 Sequence 22  
59.0 24 6 A57532 Sequence 24  
59.0 24 6 AR003689 Sequence  
59.0 25 6 AR340514 Sequence  
59.0 25 6 AX079229 Sequence  
59.0 25 6 AX079233 Sequence  
59.0 25 6 AX079239 Sequence  
59.0 25 6 AX079250 Sequence  
59.0 25 6 AX288125 Sequence  
59.0 27 6 BD140691 Nucleic a  
59.0 27 6 BD182143 Novel cha  
59.0 30 6 BD235494 Deaturas  
59.0 30 6 AR204083 Sequence  
59.0 30 6 BD077089 Lipocalin  
59.0 31 11 BX545710 Arabidops  
59.0 31 6 BD002655 Gene comp  
59.0 41 6 AX517882 Sequence  
59.0 42 6 AX612020 Sequence

C 285 11.8 59.0 42 6 AX612023  
C 286 11.8 59.0 44 6 AR058903  
C 287 11.8 59.0 44 6 I36264  
288 11.8 59.0 45 6 AR096938  
289 11.8 59.0 45 6 BD136133  
C 290 11.8 59.0 47 6 AR230943  
C 291 11.8 59.0 49 6 AX150267  
C 292 11.8 59.0 49 6 AX150276  
C 293 11.8 59.0 60 6 I87861  
294 11.6 58.0 19 6 AX130820  
295 11.6 58.0 20 6 AR268226  
296 11.6 58.0 20 6 AX613642  
297 11.6 58.0 21 6 AR183755  
C 298 11.6 58.0 22 6 A79079  
C 299 11.6 58.0 22 6 AR208215  
C 300 11.6 58.0 23 6 AX454974  
301 11.6 58.0 24 6 E39982  
302 11.6 58.0 24 6 AX292639  
303 11.6 58.0 24 6 BD174982  
C 304 11.6 58.0 25 6 AX378888  
C 305 11.6 58.0 25 6 BD170447  
306 11.6 58.0 26 6 BD160852  
C 307 11.6 58.0 27 6 A84004  
308 11.6 58.0 27 6 AR091025  
C 309 11.6 58.0 27 6 AR099333  
310 11.6 58.0 27 6 AR198060  
311 11.6 58.0 27 6 AR260214  
C 312 11.6 58.0 27 6 AR321623  
313 11.6 58.0 27 6 AR391967  
314 11.6 58.0 27 6 AX235758  
C 315 11.6 58.0 27 6 BD061174  
316 11.6 58.0 28 6 A18729  
317 11.6 58.0 28 6 A18729  
C 318 11.6 58.0 28 6 E13294  
319 11.6 58.0 28 6 BD132600  
C 320 11.6 58.0 30 6 A84929  
C 321 11.6 58.0 30 6 AR253029  
322 11.6 58.0 31 6 AX248587  
323 11.6 58.0 31 6 AX249526  
324 11.6 58.0 32 6 A18738  
C 330 11.6 58.0 34 11 C75799  
C 331 11.6 58.0 37 6 AR427970  
C 332 11.6 58.0 37 6 BD057945  
C 333 11.6 58.0 39 6 A18732  
C 334 11.6 58.0 42 6 AX283147  
335 11.6 58.0 42 6 AX283148  
336 11.6 58.0 42 6 AX787116  
337 11.6 58.0 42 6 AX787120  
338 11.6 58.0 43 6 A18731  
C 339 11.6 58.0 47 6 AR291975  
340 11.6 58.0 48 6 A79783  
341 11.6 58.0 48 6 AR018113  
C 342 11.6 58.0 48 6 AR300132  
C 343 11.6 58.0 48 6 BD082071  
C 344 11.6 58.0 50 6 AX199540  
C 345 11.6 58.0 51 6 AX159973  
C 346 11.6 58.0 51 6 AX199539  
347 11.6 58.0 51 8 AJ590706  
348 11.6 58.0 54 9 HUMC1A2A  
349 11.6 58.0 57 5 GTHR5A2  
C 350 11.6 58.0 57 6 AR138369  
C 351 11.6 58.0 57 6 AR146879  
352 11.6 58.0 57 6 AR390982  
C 353 11.6 58.0 57 6 AR390983  
354 11.6 58.0 57 6 AX089676  
C 355 11.6 58.0 57 6 AX089677  
356 11.6 58.0 57 6 AX090131  
C 357 11.6 58.0 57 6 AX090132

AX612023  
AR058903  
I36264  
AR096938  
BD136133  
AR230943  
AX150267  
AX150276  
I87861  
AX130820  
AR268226  
AX613642  
AR183755  
A79079  
AR208215  
AX454974  
E39982  
AX292639  
BD174982  
AX378888  
BD170447  
BD160852  
A84004  
AR091025  
AR099333  
AR198060  
AR260214  
AR321623  
AR391967  
AX235758  
BD061174  
A18729  
A18729  
E13294  
BD132600  
A84929  
AR253029  
AX248587  
AX249526  
A18738  
AR075177  
AR112344  
I87870  
AR212987  
I92381  
C75799  
AR427970  
BD057945  
A18732  
AX283147  
AX283148  
AX787116  
AX787120  
A18731  
AR291975  
A79783  
AR018113  
AR300132  
BD082071  
AX199540  
AX159973  
AX199539  
AJ590706  
HUMC1A2A  
GTHR5A2  
AR138369  
AR146879  
AR390982  
AR390983  
AX089676  
AX089677  
AX090131  
AX090132

58.0	57	6	AX543227	Sequence	431	11.4	57.0	60	6	AR172689	AR172689
58.0	57	6	AX543228	Sequence	432	11.4	57.0	60	6	AR178633	AR178633
58.0	57	6	BD224575	Adeno-ass	433	11.4	57.0	60	6	BD231077	BD231077
58.0	60	6	AR177888	Sequence	434	11.4	57.0	60	6	AR181204	AR181204
58.0	60	6	BD015073	Recombina	435	11.4	57.0	60	6	AR199885	AR199885
57.0	14	6	A89271	Sequence 14	436	11.4	57.0	60	6	AR231833	AR231833
57.0	14	6	BD066784	An antise	437	11.4	57.0	60	6	AR343308	AR343308
57.0	16	6	AR235525	Sequence	438	11.4	57.0	60	6	AR349626	AR349626
57.0	17	6	AX531569	Sequence	439	11.4	57.0	60	6	AR391097	AR391097
57.0	17	6	AX531570	Sequence	440	11.4	57.0	60	6	AR431540	AR431540
57.0	17	6	AX531571	Sequence	441	11.4	57.0	60	6	BD062822	BD062822
57.0	17	6	AX531572	Sequence	442	11.2	56.0	17	6	BD259296	BD259296
57.0	17	6	AX758411	Sequence	443	11.2	56.0	17	6	AX422037	AX422037
57.0	18	6	AR410492	Sequence	444	11.2	56.0	17	6	AX422038	AX422038
57.0	18	6	AR410497	Sequence	445	11.2	56.0	17	6	AX422743	AX422743
57.0	18	6	AX317302	Sequence	446	11.2	56.0	17	6	AX422744	AX422744
57.0	18	6	AX317307	Sequence	447	11.2	56.0	17	6	AX531574	AX531574
57.0	18	6	AX317450	Sequence	448	11.2	56.0	17	6	AX735662	AX735662
57.0	18	6	AX356968	Sequence	449	11.2	56.0	17	6	BD202678	BD202678
57.0	18	6	AX554986	Sequence	450	11.2	56.0	18	6	AR293569	AR293569
57.0	19	6	AX590226	Sequence	451	11.2	56.0	19	6	AR067185	AR067185
57.0	20	6	AR136257	Sequence	452	11.2	56.0	19	6	AX477615	AX477615
57.0	20	6	BD247712	Antisense	453	11.2	56.0	19	6	AX505035	AX505035
57.0	20	6	AR268227	Sequence	454	11.2	56.0	19	6	BD141129	BD141129
57.0	20	6	AX592301	Sequence	455	11.2	56.0	20	6	AR075709	AR075709
57.0	20	6	AX644649	Sequence	456	11.2	56.0	20	6	AR076702	AR076702
57.0	21	6	AR2079122	Sequence	457	11.2	56.0	20	6	AR153559	AR153559
57.0	21	6	AX057940	Sequence	458	11.2	56.0	20	6	BD262874	BD262874
57.0	24	6	AR140036	Sequence	459	11.2	56.0	20	6	BD266176	BD266176
57.0	24	6	AR165203	Sequence	460	11.2	56.0	20	6	I85587	I85587
57.0	24	6	AX443854	Sequence	461	11.2	56.0	20	6	AR182759	AR182759
57.0	25	6	AX197188	Sequence	462	11.2	56.0	20	6	AR300839	AR300839
57.0	25	6	AX197228	Sequence	463	11.2	56.0	20	6	AX224269	AX224269
57.0	25	6	AX447832	Sequence	464	11.2	56.0	20	6	AX370478	AX370478
57.0	25	6	AX533631	Sequence	465	11.2	56.0	20	6	AX719288	AX719288
57.0	25	6	AX533632	Sequence	466	11.2	56.0	20	6	AX805339	AX805339
57.0	25	6	AX533633	Sequence	467	11.2	56.0	21	6	AR124239	AR124239
57.0	25	6	AX533634	Sequence	468	11.2	56.0	21	6	I27417	I27417
57.0	26	6	AR140037	Sequence	469	11.2	56.0	21	6	I27450	I27450
57.0	27	6	AX105635	Sequence	470	11.2	56.0	22	6	E35028	E35028
57.0	27	6	AX111733	Sequence	471	11.2	56.0	22	6	I04331	I04331
57.0	28	6	AR140038	Sequence	472	11.2	56.0	22	6	BD165811	BD165811
57.0	28	6	BD097501	Novel mel	473	11.2	56.0	23	6	AX212235	AX212235
57.0	30	6	A26395	Origonucleo	474	11.2	56.0	23	6	BD143781	BD143781
57.0	30	6	AR021098	Sequence	475	11.2	56.0	23	6	BD168643	BD168643
57.0	30	6	AR140039	Sequence	476	11.2	56.0	24	6	AR004320	AR004320
57.0	30	6	BD229110	Endogeneo	477	11.2	56.0	24	6	AR080651	AR080651
57.0	30	6	AR308641	Sequence	478	11.2	56.0	24	6	AX444225	AX444225
57.0	30	6	AR431785	Sequence	479	11.2	56.0	24	6	AX548171	AX548171
57.0	31	6	AR300486	Sequence	480	11.2	56.0	25	6	AR302467	AR302467
57.0	31	6	AR428763	Sequence	481	11.2	56.0	25	6	AR302474	AR302474
57.0	32	6	AR140040	Sequence	482	11.2	56.0	25	6	AX448191	AX448191
57.0	33	6	AR027111	Sequence	483	11.2	56.0	25	6	AX533644	AX533644
57.0	36	6	E36446	DNA polymer	484	11.2	56.0	25	6	BD175838	BD175838
57.0	36	6	E36456	DNA polymer	485	11.2	56.0	25	6	BD175845	BD175845
57.0	36	6	E36458	DNA polymer	486	11.2	56.0	26	6	AX675927	AX675927
57.0	36	6	I13347	Sequence 1	487	11.2	56.0	27	6	AX023887	AX023887
57.0	36	6	I13357	Sequence 14	488	11.2	56.0	27	6	BD182141	BD182141
57.0	36	6	I13359	Sequence 16	489	11.2	56.0	27	6	BD186062	BD186062
57.0	36	6	AR359217	Sequence	490	11.2	56.0	28	6	AR197657	AR197657
57.0	36	6	BD085156	Ricin-lik	491	11.2	56.0	28	6	AR259811	AR259811
57.0	36	8	ATH552316	Arabidops	492	11.2	56.0	28	6	AR302941	AR302941
57.0	38	6	AX655083	Sequence	493	11.2	56.0	28	6	AX024605	AX024605
57.0	39	6	AR007371	Sequence	494	11.2	56.0	28	6	AX598169	AX598169
57.0	39	6	I16905	Sequence 10	495	11.2	56.0	28	6	BD091310	BD091310
57.0	39	6	I69498	Sequence 10	496	11.2	56.0	28	6	BD223220	BD223220
57.0	42	6	A79785	Sequence 12	497	11.2	56.0	28	6	AR039142	AR039142
57.0	42	6	AR018115	Sequence	498	11.2	56.0	29	6	AR065272	AR065272
57.0	45	6	AX612451	Sequence	499	11.2	56.0	29	6	BD061656	BD061656
57.0	46	6	AX665082	Sequence	500	11.2	56.0	29	6	I06862	I06862
57.0	47	6	AR291957	Sequence	501	11.2	56.0	30	6	I07313	I07313
57.0	49	6	E08249	linker. 9/1	502	11.2	56.0	30	6		
57.0	49	6	I78449	Sequence 3	503	11.2	56.0	30	6		

56.0	30	6	AR427956	AR427956 Sequence	c 577	11.2	56.0	57	6	BD141873	BD141873
56.0	30	6	AR433332	AR433332 Sequence	578	11.2	56.0	58	6	A62961	A62961 Se
56.0	30	6	AR080015	AR080015 Sequence	579	11.2	56.0	59	6	AX267016	AX267016
56.0	30	10	RRNF116B	X66573 R.rattus Hn	c 580	11.2	56.0	59	6	AX113783	AX113783
56.0	31	6	AR069595	AR069595 Sequence	c 581	11.2	56.0	60	6	E30083	E30083 No
56.0	31	6	AR091464	AR091464 Sequence	c 582	11.2	56.0	60	14	AF466492	AF466492
56.0	31	6	AR104415	AR104415 Sequence	c 583	11.2	56.0	60	14	AF466507	AF466507
56.0	31	6	AR260540	AR260540 Sequence	584	11	55.0	17	6	AX732402	AX732402
56.0	31	6	AR248269	AR248269 Sequence	585	11	55.0	17	6	BD203109	BD203109
56.0	31	6	AX329339	AX329339 Sequence	586	11	55.0	17	6	BD203110	BD203110
56.0	31	6	AX743565	AX743565 Sequence	587	11	55.0	17	6	BD203111	BD203111
56.0	31	8	ATH524599	AJ524599 Arabidops	588	11	55.0	18	6	AR073436	AR073436
56.0	32	6	AR110560	AR110560 Sequence	589	11	55.0	18	6	BD250760	BD250760
56.0	32	6	AR151780	AR151780 Sequence	c 590	11	55.0	18	6	AX443449	AX443449
56.0	32	6	AR219996	AR219996 Sequence	591	11	55.0	20	6	AR136444	AR136444
56.0	32	6	AR220713	AR220713 Sequence	c 592	11	55.0	20	6	E36664	E36664 DN
56.0	32	6	BD063041	BD063041 Protease-	593	11	55.0	20	6	AR221423	AR221423
56.0	34	6	AR302546	AR302546 Sequence	594	11	55.0	20	6	AR314814	AR314814
56.0	34	6	AX101011	AX101011 Sequence	595	11	55.0	20	6	AX429760	AX429760
56.0	34	6	AX472708	AX472708 Sequence	c 596	11	55.0	20	6	AX521736	AX521736
56.0	34	6	BD133834	BD133834 Variant B	c 597	11	55.0	20	6	AX521742	AX521742
56.0	35	6	AX188752	AX188752 Sequence	598	11	55.0	20	6	BD161947	BD161947
56.0	38	6	AX247620	AX247620 Sequence	599	11	55.0	20	6	BD170545	BD170545
56.0	38	6	AX247621	AX247621 Sequence	600	11	55.0	20	6	BD183772	BD183772
56.0	39	6	I21517	I21517 Sequence 64	601	11	55.0	20	6	BD185558	BD185558
56.0	40	6	AX057326	AX057326 Sequence	602	11	55.0	21	6	AR161457	AR161457
56.0	41	6	AX057334	AX057334 Sequence	c 603	11	55.0	21	6	AX095527	AX095527
56.0	41	6	AX097532	AX097532 Sequence	c 604	11	55.0	21	6	AX921468	AX921468
56.0	41	6	AX513862	AX513862 Sequence	605	11	55.0	22	6	AR281273	AR281273
56.0	41	6	AX515772	AX515772 Sequence	606	11	55.0	22	6	AX451373	AX451373
56.0	41	6	AX518367	AX518367 Sequence	c 607	11	55.0	23	6	AR105024	AR105024
56.0	41	6	AX519138	AX519138 Sequence	608	11	55.0	23	6	E36440	E36440 Pr
56.0	41	6	AX521270	AX521270 Sequence	609	11	55.0	23	6	AX601236	AX601236
56.0	41	6	AX543907	AX543907 Sequence	610	11	55.0	24	6	AX291334	AX291334
56.0	44	6	A06666	A06666 Deoxyoligon	c 611	11	55.0	24	6	AX447037	AX447037
56.0	44	6	AX078395	AX078395 Sequence	c 612	11	55.0	24	6	AX460288	AX460288
56.0	44	6	AX128371	AX128371 Sequence	c 613	11	55.0	24	6	AX675425	AX675425
56.0	45	9	HSU12318	U12318 Human T cel	614	11	55.0	25	6	E21017	E21017 No
56.0	46	6	AR409023	AR409023 Sequence	615	11	55.0	25	6	AX287792	AX287792
56.0	46	6	AR409024	AR409024 Sequence	c 616	11	55.0	25	6	AX536245	AX536245
56.0	47	6	AR288308	AR288308 Sequence	c 617	11	55.0	25	6	AX784662	AX784662
56.0	47	6	AR290358	AR290358 Sequence	c 618	11	55.0	25	6	AX784663	AX784663
56.0	47	6	AR230791	AR230791 Sequence	c 619	11	55.0	25	6	AX784664	AX784664
56.0	48	6	BD122070	BD122070 Sequence	c 620	11	55.0	25	6	AX784665	AX784665
56.0	48	6	BD080100	BD080100 Fusion pr	c 621	11	55.0	25	6	AX784666	AX784666
56.0	49	6	BD141898	BD141898 Polypepti	c 622	11	55.0	25	6	AX784667	AX784667
56.0	50	6	A62960	A62960 Sequence 20	c 623	11	55.0	25	6	AX784668	AX784668
56.0	50	6	AX097523	AX097523 Sequence	c 624	11	55.0	25	6	BD223553	BD223553
56.0	50	6	AX186256	AX186256 Sequence	625	11	55.0	26	6	AX537342	AX537342
56.0	50	6	AX823759	AX823759 Sequence	c 626	11	55.0	27	6	AR039974	AR039974
56.0	50	6	AX823787	AX823787 Sequence	c 627	11	55.0	27	6	AR040092	AR040092
56.0	50	9	HSKIR1	AF003116 Homo sapi	c 628	11	55.0	27	6	AR170487	AR170487
56.0	50	10	F246197S10	AF246206 Rattus no	c 629	11	55.0	27	6	AR228996	AR228996
56.0	51	6	AX159937	AX159937 Sequence	c 630	11	55.0	30	6	AR125877	AR125877
56.0	51	6	AX159938	AX159938 Sequence	c 631	11	55.0	30	6	I24244	I24244 Seq
56.0	51	6	AX190162	AX190162 Sequence	632	11	55.0	30	6	AR280222	AR280222
56.0	53	6	AX420110	AX420110 Sequence	c 633	11	55.0	30	6	BD022389	BD022389
56.0	53	6	AX684488	AX684488 Sequence	634	11	55.0	31	6	I26020	I26020 Sec
56.0	54	6	BD245085	BD245085 Regions o	c 635	11	55.0	32	6	AR050593	AR050593
56.0	54	6	BD271042	BD271042 Method an	636	11	55.0	33	6	I11484	I11484 Seq
56.0	54	6	I38084	I38084 Sequence 10	637	11	55.0	33	6	AX710182	AX710182
56.0	54	6	I94934	I94934 Sequence 10	c 638	11	55.0	35	6	AR101988	AR101988
56.0	54	6	AR195186	AR195186 Sequence	c 639	11	55.0	35	6	BD247371	BD247371
56.0	54	6	AR258448	AR258448 Sequence	c 640	11	55.0	35	6	AR234445	AR234445
56.0	54	6	BD0519300	BD0519300 Sequence	c 641	11	55.0	35	6	AR322466	AR322466
56.0	56	6	BD248116	BD248116 MEKK1 (se	c 642	11	55.0	35	6	AR372142	AR372142
56.0	56	6	BD248124	BD248124 MEKK1 (se	c 643	11	55.0	35	6	BD064233	BD064233
56.0	56	6	AR267055	AR267055 Sequence	c 644	11	55.0	36	6	AR026904	AR026904
56.0	56	6	AR285444	AR285444 Sequence	c 645	11	55.0	36	6	AR049330	AR049330
56.0	56	9	S75685	S75685 HLA DQAI (D	c 646	11	55.0	36	6	AR065588	AR065588
56.0	57	6	A17360	A17360 oligonucleo	647	11	55.0	36	6	BD056756	BD056756
56.0	57	6	AX107403	AX107403 Sequence	648	11	55.0	38	6	AX804106	AX804106
56.0	57	6			649	11	55.0	39	6	I13065	I13065 Seq

55.0	39	6	I50688	I50688 Sequence 9	723	10.8	54.0	17	6	I52441	I52441 Se
55.0	40	6	AR059118	AR059118 Sequence	724	10.8	54.0	17	6	I52443	I52443 Se
55.0	40	6	AX454071	AX454071 Sequence	725	10.8	54.0	17	6	AR191839	AR191839
55.0	40	6	BD177356	BD177356 Nucl.eic. a	726	10.8	54.0	17	6	AR191840	AR191840
55.0	44	6	AX287931	AX287931 Sequence	c 727	10.8	54.0	17	6	AR201831	AR201831
55.0	44	6	AX287932	AX287932 Sequence	728	10.8	54.0	17	6	AR201832	AR201832
55.0	44	6	AX287933	AX287933 Sequence	729	10.8	54.0	17	6	AR325734	AR325734
55.0	44	6	AX287934	AX287934 Sequence	730	10.8	54.0	17	6	AR325735	AR325735
55.0	44	6	AX287941	AX287941 Sequence	731	10.8	54.0	17	6	AX022671	AX022671
55.0	44	6	AX287942	AX287942 Sequence	c 732	10.8	54.0	17	6	AX216654	AX216654
55.0	44	6	AX287943	AX287943 Sequence	c 733	10.8	54.0	17	6	AX216926	AX216926
55.0	44	6	AX287944	AX287944 Sequence	c 734	10.8	54.0	17	6	AX216927	AX216927
55.0	44	6	BD102531	BD102531 Method fo	735	10.8	54.0	17	6	AX723776	AX723776
55.0	44	6	BD175029	BD175029 Method fo	736	10.8	54.0	17	6	AX724388	AX724388
55.0	45	6	AX055755	AX055755 Sequence	737	10.8	54.0	17	6	AX804472	AX804472
55.0	45	6	AX287922	AX287922 Sequence	738	10.8	54.0	18	6	AR073386	AR073386
55.0	45	6	AX287923	AX287923 Sequence	c 739	10.8	54.0	18	6	AR164579	AR164579
55.0	45	6	AX287924	AX287924 Sequence	740	10.8	54.0	18	6	BD250710	BD250710
55.0	45	6	AX287925	AX287925 Sequence	c 741	10.8	54.0	18	6	E36742	E36742 Pr
55.0	45	6	AX287926	AX287926 Sequence	c 742	10.8	54.0	18	6	AR241972	AR241972
55.0	47	6	AR291182	AR291182 Sequence	743	10.8	54.0	18	6	AX078804	AX078804
55.0	47	6	AX194680	AX194680 Sequence	744	10.8	54.0	18	6	AX078806	AX078806
55.0	51	6	AX158809	AX158809 Sequence	745	10.8	54.0	19	6	A95029	A95029 Se
55.0	51	6	AX158810	AX158810 Sequence	746	10.8	54.0	19	6	E05500	E05500 Pr
55.0	51	6	AX159945	AX159945 Sequence	747	10.8	54.0	19	6	E38381	E38381 B1
55.0	51	6	AX160399	AX160399 Sequence	748	10.8	54.0	19	6	E39025	E39025 Nu
55.0	51	6	AX160607	AX160607 Sequence	749	10.8	54.0	19	6	AX022673	AX022673
55.0	51	6	AX160608	AX160608 Sequence	750	10.8	54.0	19	6	AX131031	AX131031
55.0	51	6	AX164995	AX164995 Sequence	751	10.8	54.0	19	6	AX131032	AX131032
55.0	51	6	AX165384	AX165384 Sequence	752	10.8	54.0	19	6	AX131033	AX131033
55.0	51	6	AX204124	AX204124 Sequence	c 753	10.8	54.0	19	6	AX131243	AX131243
55.0	51	6	AX204515	AX204515 Sequence	c 754	10.8	54.0	19	6	AX131244	AX131244
55.0	52	6	BD267583	BD267583 Sphingos	755	10.8	54.0	19	6	AX742738	AX742738
55.0	53	6	I44614	I44614 Sequence 43	756	10.8	54.0	19	6	AX742793	AX742793
55.0	53	6	I71019	I71019 Sequence 43	757	10.8	54.0	19	6	BD184591	BD184591
55.0	53	9	HSBRUN	X95500 H.sapiens D	758	10.8	54.0	19	6	BD184646	BD184646
55.0	54	6	E33812	E33812 Cell cycle	c 759	10.8	54.0	20	6	AR016182	AR016182
55.0	54	6	BD105360	BD105360 Novel ins	c 760	10.8	54.0	20	6	AR019180	AR019180
55.0	57	6	AX326592	AX326592 Sequence	761	10.8	54.0	20	6	AR117576	AR117576
55.0	57	6	A38675	A38675 Sequence 6	c 762	10.8	54.0	20	6	AR117653	AR117653
55.0	58	6	A51709	A51709 Sequence 15	763	10.8	54.0	20	6	BD250312	BD250312
55.0	58	6	AR122569	AR122569 Sequence	c 764	10.8	54.0	20	6	E31854	E31854 NC
55.0	58	6	AR167588	AR167588 Sequence	765	10.8	54.0	20	6	AR222140	AR222140
55.0	58	6	AR178298	AR178298 Sequence	766	10.8	54.0	20	6	AR228861	AR228861
55.0	58	6	AX323380	AX323380 Sequence	c 767	10.8	54.0	20	6	AR229533	AR229533
55.0	58	6	AX686850	AX686850 Sequence	768	10.8	54.0	20	6	AR373463	AR373463
55.0	59	6	A82601	A82601 Sequence 3	769	10.8	54.0	20	6	AR373537	AR373537
55.0	59	6	AR399106	AR399106 Sequence	770	10.8	54.0	20	6	AX295967	AX295967
55.0	59	6	BD107700	BD107700 Ribosome	c 771	10.8	54.0	20	6	AX399127	AX399127
55.0	60	6	AR100866	AR100866 Sequence	c 772	10.8	54.0	20	6	AX462560	AX462560
55.0	60	6	AX601358	AX601358 Sequence	c 773	10.8	54.0	20	6	AX785621	AX785621
54.0	14	6	A88216	A88216 Sequence 36	c 774	10.8	54.0	20	6	AX785623	AX785623
54.0	14	6	A90183	A90183 Sequence 36	c 775	10.8	54.0	20	6	AX785626	AX785626
54.0	14	6	BD065729	BD065729 An anti-se	c 776	10.8	54.0	20	6	AX785628	AX785628
54.0	15	6	AR061290	AR061290 Sequence	c 777	10.8	54.0	20	6	AX785629	AX785629
54.0	15	6	AR061299	AR061299 Sequence	778	10.8	54.0	20	6	BD092012	BD092012
54.0	15	6	I34737	I34737 Sequence 3	c 779	10.8	54.0	20	6	BD141127	BD141127
54.0	15	6	I34746	I34746 Sequence 12	780	10.8	54.0	21	6	E04603	E04603 Pr
54.0	17	6	A95027	A95027 Sequence 33	c 781	10.8	54.0	21	6	AX095867	AX095867
54.0	17	6	AR036431	AR036431 Sequence	c 782	10.8	54.0	21	6	AX203485	AX203485
54.0	17	6	AR045389	AR045389 Sequence	783	10.8	54.0	21	6	AX253531	AX253531
54.0	17	6	AR045391	AR045391 Sequence	784	10.8	54.0	21	6	AX553620	AX553620
54.0	17	6	AR053034	AR053034 Sequence	c 785	10.8	54.0	22	6	E15339	E15339 An
54.0	17	6	AR053065	AR053065 Sequence	786	10.8	54.0	22	6	AX040635	AX040635
54.0	17	6	AR064995	AR064995 Sequence	c 787	10.8	54.0	23	6	AR116730	AR116730
54.0	17	6	AR065026	AR065026 Sequence	c 788	10.8	54.0	23	6	BD269669	BD269669
54.0	17	6	BD255012	BD255012 Regulatio	c 789	10.8	54.0	23	6	I89280	I89280 Se
54.0	17	6	E38379	E38379 Binding par	c 790	10.8	54.0	23	6	AX035299	AX035299
54.0	17	6	E39023	E39023 Nucl.eic aci	791	10.8	54.0	24	6	A57528	A57528 Se
54.0	17	6	I29872	I29872 Sequence 23	792	10.8	54.0	24	6	A57534	A57534 Se
54.0	17	6	I32540	I32540 Sequence 4	793	10.8	54.0	24	6	AX45237	AX45237
54.0	17	6	I32571	I32571 Sequence 35	794	10.8	54.0	24	6	BD141713	BD141713
54.0	17	6	I43714	I43714 Sequence 3	795	10.8	54.0	24	6	BD183265	BD183265

14.0	25	6	AR049986	Sequence	C 869	10.8	54.0	36	6	AR142182	S
14.0	25	6	AR090567	Sequence	C 870	10.8	54.0	36	6	AR179634	S
14.0	25	6	AR182522	Sequence	C 871	10.8	54.0	36	6	AR179637	S
14.0	25	6	AR197602	Sequence	C 872	10.8	54.0	36	6	AX009452	S
14.0	25	6	AR259756	Sequence	C 873	10.8	54.0	37	6	AX183625	S
14.0	25	6	AR362014	Sequence	C 874	10.8	54.0	38	6	BD231603	C
14.0	25	6	AX078120	Sequence	C 875	10.8	54.0	39	6	AX283648	C
14.0	25	6	AX078148	Sequence	C 876	10.8	54.0	39	6	AX537706	C
14.0	25	6	AX399696	Sequence	C 877	10.8	54.0	39	6	AX538085	S
14.0	25	6	AX399703	Sequence	C 878	10.8	54.0	40	6	AR059117	S
14.0	25	6	AX504312	Sequence	C 879	10.8	54.0	40	6	BD266464	U
14.0	25	6	AX504329	Sequence	C 880	10.8	54.0	40	6	I30261	Seq
14.0	25	6	AX611003	Sequence	C 881	10.8	54.0	41	6	AX515741	S
14.0	25	6	BD209774	Electroni	C 882	10.8	54.0	41	6	AX516178	S
14.0	25	6	BD209802	Electroni	C 883	10.8	54.0	41	6	AX517033	S
14.0	26	6	AR091142	Sequence	C 884	10.8	54.0	41	6	AX518336	S
14.0	26	6	BD272782	Detection	C 885	10.8	54.0	41	6	AX519546	S
14.0	26	6	BD272789	Detection	C 886	10.8	54.0	42	6	BD074125	C
14.0	26	6	BD272804	Detection	C 887	10.8	54.0	43	6	I55966	Seq
14.0	26	6	BD272811	Detection	C 888	10.8	54.0	45	6	A02009	Art
14.0	26	6	AR198177	Sequence	C 889	10.8	54.0	45	6	A06779	Nuc
14.0	26	6	AR260331	Sequence	C 890	10.8	54.0	45	6	AR062574	S
14.0	26	6	AR279411	Sequence	C 891	10.8	54.0	45	6	I30284	Seq
14.0	26	6	AR279418	Sequence	C 892	10.8	54.0	45	9	H5U14047	Hum
14.0	26	6	AR279433	Sequence	C 893	10.8	54.0	47	6	AR211831	S
14.0	26	6	AR279440	Sequence	C 894	10.8	54.0	47	6	AR211852	S
14.0	26	6	AX197239	Sequence	C 895	10.8	54.0	47	6	AR288955	S
14.0	26	6	AX717038	Sequence	C 896	10.8	54.0	47	6	AR289184	S
14.0	26	6	AX742337	Sequence	C 897	10.8	54.0	47	6	AR291909	S
14.0	26	6	AX742412	Sequence	C 898	10.8	54.0	47	6	AR365554	S
14.0	26	6	BD184161	Method an	C 899	10.8	54.0	47	6	AX378321	S
14.0	26	6	BD184265	Method an	C 900	10.8	54.0	47	6	AX752735	S
14.0	27	6	AR072924	Sequence	C 901	10.8	54.0	47	6	BD221901	N
14.0	27	6	AR220057	Sequence	C 902	10.8	54.0	47	6	BD221922	N
14.0	27	6	AX022989	Sequence	C 903	10.8	54.0	48	6	AX229400	S
14.0	27	6	AX026382	Sequence	C 904	10.8	54.0	48	6	AX426269	S
14.0	27	6	BD002251	Cellulase	C 905	10.8	54.0	48	6	AX426403	S
14.0	27	6	BD010855	Cellulase	C 906	10.8	54.0	48	6	AX426707	S
14.0	27	6	BD144789	A method	C 907	10.8	54.0	48	6	AX426852	S
14.0	28	6	AR120087	Sequence	C 908	10.8	54.0	49	6	AR362008	S
14.0	28	6	BD269053	Promoters	C 909	10.8	54.0	49	6	AX078114	S
14.0	28	6	E39416	Novel physi	C 910	10.8	54.0	49	6	AX147410	S
14.0	28	6	AR202183	Sequence	C 911	10.8	54.0	49	6	BD209768	E
14.0	28	6	AR280202	Sequence	C 912	10.8	54.0	50	6	AR032899	S
14.0	28	6	AR302979	Sequence	C 913	10.8	54.0	50	6	I29639	Seq
14.0	28	6	AX223974	Sequence	C 914	10.8	54.0	50	6	I91313	Seq
14.0	28	6	AX224433	Sequence	C 915	10.8	54.0	50	6	AR209563	S
14.0	28	6	AX598045	Sequence	C 916	10.8	54.0	50	6	AX165846	S
14.0	28	6	AX766010	Sequence	C 917	10.8	54.0	50	6	BD177540	M
14.0	28	6	AX766011	Sequence	C 918	10.8	54.0	50	6	BD177541	M
14.0	28	6	BD097269	Novel col	C 919	10.8	54.0	51	6	AX157832	S
14.0	28	6	BD171060	Process f	C 920	10.8	54.0	51	6	AX158319	S
14.0	28	6	BD171140	Process f	C 921	10.8	54.0	51	6	AX158320	S
14.0	28	6	BD173733	Use of ga	C 922	10.8	54.0	51	6	AX159029	S
14.0	28	6	BD185413	Use of ga	C 923	10.8	54.0	51	6	AX160433	S
14.0	29	6	AX405171	Sequence	C 924	10.8	54.0	51	6	AX160434	S
14.0	30	6	E36190	Upstream re	C 925	10.8	54.0	51	6	AX165213	S
14.0	31	6	AX249129	Sequence	C 926	10.8	54.0	51	6	AX165648	S
14.0	31	6	AX249294	Sequence	C 927	10.8	54.0	51	6	AX204467	S
14.0	31	6	AX537793	Sequence	C 928	10.8	54.0	51	8	AJ601325	A
14.0	31	6	AX538102	Sequence	C 929	10.8	54.0	51	10	AF005556	
14.0	32	6	AX3688	Sequence 4	C 930	10.8	54.0	52	6	A14704	Nuc
14.0	32	6	AX3690	Sequence 6	C 931	10.8	54.0	54	6	I38032	Seq
14.0	32	6	AR050261	Sequence	C 932	10.8	54.0	54	6	I94882	Seq
14.0	32	6	AR050263	Sequence	C 933	10.8	54.0	55	6	AR050474	S
14.0	33	6	E09067	DNA encodin	C 934	10.8	54.0	55	6	AR124602	S
14.0	33	6	AX828564	Sequence	C 935	10.8	54.0	55	6	AR302982	S
14.0	34	6	E00476	Synthetic D	C 936	10.8	54.0	56	6	AR071026	S
14.0	34	6	I00945	Sequence 2	C 937	10.8	54.0	56	6	BD272327	S
14.0	35	6	AR127676	Sequence 94	C 938	10.8	54.0	56	6	BD272328	S
14.0	35	6	I75345	Sequence 94	C 939	10.8	54.0	56	9	HUMTCVD1FC	Hum
14.0	36	6	A59370	Sequence 20	C 940	10.8	54.0	57	6	AR127708	S
14.0	36	6	A59373	Sequence 23	C 941	10.8	54.0	57	6	I75377	Seq

54.0 57 6 AR362025 Sequence  
 54.0 57 6 AX078131 Sequence  
 54.0 57 6 AX078149 Sequence  
 54.0 57 6 BD209785 Sequence  
 54.0 57 6 BD209803 Sequence  
 54.0 57 6 BD209803 Electroni  
 54.0 57 6 M63733 Human argin  
 54.0 60 6 AX538331 Sequence  
 53.0 17 6 AR057627 Sequence  
 53.0 17 6 AR115385 Sequence  
 53.0 17 6 AX634704 Sequence  
 53.0 17 6 AX687771 Sequence  
 53.0 18 6 I28018 Sequence 19  
 53.0 18 6 AX522112 Sequence  
 53.0 18 6 AX838257 Sequence  
 53.0 19 6 AR098544 Sequence  
 53.0 19 6 AR108889 Sequence  
 53.0 19 6 AX286819 Sequence  
 53.0 20 6 AX8857 Sequence 9  
 53.0 20 6 AR124991 Sequence  
 53.0 20 6 AR143108 Sequence  
 53.0 20 6 AR162549 Sequence  
 53.0 20 6 AR163943 Sequence  
 53.0 20 6 AR163944 Sequence  
 53.0 20 6 BD243081 Antisense  
 53.0 20 6 AR182240 Sequence  
 53.0 20 6 AR262060 Sequence  
 53.0 20 6 AR311970 Sequence  
 53.0 20 6 AX268988 Sequence  
 53.0 20 6 AX364584 Sequence  
 53.0 20 6 BD177769 A method  
 53.0 21 6 I46605 Sequence 58  
 53.0 21 6 AR217314 Sequence  
 53.0 21 6 AR307352 Sequence  
 53.0 21 6 AX536232 Sequence  
 53.0 21 6 BD070791 Method to  
 53.0 22 6 A91364 Sequence 26  
 53.0 22 6 AR148613 Sequence  
 53.0 22 6 BD265734 Heat-indu  
 53.0 22 6 I29988 Sequence 22  
 53.0 22 6 AX033769 Sequence  
 53.0 22 6 AX802611 Sequence  
 53.0 22 6 AX803166 Sequence  
 53.0 22 6 BD136180 Inhibitor  
 53.0 23 6 BD234235 ATP-bindi  
 53.0 23 6 E30632 Antibody an  
 53.0 23 6 E31241 Device for  
 53.0 23 6 AX183988 Sequence  
 53.0 23 6 AX553853 Sequence  
 53.0 23 6 BD173646 Novel phy  
 53.0 24 6 A91363 Sequence 25  
 53.0 24 6 BD234780 Polypepti  
 53.0 24 6 E33981 Novel RpoA.  
 53.0 24 6 AX011543 Sequence  
 53.0 25 6 AR216121 Sequence  
 53.0 25 6 AR216123 Sequence  
 53.0 25 6 AR216125 Sequence  
 53.0 25 6 AR235663 Sequence  
 53.0 25 6 AX197038 Sequence  
 53.0 25 6 AX689268 Sequence

## ALIGNMENTS

3803 17 bp DNA  
 ence 1490 from Patent WO03025176.  
 3803  
 3803.1 GI:30503146  
 musculus (house mouse)  
 musculus

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 FEATURES  
 source  
 ORIGIN  
 Query Match 75.0%; Score 15; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03; Indels 0;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0;  
 Qy 1 ATCTTGTCTCTCCAC 15  
 Db 2 ATCTTGTCTCTCCAC 16  
 RESULT 2  
 BD268717 20 bp DNA linear PAT  
 LOCUS  
 DEFINITION Inhibitors for use in hemostasis and immune function.  
 ACCESSION BD268717  
 VERSION BD268717.1 GI:33078485  
 KEYWORDS JP 2002537270-A/10.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 20)  
 AUTHORS Sheppard,P.O., Lasser,G.W. and Bishop,P.D.  
 TITLE Inhibitors for use in hemostasis and immune function  
 JOURNAL Patent: JP 2002537270-A 10 05-NOV-2002;  
 COMMENT ZYMOGENETICS INC  
 OS Artificial Sequence  
 PN JP 2002537270-A/10  
 PD 05-NOV-2002  
 PF 17-FEB-2000 JP 2000599415 09/44  
 PR 19-FEB-1999 US 09/253604,22-NOV-1999 US  
 PAUL O SHEPPARD,GERALD W LASSER,PAUL D BISHOP PC  
 A61K38/00,A61P7/04,A61P9/08,A61P9/10,A61P17/02,A61P43/00  
 A61K39/395  
 PC A61K39/395,A61K45/00,C07K14/47,C12N15/09,A61K37/02,  
 CC Oligonucleotide ZC13651  
 FH Key Location/Qualifiers  
 FT source 1..20  
 FT /organism='Artificial Sequence'.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..20  
 /organism='synthetic construct'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32630'  
 ORIGIN  
 Query Match 74.0%; Score 14.8; DB 6; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03; Indels 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 Qy 3 CCTTGTCTCTCCACGGTT 20  
 Db 1 CTTTGTCTCTCCACGGTT 18  
 RESULT 3  
 BD268720/c  
 LOCUS 20 bp DNA linear PAT  
 DEFINITION Inhibitors for use in hemostasis and immune function.

**us-10-090-326-7.max.rge**

ACCESSION	AR229117	AR229117.1	GI:27269262	
VERSION	AR229117.1			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 20)			
TITLE	Sheppard,P.O., Lasser,G.W. and Bishop,P.D.			
JOURNAL	Methods of promoting blood flow within the vasculature o			
FEATURES	Patent: US 648221-A 15 10-SEP-2002;			
source	Location/Qualifiers			
	1..20			
	/organism="unknown"			
	/mol_type="genomic DNA"			
ORIGIN				
Query Match	74.0%;	Score 14.8;	DB 6;	Length 20;
Best Local Similarity	88.9%;	Pred. No. 6.9e+03;		
Matches	16;	Conservative	0;	Mismatches 2;
				Indels 0;
QY	3	CCTTGTCCTCCACGGGTT	20	
Db	20	CTTTGTCCTCCACGGGTTT	3	
RESULT 6				
LOCUS	AR281377	AR281377	20 bp	DNA
DEFINITION	Sequence 12 from patent US 6518403.			linear
ACCESSION	AR281377			
VERSION	AR281377.1	GI:29717043		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 20)			
TITLE	Sheppard,P.O.			
JOURNAL	Antibodies that bind an adipocyte-specific protein homol			
FEATURES	Patent: US 6518403-A 12 11-FEB-2003;			
source	Location/Qualifiers			
	1..20			
	/organism="unknown"			
	/mol_type="genomic DNA"			
ORIGIN				
Query Match	74.0%;	Score 14.8;	DB 6;	Length 20;
Best Local Similarity	88.9%;	Pred. No. 6.9e+03;		
Matches	16;	Conservative	0;	Mismatches 2;
				Indels 0;
QY	3	CCTTGTCCTCCACGGGTT	20	
Db	1	CTTTGTCCTCCACGGGTTT	18	
RESULT 7				
LOCUS	AR281380/c	AR281380	20 bp	DNA
DEFINITION	Sequence 15 from patent US 6518403.			linear
ACCESSION	AR281380			
VERSION	AR281380.1	GI:29717046		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 20)			
TITLE	Sheppard,P.O.			
JOURNAL	Antibodies that bind an adipocyte-specific protein homol			
FEATURES	Patent: US 6518403-A 15 11-FEB-2003;			
source	Location/Qualifiers			
	1..20			
	/organism="unknown"			
	/mol_type="genomic DNA"			
ORIGIN				



74.0%; Score 14.8; DB 6; Length 20;  
ilarity 88.9%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0;  
TTTGTCCTCCACGGTT 20  
|||||  
TTTGTCCTCCACGGTTT 3

4586 20 bp DNA PAT 12-JUN-2003  
ence 12 from patent US 6544946.  
4586  
4586.1 GI:31693749  
OWN.  
OWN.  
assified.  
bases 1 to 20)  
pard,P.O., Lasser,G.W. and Bishop,P.D.  
bitors for use in hemostasis and immune function  
nt: US 6544946-A 12 08-APR-2003;  
Location/Qualifiers  
1. .20  
/organism="unknown"  
/mol\_type="genomic DNA"

74.0%; Score 14.8; DB 6; Length 20;  
ilarity 88.9%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0;  
TTTGTCCTCCACGGTT 20  
|||||  
TTTGTCCTCCACGGTTT 18

4589 20 bp DNA PAT 12-JUN-2003  
ence 15 from patent US 6544946.  
4589  
4589.1 GI:31693752  
OWN.  
OWN.  
assified.  
bases 1 to 20)  
pard,P.O., Lasser,G.W. and Bishop,P.D.  
bitors for use in hemostasis and immune function  
nt: US 6544946-A 15 08-APR-2003;  
Location/Qualifiers  
1. .20  
/organism="unknown"  
/mol\_type="genomic DNA"

74.0%; Score 14.8; DB 6; Length 20;  
ilarity 88.9%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0;  
TTTGTCCTCCACGGTT 20  
|||||  
TTTGTCCTCCACGGTTT 3

.7582 20 bp DNA PAT 17-AUG-2003  
ence 12 from patent US 6566499.  
.7582

AR337582.1 GI:33723983  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sheppard,P.O.  
TITLE Adipocyte-specific protein homologs  
JOURNAL Patent: US 6566499-A 12 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .20  
source /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 74.0%; Score 14.8; DB 6; Length 20;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
QY 3 CCTTGTCCTCCACGGTT 20  
|||||  
Db 1 CTTTGTCCTCCACGGTTT 18  
|||||

RESULT 11  
AR337585/c  
LOCUS AR337585 20 bp DNA linear PAT  
DEFINITION Sequence 15 from patent US 6566499.  
ACCESSION AR337585  
VERSION AR337585.1 GI:33723986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Sheppard,P.O.  
TITLE Adipocyte-specific protein homologs  
JOURNAL Patent: US 6566499-A 15 20-MAY-2003;  
FEATURES Location/Qualifiers  
1. .20  
source /organism="unknown"  
/mol\_type="genomic DNA"

Query Match 74.0%; Score 14.8; DB 6; Length 20;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
QY 3 CCTTGTCCTCCACGGTT 20  
|||||  
Db 20 CTTTGTCCTCCACGGTTT 3  
|||||

RESULT 12  
AX696154 20 bp DNA linear PAT  
LOCUS AX696154  
DEFINITION Sequence 53 from Patent WO03008640.  
ACCESSION AX696154  
VERSION AX696154.1 GI:29419314  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom  
1  
REFERENCE Whittaker,P.A., Meyers,D.A., Postma,D.S. and Bleesker,E.  
AUTHORS Asthma-associated gene  
TITLE Patent: WO 03008640-A 53 30-JAN-2003;  
JOURNAL Novartis AG (CH); Novartis Pharma GmbH (AT); Wake Fore  
University Health Sciences (US); Rijksuniversiteit te G  
(NL)

FEATURES Location/Qualifiers  
1. .20  
source

09:38:25 2004

us-10-090-326-7.max.rge

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

74.0%; Score 14.8; DB 6; Length 20;  
ilarity 88.9%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTGCTCCACGG 18  
|||||  
CTGCTCTCCACGG 20

216 38 bp DNA linear PAT 25-SEP-2002  
nce 2 from patent US 6410710.  
216  
216.1 GI:23314670

wn.  
wn.  
ssified.  
ases 1 to 38)  
man,S. and Van Eyndhoven,W.  
ic acid encoding a TRAF-3 deletion isoform  
it: US 6410710-A 2 25-JUN-2002;  
Location/Qualifiers  
1. .38  
/organism="unknown"  
/mol\_type="genomic DNA"

72.0%; Score 14.4; DB 6; Length 38;  
ilarity 93.8%; Pred. No. 1.2e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCTCCACGG 17  
|||||  
TTGTCTCTCCACGG 17

10 33 bp DNA linear PAT 26-JUL-1995  
nce 44 from Patent US 5407795.  
10.1 GI:909008

wn.  
wn.  
ssified.  
ases 1 to 33)  
rg,J.A., Shen,L.-P. and Urdea,M.S.  
probes for use in solution phase sandwich  
it: US 5407795-A 44 18-APR-1995;  
Location/Qualifiers  
1. .33  
/organism="unknown"  
/mol\_type="unassigned DNA"

70.0%; Score 14; DB 6; Length 33;  
ilarity 100.0%; Pred. No. 1.9e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTGTCTCTCCACG 16  
|||||  
TTGTCTCTCCACG 31

BD234781/c  
LOCUS  
DEFINITION

24 bp DNA linear PAT  
Polypeptide having immunogenic properties and modified b  
protein function.

ACCESSION  
BD234781  
VERSION  
BD234781.1 GI:33044551  
KEYWORDS  
JP 2002512801-A/4.  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 24)  
Gissmann,L. and Jochmus,I.  
Polypeptide having immunogenic properties and modified b  
protein function

JOURNAL

Patent: JP 2002512801-A 4 08-MAY-2002;  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICH

COMMENT

OS Artificial Sequence  
PN JP 2002512801-A/4

PD

PD 08-MAY-2002  
PF 30-APR-1999 JP 2000546020  
PF 30-APR-1998 DE 198 19 476.5

PI

PI LUTZ GISSMANN,INGRID JOCHMUS  
PC C12N15/09,A61K38/00,A61K48/00,C07K14/025,C12N1/15,C

PC

PC C12N1/21,  
PC C12N5/10,C12P21/02,C12N15/00,A61K37/02,C12N5/00 CC

Description of Artificial Sequence: Primer

PH Key

Location/Qualifiers  
FT source 1. .24

FT

/organism='Artificial Sequence'.  
Location/Qualifiers  
1. .24

FEATURES

source

/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 24;  
Best Local Similarity 80.0%; Pred. No. 3e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 1 ATCCTTGCTCTCCACGGTT 20

|||||  
21 ATCCTCTCTCTCTCGGTT 2


RESULT 16

AX011544/c

LOCUS

24 bp DNA linear PAT  
Sequence 6 from Patent WO955876.

DEFINITION

AX011544

ACCESSION

AX011544.1

VERSION

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

1

AUTHORS

Gissmann,L. and Jochmus,I.

Polyptide with immunogenic properties and with a prote

modified biological functions

PATENT: WO 955876-A 6 04-NOV-1999;

JOURNAL

DEUTSCHES KREBSFORSCH (DE); GISSMANN LUTZ (DE); JOCHMUS :

Location/Qualifiers

1. .24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Primer"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 24;

Best Local Similarity 80.0%; Pred. No. 3e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

CTTGTCTCCACGGGTT 20  
|||||  
CTCTCTCTCTCTGGTT 2

9510 32 bp DNA linear PAT 21-MAR-2001  
ence 2 from Patent WO0116299.

9510  
9510.1 GI:13443747

etic construct  
etic construct  
icial sequences.

J.P.M., Riggs, B.L., Khosla, S. and Russel, S.T.  
of dna encoding osteoprotegerin to prevent or inhibit metabolic  
disorders  
at: WO 0116299-A 2 08-MAR-2001;  
FOUNDATION (US)

Location/Qualifiers  
1..32  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="A primer"

68.0%; Score 13.6; DB 6; Length 32;  
ilarity 80.0%; Pred. No. 3.1e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTTGTCTCCACGGGTT 20  
|||||  
CTTATCATCCATGGGAT 28

1037 20 bp DNA linear PAT 17-FEB-2003  
ence 132 from Patent WO02092851.

1037  
1037.1 GI:28401110

etic construct  
etic construct  
ficial sequences.

S.M.M. and Swinburne, J.E.

tic typing  
nt: WO 02092851-A 132 21-NOV-2002;  
AL HEALTH TRUST (GB); The British Horseracing Board (GB)

Location/Qualifiers  
1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

67.0%; Score 13.4; DB 6; Length 20;  
ilarity 93.3%; Pred. No. 3.8e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTTGTCTCCAC 15  
|||||  
CCTTGGCCTCCAC 6

6562 29 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 5 from patent US 6312892.

ACCESSION AR176562  
VERSION AR176562.1 GI:17918917

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.  
TITLE High fidelity detection of nucleic acid differences by 1:  
detection reaction  
JOURNAL Patent: US 6312892-A 5 06-NOV-2001;  
FEATURES Location/Qualifiers  
1..29  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 29;  
Best Local Similarity 93.3%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CCTTGTCTCCACGG 17  
|||||

Db 14 CCTTGTCTCCACGG 28  
|||||

RESULT 20

AR176564

LOCUS AR176564 29 bp DNA linear PAT  
DEFINITION Sequence 7 from patent US 6312892.

ACCESSION AR176564  
VERSION AR176564.1 GI:17918919

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.  
TITLE High fidelity detection of nucleic acid differences by 1:  
detection reaction  
JOURNAL Patent: US 6312892-A 7 06-NOV-2001;  
FEATURES Location/Qualifiers  
1..29  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 29;  
Best Local Similarity 93.3%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CCTTGTCTCCACGG 17  
|||||

Db 14 CCTTGTCTCCACGG 28  
|||||

RESULT 21

AR342701

LOCUS AR342701 29 bp DNA linear PAT  
DEFINITION Sequence 5 from patent US 6576453.

ACCESSION AR342701  
VERSION AR342701.1 GI:33737888

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.  
TITLE Thermostable DNA ligase mutants  
JOURNAL Patent: US 6576453-A 5 10-JUN-2003;  
FEATURES Location/Qualifiers  
1..29

09:38:25 2004

us-10-090-326-7.max.rge

/organism="unknown"  
/mol\_type="genomic DNA"

67.0%; Score 13.4; DB 6; Length 29;  
ilarity 93.3%; Pred. No. 3.9e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCCACGG 17  
|||||  
TTGTCTCCACGG 28

2703 29 bp DNA linear PAT 17-AUG-2003  
ence 7 from patent US 6576453.  
2703  
2703.1 GI:33737890

own.  
own.  
assified.  
ases 1 to 29)  
y, F., Luo, J., Khanna, M. and Bergstrom, D. B.  
ostable DNA ligase mutants  
at: US 6576453-A 7 10-JUN-2003;  
Location/Qualifiers  
1. .29  
/organism="unknown"  
/mol\_type="genomic DNA"

67.0%; Score 13.4; DB 6; Length 29;  
ilarity 93.3%; Pred. No. 3.9e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCCACGG 17  
|||||  
TTGTCTCCACGG 28

7020 41 bp DNA linear PAT 05-OCT-2002  
ence 3218 from Patent WO02052044.  
7020  
7020.1 GI:23565323

sapiens (human)  
sapiens  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
mura, Y., Sekine, A., Iida, A. and Saito, S.  
ction of genetic polymorphisms  
nt: WO 02052044-A 3218 04-JUL-2002;  
n (JP)

Location/Qualifiers  
1. .41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

67.0%; Score 13.4; DB 6; Length 41;  
ilarity 82.4%; Pred. No. 3.9e+04;  
Conservative 1; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGT 19  
|||||  
TTGTCTCCACGGGT 17

RESULT 24  
AX519531/c  
LOCUS  
DEFINITION  
Sequence 5729 from Patent WO02052044.  
ACCESSION  
AX519531  
VERSION  
AX519531.1 GI:23569850  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

41 bp DNA linear PAT

REFERENCE  
1  
AUTHORS  
Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE  
Detection of genetic polymorphisms  
JOURNAL  
Patent: WO 02052044-A 5729 04-JUL-2002;  
Riken (JP)  
FEATURES  
Location/Qualifiers  
1. .41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 82.4%; Pred. No. 3.9e+04;  
Matches 14; Conservative 1; Mismatches 2; Indels 0;

QY 3 CCTGTCTCCACGGGT 19  
|||||  
Db 33 CCTGTCTCCACGGGT 17

RESULT 25  
AX167919/c  
LOCUS  
DEFINITION  
Sequence 103 from Patent WO0142307.  
ACCESSION  
AX167919  
VERSION  
AX167919.1 GI:14597239  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

20 bp DNA linear PAT

REFERENCE  
1  
AUTHORS  
Saito, K., Ohe, N. and Sato, H.  
TITLE  
Mutant er g(a) and test systems for transactivation  
JOURNAL  
Patent: WO 0142307-A 103 14-JUN-2001;  
Sumitomo Chemical Company, Limited (JP)  
FEATURES  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Designed oligonucleotide primer for PCR"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.8e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGTCTCCACGGGT 19  
|||||  
Db 20 TCCTTGTCTCCACGGAT 3

RESULT 26

AR095317/c  
LOCUS  
DEFINITION  
Sequence 8 from patent US 6004557.  
ACCESSION  
AR095317  
VERSION  
AR095317.1 GI:10023086  
KEYWORDS  
SOURCE  
Unknown.

30 bp DNA linear PAT



sapiens  
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ases 1 to 54)  
rup, R.J., Cohn, D.H., Cohen, T., and Byers, P.H.  
line for glycine substitution in the triple-helical domain of  
products of one alpha 2(I) collagen allele (COL1A2) produces  
steogenesis imperfecta type IV phenotype  
ol. Chem. 263 (16), 7734-7740 (1988)

725  
63  
nal source text: Human (individuals I-1 and II-4) skin  
blast DNA.  
utant alpha-2 type I collagen causes osteogenesis imperfecta.

Location/Qualifiers  
1. .54  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="7q21.3-q22.1"  
1. .54  
/gene="COL1A2"  
<1. >54  
/gene="COL1A2"  
/note="OI alpha-2 type I collagen"  
/codon\_start=1  
/protein\_id="AA51846.1"  
/db\_xref="GI:179607"  
/db\_xref="GDB:G00-119-062"  
/translation="GPPGPPGPPRVSGG"  
osome 7q21.3-q22.1.

66.0%; Score 13.2; DB 9; Length 54;  
ilarity 83.3%; Pred. No. 5.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGT 19  
|||||  
TGGACCTCCACGTGT 41

1169  
nce 13666 from patent US 6639063.  
1169  
169.1 GI:40177279

wn.  
wn.  
ssified.  
ases 1 to 55)  
ds, J.-B.D.M., Jobert, S. and Giordano, J.-Y.  
and encoded human proteins  
it: US 6639063-A 13666 28-OCT-2003;  
Location/Qualifiers  
1. .55  
/organism="unknown"  
/mol\_type="genomic DNA"

66.0%; Score 13.2; DB 6; Length 55;  
ilarity 83.3%; Pred. No. 5.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGT 19  
|||||  
TCTCTCTCCACGGCT 1

7722  
55 bp DNA linear PAT 18-SEP-2002

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST and encoded human protein.

BD117722  
BD117722.1 GI:23212626

JP 2002010789-A/9799.  
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

EST and encoded human protein

Patent: JP 2002010789-A 9799 15-JAN-2002;

GENSET CORP

OS Homo sapiens (human)

PN JP 2002010789-A/9799

PD 15-JAN-2002

PF 07-AUG-2000 JP 2000280989

PR 05-AUG-1999 US 60/147499

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEI

GIORDANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12

C12N1/21,

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12

C12N15/00

CC EST and encoded human protein

EH Key Location/Qualifiers

FT source 1. .55

FT Location/Qualifiers

1. .55

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 55;  
Best Local Similarity 83.3%; Pred. No. 5.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTCTCTCCACGGGT 19  
|||||  
DB 18 TCCTCTCTCTCCACGGCT 1

RESULT 34  
AX248870/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

REFERENCE

AUTHORS

TITLE

JOURNAL

WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES

source

1. .31

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 31;  
Best Local Similarity 86.7%; Pred. No. 6.3e+04;  
Matches 13; Conservative 1; Mismatches 1; Indels 0;

QY 3 CCTTGTCTCTCCACGG 17  
|||||

TTGTCWCACGG 10

4698 55 bp DNA linear PLN 23-OCT-2003  
 idopsis thaliana T-DNA flanking sequence, left border, clone  
 08.

4698

4698.1 GI:37944322  
 border; T-DNA flanking sequence.

idopsis thaliana (thale cress)

idopsis thaliana

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

aud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,

vin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,

nec, L., Caboche, M. and Lecharny, A.

A integration into the Arabidopsis genome depends on sequences  
 re-insertion sites

Rep. 3 (12), 1152-1157 (2002)

3535

6565

bases 1 to 55)

ergue, S.

ct Submission

itted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

on Cremieux, 91057 Evry cedex, FRANCE

was performed on DNA from transformants of Arabidopsis thaliana  
 its from INRA (Versailles). The DNA fragment (s) resulting from  
 PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

ved sequences were removed. Information to order the

responding mutant line and a link to a database providing a

hical display of the insertion site are available at

://dbgap.versailles.inra.fr/publiclines/. This sequence has

generated in the framework of the French plant genomics

ram 'Genoplante' (<http://www.genoplante.com> and

://genoplante-info.infobiogen.fr).

Location/Qualifiers

1..55

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/cultivar="Wassillewskija"

/db\_xref="taxon:3702"

/clone="404C08"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

1..55

/note="T-DNA flanking sequence

left border"

55.0%; Score 13; DB 8; Length 55;

ilarity 100.0%; Pred. No. 6.5e+04;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GTCTCCACGG 17

|||||

GTCTCCACGG 17

74525 17 bp DNA linear PAT 27-MAR-2003

ence 2970 from Patent WO03004526.

74525

74525.1 GI:29332873

sapiens (human)

sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: WO 03004526-A 2970 16-JAN-2003;

Molecular Engines Laboratories (FR)

FEATURES

source

1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 17;

Best Local Similarity 87.5%; Pred. No. 7.8e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTTGCTCCACGGGT 19

|||||

Db 17 CTTGCTCCACAGAT 2

|||||

RESULT 37

BD226165

LOCUS

DEFINITION

Glaucoma therapeutics and diagnostics based on a novel T

transcription factor.

ACCESSION

BD226165

VERSION

BD226165.1

KEYWORDS

JP 2002511265-A/16.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS Artificial Sequence

PN JP 2002511265-A/16

PD 16-APR-2002

PF 14-APR-1999

PR 15-APR-1998

VAL C SHEFFIELD, WALLACE L M ALWARD, EDWIN M STONE, DARRYL

NISHIMURA,

PI SHIVA PATIL

PC C12N15/00, A61K45/00, A61P27/06, C07K14/47, C12N1/15, C1

PC C12N5/10, C12P21/02, C12Q1/68, G01N33/15, G01N33/50, C12

C12N5/00

CC Description of Artificial Sequence: primer

FH Key Location/Qualifiers

FT source 1..21

FT /organism='Artificial Sequence'.

FEATURES

source

1..21

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 21;

Best Local Similarity 87.5%; Pred. No. 7.9e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTGTCTCCACGG 17

|||||

Db 3 TCCTGTCTCCACGG 18

|||||

09:38:25 2004

us-10-090-326-7.max.rge

735 22 bp DNA linear PAT 22-MAR-2003

nce 110 from Patent WO02097127.

735 GI:29163915

etic construct  
etic construct  
ical sequences.

rs.N., Gehrman.M., Kallabis.H., Hall,R., Schulze,T. and  
el,C.

and proteins for prevention, prediction, diagnosis, prognosis  
reatment of chronic lung disease  
t: WO 02097127-A 110 05-DEC-2002;  
Aktiengesellschaft (DE)

Location/Qualifiers

1..22

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="M96233 reverse primer"

64.0%; Score 12.8; DB 6; Length 22;

larity 87.5%; Pred. No. 7.9e+04;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTCTCTCCACCG 17

|||||

TTGACCTCCACCG 4

427 22 bp DNA linear PAT 18-SEP-2002

d for assaying glutathione S-transferase, and probe and kit

for.

427

427.1 GI:23228372

02058483-A/25.

ntified

ntified

assified.

ases 1 to 22)

mura,M., Yaguchi,H., Naito,S. and Hiraoka,I.

d for assaying glutathione S-transferase, and probe and kit

for

it: JP 2002058483-A 25 26-FEB-2002;

TA PHARMACEUTICAL FACTORY INC

human GSTM1B gene

JP 2002058483-A/25

26-FEB-2002

14-AUG-2000 JP 2000245951

MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAOKA

C12N15/09,C12Q1/68,G01N21/64,G01N33/53,G01N33/566,

C12N15/00

Method for assaying glutathione S-transferase, and probe and

kit therefor

Location/Qualifiers

1..22

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

64.0%; Score 12.8; DB 6; Length 22;

larity 87.5%; Pred. No. 7.9e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACCG 17

|||||

Db 18 TCCTTGACCTCCACCG 3

RESULT 40

AX289046

LOCUS

DEFINITION

AX289046

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Hypothetical Probe Sequence"

ORIGIN

Query Match

Best Local Similarity

Matches 14; Conservative

0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACCG 17

|||||

Db 1 TCCTTGCTCTCCACCG 16

RESULT 41

AR090871

LOCUS

DEFINITION

AR090871

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..28

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match

Best Local Similarity

Matches 14; Conservative

0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACCG 17

|||||

Db 9 TCCTTGACCTCCACCG 24

RESULT 42

AR197906

LOCUS

DEFINITION

Sequence 991 from patent US 6352829.



7906  
7906.1 GI:20247755  
DOWN.  
DOWN.  
assified.  
bases 1 to 28)  
chik,A., Jokhadze,G. and Bibilashvilli,R.  
ods of assaying differential expression  
nt: US 6352829-A 991 05-MAR-2002;  
Location/Qualifiers  
1..28  
/organism="unknown"  
/mol\_type="unassigned DNA"  
64.0%; Score 12.8; DB 6; Length 28;  
ilarity 87.5%; Pred. No. 8e+04; Length 28;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
:CTTGCTCTCCACCG 17  
|||||  
:CTTGACCTCCACCG 24  
:0060  
ence 991 from patent US 6489455.  
:0060.1 GI:27310571  
DOWN.  
DOWN.  
assified.  
bases 1 to 28)  
chik,A., Jokhadze,G. and Bibilashvilli,R.  
ods of assaying differential expression  
nt: US 6489455-A 991 03-DEC-2002;  
Location/Qualifiers  
1..28  
/organism="unknown"  
/mol\_type="genomic DNA"  
64.0%; Score 12.8; DB 6; Length 28;  
ilarity 87.5%; Pred. No. 8e+04; Length 28;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
:CTTGCTCTCCACCG 17  
|||||  
:CTTGACCTCCACCG 24  
:0113  
idopsis thaliana T-DNA flanking sequence, left border, clone  
:02.  
:0113  
:0113.1 GI:37939737  
: border; T-DNA flanking sequence.  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
aud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,  
ivin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,  
nec,L., Caboche,M. and Lecharny,A.  
TA integration into the Arabidopsis genome depends on sequences  
re-insertion sites

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
EMBO Rep. 3 (12), 1152-1157 (2002)  
22363535  
12446565  
2 (bases 1 to 37)  
Balzergue,S.  
Direct Submission  
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS,  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of Arabidopsi  
plants from INRA (Versailles). The DNA fragment(s) resul  
the PCR were directly sequenced from the left or the rig  
to determine the genomic sequence flanking the insertion  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database provi  
graphical display of the insertion site are available at  
http://dbgap.versailles.inra.fr/publiclines/. This seq  
been generated in the framework of the French plant gen  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).  
Location/Qualifiers  
1..37  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="WassiljewskiJa"  
/db\_xref="taxon:3702"  
/clone="563F02"  
/clone\_lib="Arabidopsis thaliana T-DNA inserti  
misc\_feature  
1..37  
/note="T-DNA flanking sequence  
left border"  
ORIGIN  
Query Match 64.0%; Score 12.8; DB 8; Length 37;  
Best Local Similarity 87.5%; Pred. No. 8.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 4 CTTCGCTCTCCACCGGT 19  
|||||  
Db 17 CGTGTCTCTCCACCGGT 32  
|||||  
RESULT 45  
AX516800/C  
AX516800 41 bp DNA linear PAT  
LOCUS  
DEFINITION Sequence 2998 from Patent WO02052044.  
ACCESSION AX516800  
VERSION AX516800.1 GI:23564873  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hor  
1  
REFERENCE  
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 2998 04-JUL-2002;  
Riken (JP)  
FEATURES  
source  
1..41  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 64.0%; Score 12.8; DB 6; Length 41;  
Best Local Similarity 77.8%; Pred. No. 8.2e+04;  
Matches 14; Conservative 1; Mismatches 3; Indels 0;  
Qy 2 TCCTGTCTCTCCACCGGT 19  
:|||||  
Db 21 YCCTGTCTCTCCACAGCT 4  
:|||||

09:38:25 2004

us-10-090-326-7.max.rge

: February 29, 2004, 09:43:11  
16 secs

09:38:25 2004

us-10-090-326-7.max.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

.eic search, using sw model

February 29, 2004, 07:46:14 ; Search time 170.649 Seconds  
(without alignments)  
497.886 Million cell updates/sec

JS-10-090-326-7

l atctgtgtctccacgggtt 20

IDENTITY NUC

hapop 10.0 , Gapext 1.0

1373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

N Geneseq\_29Jan04:.\*  
l: Geneseqn1980s:.\*  
l: Geneseqn1990s:.\*  
l: Geneseqn2000s:.\*  
l: Geneseqn2001as:.\*  
l: Geneseqn2001bs:.\*  
l: Geneseqn2002s:.\*  
l: Geneseqn2003as:.\*  
l: Geneseqn2003bs:.\*  
l: Geneseqn2003cs:.\*  
l: Geneseqn2004s:.\*

is the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

SUMMARIES

%	Query	Match	Length	DB	ID	Description
100.0	20	6	ABQ82541			Abq82541 Human CEA
95.0	47	9	Adel13859			Adel13859 CEA(6D)-1
75.0	17	7	ACC64243			Acc64243 Murine ol
75.0	25	8	ACI58088			ACI58088 Human mic
74.0	20	7	ABX99012			ABX99012 Human AAG
74.0	20	7	ACD02563			ACD02563 Novel hum
74.0	20	7	ACD02560			ACD02560 Novel hum
74.0	20	7	ABX04524			ABX04524 Human adi
74.0	20	7	ABX04521			ABX04521 Human adi
74.0	20	9	ADC01943			ADC01943 Human zsi
74.0	20	9	ADC01940			ADC01940 Human zsi
74.0	20	9	AAD59886			AAD59886 ZC13651 o
74.0	20	9	AAD59889			AAD59889 ZC13650 o
74.0	25	8	ACK19038			ACK19038 Human mic
72.0	38	3	AAA95956			AAA95956 Human TRA
72.0	38	3	AAA95963			AAA95963 1.8 kb TR
71.0	25	8	ACI76567			ACI76567 Human mic
71.0	36	4	AAF84148			AAF84148 Human nov
70.0	33	2	AAQ45878			AAQ45878 CMV captu
69.0	25	8	ACI54322			ACI54322 Human mic
69.0	60	6	ABN35794			ABN35794 Human spl
68.0	24	3	AAZ24132			AAZ24132 HPV16 E7
68.0	24	6	AAK99483			AAK99483 Lipophili

62.0	14	2	AAV48580	Aav48580 junB gene	C 170	12.2	61.0	45	4	AAF31453	Aaf31453
62.0	17	7	ACC68623	Acc68623 Murine ol	C 171	12.2	61.0	45	8	ACD68356	Ac68356
62.0	18	4	AAF60706	Aaf60706 Human som	C 172	12.2	61.0	45	8	ACH04458	AcH04458
62.0	21	7	ACC41024	Acc41024 Perennial	C 173	12.2	61.0	45	8	ACD68002	Ac68002
62.0	21	9	ADC19995	Adc19995 Human COM	C 174	12.2	61.0	45	9	ADC18037	Adc18037
62.0	25	2	AAE65132	Aae65132 Primer 31	C 175	12.2	61.0	45	9	ADD70683	Ad70683
62.0	25	8	ACI55189	AcI55189 Human mic	C 176	12.2	61.0	45	9	ADD39760	Ad39760
62.0	25	8	ACI82928	AcI82928 Human mic	C 177	12.2	61.0	45	9	ADD70206	Ad70206
62.0	25	8	ACK29672	Ack29672 Human mic	C 178	12.2	61.0	45	9	ADD38327	Ad38327
62.0	25	8	ACK16061	Ack16061 Human mic	C 179	12.2	61.0	45	9	ADD39283	Ad39283
62.0	25	8	ACT186036	Act186036 Human mic	C 180	12.2	61.0	45	9	ADD38806	Ad38806
62.0	25	8	ACH53289	Ach53289 DNA targe	C 181	12.2	61.0	45	9	ADD40237	Ad40237
62.0	25	8	ACH54112	Ach54112 DNA targe	C 182	12.2	61.0	45	9	ADE50458	Ad50458
62.0	33	6	ABZ70235	Abz70235 Ribosomal	C 183	12.2	61.0	45	9	ADE20070	Ad20070
62.0	36	7	AA49055	Aa49055 RO38, re	C 184	12.2	61.0	45	9	ADE49981	Ad49981
62.0	36	7	ABX10180	Abx10180 Delta-des	C 185	12.2	61.0	45	9	ADE21539	Ad21539
62.0	47	6	ABK40861	Abk40861 Human obe	C 186	12.2	61.0	48	4	AAI76614	Aai76614
62.0	60	6	ABN50057	Abn50057 Human spl	C 187	12.2	61.0	50	4	AAI34322	Aai34322
61.0	17	6	ABV90369	Abv90369 Human POS	C 188	12.2	61.0	50	4	AAI34323	Aai34323
61.0	20	2	AAZ02725	Aaz02725 PCR prime	C 189	12.2	61.0	50	4	AAI34066	Aai34066
61.0	20	6	AB194148	Abi94148 Capture o	C 190	12.2	61.0	51	2	AAI34066	Aai34066
61.0	20	7	ABZ87914	Abz87914 Human oli	C 191	12.2	61.0	51	3	AAI33152	Aai33152
61.0	20	8	ACF79179	Acf79179 Mouse ger	C 192	12.2	61.0	51	3	AAI77274	Aai77274
61.0	21	2	AAZ25980	Aaz25980 Human POS	C 193	12.2	61.0	51	3	AAI28243	Aai28243
61.0	21	2	AAV99832	Aav99832 Human Fia	C 194	12.2	61.0	51	4	AAI33152	Aai33152
61.0	24	6	ABK15074	Abk15074 Human HBG	C 195	12.2	61.0	51	6	ABT12805	Abt12805
61.0	24	6	AB184866	Abi84866 Capture o	C 196	12.2	61.0	54	1	AAI33152	Aai33152
61.0	24	6	AB184867	Abi84867 Capture o	C 197	12.2	61.0	54	1	AAI33152	Aai33152
61.0	25	6	ABV92434	Abv92434 Human POS	C 198	12.2	61.0	57	6	AB151925	Ab151925
61.0	25	6	ABV92438	Abv92438 Human POS	C 199	12.2	61.0	57	6	AB151925	Ab151925
61.0	25	6	ABV92431	Abv92431 Human POS	C 200	12.2	61.0	60	3	AAZ62394	Aaz62394
61.0	25	6	ABV92435	Abv92435 Human POS	C 201	12.2	61.0	60	3	AAZ62394	Aaz62394
61.0	25	6	ABV92436	Abv92436 Human POS	C 202	12.2	61.0	60	6	ABN35991	Abn35991
61.0	25	6	ABV92437	Abv92437 Human POS	C 203	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	6	ABV92432	Abv92432 Human POS	C 204	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	6	ABV92433	Abv92433 Human POS	C 205	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	6	ABV92439	Abv92439 Human POS	C 206	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	8	ACI93767	AcI93767 Human mic	C 207	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	8	ACK07633	Ack07633 Human mic	C 208	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	8	ACI54323	AcI54323 Human mic	C 209	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	8	ACK22927	Ack22927 Human mic	C 210	12.2	61.0	60	6	ABN37303	Abn37303
61.0	27	6	ABX03800	Abx03800 DNA encod	C 211	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAQ71881	Aaq71881 Lo-CD2a V	C 212	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAV62599	Aav62599 Lo-CD2a c	C 213	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAV22857	Aav22857 Lo-CD2a h	C 214	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAV38592	Aav38592 Human gen	C 215	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAZ10124	Aaz10124 PCR prime	C 216	12.2	61.0	60	6	ABN37303	Abn37303
61.0	31	2	AAZ06194	Aaz06194 Human bia	C 217	12.2	61.0	60	6	ABN37303	Abn37303
61.0	32	2	AAZ32839	Aaz32839 Yeast GCN	C 218	12.2	61.0	60	6	ABN37303	Abn37303
61.0	32	2	AAQ30574	Aaq30574 Encodes r	C 219	12.2	61.0	60	6	ABN37303	Abn37303
61.0	32	2	AAQ30571	Aaq30571 Encodes r	C 220	12.2	61.0	60	6	ABN37303	Abn37303
61.0	32	2	AAZ47122	Aaz47122 Primer #2	C 221	12.2	61.0	60	6	ABN37303	Abn37303
61.0	32	2	AAZ47121	Aaz47121 Primer #1	C 222	12.2	61.0	60	6	ABN37303	Abn37303
61.0	33	4	AAZ08995	Aaz08995 Bacillus	C 223	12.2	61.0	60	6	ABN37303	Abn37303
61.0	36	6	ABK98981	Abk98981 Feline PC	C 224	12.2	61.0	60	6	ABN37303	Abn37303
61.0	36	6	ABN88049	Abn88049 Taxadiene	C 225	12.2	61.0	60	6	ABN37303	Abn37303
61.0	37	2	AAQ65478	Aaq65478 PCR prime	C 226	12.2	61.0	60	6	ABN37303	Abn37303
61.0	37	2	AAV65699	Aav65699 Helicobac	C 227	12.2	61.0	60	6	ABN37303	Abn37303
61.0	37	9	ADC64348	Adc64348 Oligonuc	C 228	12.2	61.0	60	6	ABN37303	Abn37303
61.0	39	7	ACC69760	Acc69760 FLAG olig	C 229	12.2	61.0	60	6	ABN37303	Abn37303
61.0	39	7	ACC69761	Acc69761 FLAG olig	C 230	12.2	61.0	60	6	ABN37303	Abn37303
61.0	39	8	ADA38057	Ada38057 Flag olig	C 231	12.2	61.0	60	6	ABN37303	Abn37303
61.0	39	8	ADA38058	Ada38058 Flag olig	C 232	12.2	61.0	60	6	ABN37303	Abn37303
61.0	40	7	ACA55276	AcA55276 Rat Ige C	C 233	12.2	61.0	60	6	ABN37303	Abn37303
61.0	41	6	ABZ46434	Abz46434 Human ald	C 234	12.2	61.0	60	6	ABN37303	Abn37303
61.0	41	6	ABZ46214	Abz46214 Human org	C 235	12.2	61.0	60	6	ABN37303	Abn37303
61.0	41	6	ABZ48946	Abz48946 Human ald	C 236	12.2	61.0	60	6	ABN37303	Abn37303
61.0	41	6	ABZ48371	Abz48371 Human org	C 237	11.8	59.0	60	6	ABN37303	Abn37303
61.0	45	2	AAQ14604	Aaq14604 5TG-Apal	C 238	11.8	59.0	60	6	ABN37303	Abn37303
61.0	45	2	AAV08809	Aav08809 PCR prime	C 239	11.8	59.0	60	6	ABN37303	Abn37303
61.0	45	3	AAV58499	Aav58499 Human PRO	C 240	11.8	59.0	60	6	ABN37303	Abn37303
61.0	45	3	AAA37213	Aaa37213 Human PRO	C 241	11.8	59.0	60	6	ABN37303	Abn37303
61.0	45	4	AAF54319	Aaf54319 Probe #26	C 242	11.8	59.0	60	6	ABN37303	Abn37303

59.0	20	6	ABT07420	Abt07420 Mammalian	C 316	11.6	58.0	25	6	ABK39852	Abk39852
59.0	20	6	AAD38471	Rad38471 Bovine MH	C 317	11.6	58.0	25	6	ABN89410	Abn89410
59.0	20	7	ACC70236	Acc70236 PCR prime	C 318	11.6	58.0	25	7	ABK89041	Abk89041
59.0	21	8	AAD56927	Aad56927 Human 604	C 319	11.6	58.0	25	8	ABX12293	Abx12293
59.0	22	2	AAQ94129	Aaq94129 Human mpl	C 320	11.6	58.0	25	8	ACK18832	Ack18832
59.0	22	6	ABZ29902	Abz29902 Candida a	C 321	11.6	58.0	25	8	ACK26905	Ack26905
59.0	22	3	AAA07348	Aaa07348 PCR prime	C 322	11.6	58.0	25	8	ACI01073	Act01073
59.0	23	3	AAO7348	Aao7348 M. tuberc	C 323	11.6	58.0	25	8	ACI09664	Acti09664
59.0	24	2	AAAX59906	Aax59906 PCR prime	C 324	11.6	58.0	25	8	ACK11841	Ack11841
59.0	24	4	AAO8718	Aao8718 Forward p	C 325	11.6	58.0	25	8	ACI38055	Acti38055
59.0	25	3	AAAR7583	Aaar7583 Rat hepat	C 326	11.6	58.0	25	8	ACI64770	Acti64770
59.0	25	4	AAD02664	Aad02664 Human WTI	C 327	11.6	58.0	25	8	ACI67995	Acti67995
59.0	25	6	AAD21935	Aad21935 Target nu	C 328	11.6	58.0	25	8	ACK19316	Ack19316
59.0	25	7	ABZ84508	Abz84508 Toxicolog	C 329	11.6	58.0	25	8	ACI23979	Acti23979
59.0	25	8	ACI27143	Acti27143 Human mic	C 330	11.6	58.0	25	8	ACI01519	Acti01519
59.0	25	8	ACI16451	Acti16451 Human mic	C 331	11.6	58.0	25	8	ACK09850	Ack09850
59.0	25	8	ACI38421	Acti38421 Human mic	C 332	11.6	58.0	25	8	ACI72440	Acti72440
59.0	25	8	ACK28100	Act28100 Human mic	C 333	11.6	58.0	25	8	ACI64256	Acti64256
59.0	25	8	ACK22222	Act22222 Human mic	C 334	11.6	58.0	25	8	ACK24323	Ack24323
59.0	25	8	ACI35185	Acti35185 Human mic	C 335	11.6	58.0	26	6	ABQ75990	Abq75990
59.0	25	8	ACI16450	Acti16450 Human mic	C 336	11.6	58.0	27	2	AAV41481	Aav41481
59.0	25	8	ACI67728	Acti67728 Human mic	C 337	11.6	58.0	27	2	AAX09730	Aax09730
59.0	25	8	ACI51610	Acti51610 Human mic	C 338	11.6	58.0	27	5	AAH78365	Aah78365
59.0	25	8	ACI78487	Acti78487 Human mic	C 339	11.6	58.0	27	6	ABK67057	Abk67057
59.0	25	8	ACI83089	Acti83089 Human mic	C 340	11.6	58.0	28	2	AAT02385	Aat02385
59.0	25	8	ACI28252	Acti28252 Human mic	C 341	11.6	58.0	28	2	AAX03202	Aax03202
59.0	26	4	AAD06276	Aad06276 Domestic	C 342	11.6	58.0	28	6	AAV69768	Aav69768
59.0	26	2	AAD06278	Aad06278 Domestic	C 343	11.6	58.0	28	6	AAV69768	Aav69768
59.0	27	4	AAX80203	Aax80203 Beta-glob	C 344	11.6	58.0	30	2	AAV60371	Aav60371
59.0	27	7	ABZ21545	Abz21545 Humulus l	C 345	11.6	58.0	31	4	AAI29860	Aai29860
59.0	28	2	AAX86510	Aax86510 Forward p	C 346	11.6	58.0	31	4	AAI30178	Aai30178
59.0	28	5	AAF80037	Aaf80037 PCR prime	C 347	11.6	58.0	31	4	AAI31117	Aai31117
59.0	28	9	AAD36214	Aad36214 Weed cont	C 348	11.6	58.0	33	2	AAT17180	Aat17180
59.0	30	2	AAT41641	Aat41641 Endo-xylo	C 349	11.6	58.0	33	2	AAV05297	Aav05297
59.0	30	2	AAI19510	Aai19510 Human lip	C 350	11.6	58.0	33	2	AAX09602	Aax09602
59.0	30	3	AAZ35207	Aaz35207 Corn glob	C 351	11.6	58.0	33	3	AAK63731	Aak63731
59.0	31	2	AAV67924	Aav67924 Nucleotid	C 352	11.6	58.0	33	6	ABD41984	Abd41984
59.0	31	3	AAA78951	Aaa78951 Human gen	C 353	11.6	58.0	33	6	ABZ25996	Abz25996
59.0	33	6	ABV74474	Abv74474 UGT and c	C 354	11.6	58.0	35	2	AAQ24138	Aaq24138
59.0	40	2	AAT28122	Aat28122 Probe for	C 355	11.6	58.0	36	2	AAQ58217	Aaq58217
59.0	40	2	AAT87111	Aat87111 IFN-gamma	C 356	11.6	58.0	37	2	AAV63966	Aav63966
59.0	40	2	AAT87110	Aat87110 IFN-gamma	C 357	11.6	58.0	37	2	AAV63966	Aav63966
59.0	44	2	AAT62424	Aat62424 Bovine be	C 358	11.6	58.0	37	7	ACA54711	Acta54711
59.0	44	2	AAV64121	Aav64121 Bovine be	C 359	11.6	58.0	39	7	ABT19445	Abt19445
59.0	45	2	AAT97216	Aat97216 Immunoglo	C 360	11.6	58.0	41	6	ABG60440	Abg60440
59.0	47	3	AAZ68331	Aaz68331 Human map	C 361	11.6	58.0	41	6	ABZ48553	Abz48553
59.0	49	4	AAD06895	Aad06895 Human oli	C 362	11.6	58.0	41	6	ABZ43276	Abz43276
59.0	49	4	AAD06904	Aad06904 Human oli	C 363	11.6	58.0	41	6	ABA95666	Aba95666
59.0	50	4	AAZ29516	Aaz29516 Human SNP	C 364	11.6	58.0	41	7	ABZ79598	Abz79598
59.0	50	6	ABZ03355	Abz03355 Human SNP	C 365	11.6	58.0	41	7	AAZ54344	Aaz54344
59.0	50	6	ADD41480	Add41480 Synthetic	C 366	11.6	58.0	42	4	AAI66856	Aai66856
59.0	51	4	AAZ27563	Aaz27563 Human SNP	C 367	11.6	58.0	42	4	AAI66857	Aai66857
59.0	51	4	AAZ27563	Aaz27563 Human SNP	C 368	11.6	58.0	42	6	AAD28168	Aad28168
59.0	51	4	AAZ31121	Aaz31121 Human SNP	C 369	11.6	58.0	42	6	AAD28169	Aad28169
59.0	51	4	AAZ31121	Aaz31121 Human SNP	C 370	11.6	58.0	42	7	ACC72627	Acc72627
59.0	51	4	AAZ31121	Aaz31121 Human SNP	C 371	11.6	58.0	42	7	ACC72628	Acc72628
59.0	60	2	AAV13216	Aav13216 Primer AS	C 372	11.6	58.0	42	7	ACC43213	Acc43213
59.0	60	6	ABN50088	Abn50088 Human spl	C 373	11.6	58.0	42	7	ACC43209	Acc43209
59.0	60	6	ABN59445	Abn59445 Human spl	C 374	11.6	58.0	48	2	AAT77147	Aat77147
59.0	60	6	ABN46833	Abn46833 Human spl	C 375	11.6	58.0	48	2	AAV07413	Aav07413
58.0	19	3	AAA84452	Aaa84452 Cyclin D3	C 376	11.6	58.0	50	4	AAH89689	Aah89689
58.0	19	5	AAH59614	Aah59614 Cyclin D3	C 377	11.6	58.0	50	6	ABZ05446	Abz05446
58.0	20	6	AAD34730	Aad34730 Human MEK	C 378	11.6	58.0	50	6	AAZ06001	Aaz06001
58.0	21	2	AAZ61027	Aaz61027 PCR prime	C 379	11.6	58.0	51	3	AAA07020	Aaa07020
58.0	21	8	ADA27332	Ada27332 Human mic	C 380	11.6	58.0	51	3	AAZ77148	Aaz77148
58.0	22	2	AAV35216	Aav35216 ICE gene	C 381	11.6	58.0	51	4	AAZ77148	Aaz77148
58.0	23	6	ABX09450	Abx09450 Arteriosc	C 382	11.6	58.0	51	4	AAI33955	Aai33955
58.0	23	6	ABL99402	AbL99402 Left PCR	C 383	11.6	58.0	51	4	AAI76360	Aai76360
58.0	24	4	AAH45836	Aah45836 C album c	C 384	11.6	58.0	54	8	AAH89688	Aah89688
58.0	24	6	ABS55114	Abs55114 C. Album	C 385	11.6	58.0	57	3	AAD00113	Aad00113
58.0	24	6	ABI91199	Abi91199 Capture o	C 386	11.6	58.0	57	4	AAE94539	Aae94539
58.0	24	6	ABI91199	Abi91199 Capture o	C 387	11.6	58.0	57	4	AAF93107	Aaf93107
58.0	24	6	ABI91198	Abi91198 Capture o	C 388	11.6	58.0	57	4	AAF93106	Aaf93106

58.0	57	4	AAD08604	Primer IN	462	11.4	57.0	25	8	ACI10408	ACI10408
58.0	57	6	ABT03446	Human HIV	463	11.4	57.0	25	8	ACI43231	ACI43231
58.0	57	6	ABT03447	Human HIV	C 464	11.4	57.0	25	8	ACH57316	ACH57316
58.0	60	2	AAT051027	5' fragme	465	11.4	57.0	26	4	AAF30582	AAF30582
58.0	60	6	ABN44635	Human spl	C 466	11.4	57.0	27	4	AAF57678	AAF57678
58.0	60	6	ABN40334	Human spl	C 467	11.4	57.0	27	4	AAF30672	AAF30672
58.0	60	6	ABN41630	Human spl	468	11.4	57.0	28	4	AAF30583	AAF30583
58.0	60	6	ABN41074	Human spl	C 469	11.4	57.0	28	5	AAI71936	AAI71936
58.0	60	6	ABN38683	Human spl	470	11.4	57.0	30	2	AAQ14283	AAQ14283
58.0	60	6	ABN46459	Human spl	471	11.4	57.0	30	2	AAQ37670	AAQ37670
58.0	60	6	ABN43803	Human spl	C 472	11.4	57.0	30	3	AAZ50560	AAZ50560
58.0	60	6	ABN32832	Human spl	C 473	11.4	57.0	30	3	AAA30665	AAA30665
58.0	60	6	ABN34626	Human spl	474	11.4	57.0	30	4	AAF30584	AAF30584
58.0	60	6	ABN33037	Human spl	C 475	11.4	57.0	30	9	ADC22635	ADC22635
58.0	60	6	ABN39120	Human spl	476	11.4	57.0	31	4	ACC81025	ACC81025
58.0	60	6	ABN44650	Human spl	477	11.4	57.0	31	4	AAF84963	AAF84963
57.0	16	2	AXX61158	Human chr	478	11.4	57.0	32	4	AAF30585	AAF30585
57.0	16	7	ACC42403	Mouse acy	C 479	11.4	57.0	33	2	AAT31736	AAT31736
57.0	17	6	ABV90365	Human POS	480	11.4	57.0	33	6	ABL58191	ABL58191
57.0	17	6	ABV90368	Human POS	481	11.4	57.0	36	2	AAQ79555	AAQ79555
57.0	17	6	ABV90366	Human POS	482	11.4	57.0	36	2	AAQ79543	AAQ79543
57.0	17	6	ABV90367	Human POS	483	11.4	57.0	36	2	AAQ79553	AAQ79553
57.0	17	7	ABZ61854	Human H-R	C 484	11.4	57.0	36	2	AXX04258	AXX04258
57.0	17	7	ACD64741	HCV minus	485	11.4	57.0	36	6	AAD42545	AAD42545
57.0	17	7	ACD57928	HCV DNazzy	486	11.4	57.0	36	6	AAD42535	AAD42535
57.0	17	9	ADB41409	Tumour su	487	11.4	57.0	36	6	AAD42547	AAD42547
57.0	18	2	AAV44606	Human unc	488	11.4	57.0	36	8	ACH00389	ACH00389
57.0	18	2	AXX54355	NK-KB ant	489	11.4	57.0	36	8	ACH00377	ACH00377
57.0	18	3	AA333799	Low adeno	490	11.4	57.0	36	8	ACH00387	ACH00387
57.0	18	3	AAF19921	Human NF-	491	11.4	57.0	38	9	ADC64130	ADC64130
57.0	18	6	AD301081	Human UGT	492	11.4	57.0	41	8	ACC41994	ACC41994
57.0	18	6	ABK98395	Mouse sma	C 493	11.4	57.0	42	2	AAT77149	AAT77149
57.0	18	7	ABZ95615	Human NF-	C 494	11.4	57.0	46	9	ADC64129	ADC64129
57.0	19	6	ABX03574	Human ner	C 495	11.4	57.0	47	3	AAZ68568	AAZ68568
57.0	20	2	AAV36332	Human BRC	496	11.4	57.0	50	6	ABZ02282	ABZ02282
57.0	20	3	AACT3707	Human IL-	C 497	11.4	57.0	50	6	ABZ01231	ABZ01231
57.0	20	6	ABN85727	Human FSA	498	11.4	57.0	51	4	AAI32625	AAI32625
57.0	20	6	AA34731	Human MEK	499	11.4	57.0	51	4	AAI32787	AAI32787
57.0	20	7	ABX04361	Human Int	C 500	11.4	57.0	51	4	AAI27191	AAI27191
57.0	20	7	ACC49981	sox9f pri	501	11.4	57.0	60	2	AAV40187	AAV40187
57.0	20	7	AD531148	SOX-9 DNA	C 502	11.4	57.0	60	6	ABN32962	ABN32962
57.0	20	9	ADD22547	Flatfish	C 503	11.4	57.0	60	6	ABN58762	ABN58762
57.0	21	2	AAQ71316	Primer fo	C 504	11.4	57.0	60	6	ABN37104	ABN37104
57.0	21	2	AAAX91386	Primer fo	C 505	11.4	57.0	60	6	ABN39406	ABN39406
57.0	21	4	AAAC84519	Human gly	506	11.2	56.0	17	2	AAA22478	AAA22478
57.0	21	4	AAAF95940	Human gen	507	11.2	56.0	17	3	AAF07098	AAF07098
57.0	21	4	AA542709	T. gondii	C 508	11.2	56.0	17	6	ABN08564	ABN08564
57.0	21	4	ABL51705	Human GFR	C 509	11.2	56.0	17	6	ABN08565	ABN08565
57.0	22	9	ABE16166	G-coupled	510	11.2	56.0	17	6	ABK18433	ABK18433
57.0	23	7	ABZ76186	Arabidops	511	11.2	56.0	17	6	ABK17727	ABK17727
57.0	24	2	AAAT17881	IL-11 rec	512	11.2	56.0	17	6	ABK17726	ABK17726
57.0	24	4	AAF30581	Human COM	513	11.2	56.0	17	6	ABK18432	ABK18432
57.0	24	6	ABQ04620	Oligonucl	514	11.2	56.0	17	6	ABV90370	ABV90370
57.0	24	6	ABQ04579	Oligonucl	515	11.2	56.0	18	3	AAZ91442	AAZ91442
57.0	24	6	ABQ10907	Oligonucl	C 516	11.2	56.0	18	3	AAZ70948	AAZ70948
57.0	24	6	ABQ00302	Oligonucl	C 517	11.2	56.0	18	9	ADE43411	ADE43411
57.0	24	6	ABQ10948	Oligonucl	518	11.2	56.0	19	2	AAQ82533	AAQ82533
57.0	25	5	AAI62264	Soybean 3	C 519	11.2	56.0	19	6	ABK18432	ABK18432
57.0	25	5	AAI62304	Soybean 3	C 520	11.2	56.0	19	6	ABK44408	ABK44408
57.0	25	6	ABQ12443	Oligonucl	C 521	11.2	56.0	19	6	ABT03925	ABT03925
57.0	25	6	ABQ12484	Oligonucl	C 522	11.2	56.0	19	7	ABZ84512	ABZ84512
57.0	25	6	ABV52430	Human POS	C 523	11.2	56.0	19	8	ACD13528	ACD13528
57.0	25	6	ABV92428	Human POS	C 524	11.2	56.0	19	8	ADA97829	ADA97829
57.0	25	6	ABV92427	Human POS	C 525	11.2	56.0	20	2	AAT00612	AAT00612
57.0	25	6	ABV92429	Human POS	526	11.2	56.0	20	2	AAZ22628	AAZ22628
57.0	25	8	ACI65495	Human mic	527	11.2	56.0	20	2	AAZ78590	AAZ78590
57.0	25	8	ACI30050	Human mic	C 528	11.2	56.0	20	2	AAZ06158	AAZ06158
57.0	25	8	ACI17094	Human mic	C 529	11.2	56.0	20	2	AAZ01942	AAZ01942
57.0	25	8	ACK29930	Human mic	530	11.2	56.0	20	2	AAZ83697	AAZ83697
57.0	25	8	ACI34056	Human mic	531	11.2	56.0	20	2	AAI19193	AAI19193
57.0	25	8	ACI18817	Human mic	532	11.2	56.0	20	2	AAZ27332	AAZ27332
57.0	25	8	ACI86651	Human mic	533	11.2	56.0	20	3	AACT1588	AACT1588
57.0	25	8	ACK12962	Human mic	534	11.2	56.0	20	3	AACT1591	AACT1591

56.0	20	3	AAC73141	Aac73141	Forward p	c 608	11.2	56.0	25	8	ACH53698	Ach53698
56.0	20	4	AA14641	Aad14641	DEN-1 PDK	c 609	11.2	56.0	25	8	ACH64773	Ach64773
56.0	20	4	AAC84227	Aac84227	Human PKC	c 610	11.2	56.0	25	8	ACH55441	Ach55441
56.0	20	6	ABL90920	Ab190920	Human pro	c 611	11.2	56.0	25	8	ACH55317	Ach55317
56.0	20	7	ABZ85243	Abz85243	Human Oli	c 612	11.2	56.0	25	9	ADE86830	Ade86830
56.0	20	7	ABZ98576	Abz98576	Human ICA	c 613	11.2	56.0	26	2	AAT10247	Aat10247
56.0	20	7	ACC43096	Acc43096	Probe use	c 614	11.2	56.0	26	6	ABS51750	Ab51750
56.0	20	8	ACC99689	Acc99689	Apol PCR	c 615	11.2	56.0	27	3	AAA39575	Aaa39575
56.0	20	8	ACH11199	Ach11199	Human pro	c 616	11.2	56.0	27	3	ADA01452	Ada01452
56.0	20	9	ACF79244	Acf79244	Human neu	c 617	11.2	56.0	27	7	ADA01448	Ada01448
56.0	20	9	ADE13476	Ade13476	HLA Class	c 618	11.2	56.0	27	7	ABZ21543	Abz21543
56.0	21	2	AA705918	Aat05918	COX II se	c 619	11.2	56.0	28	2	AAQ24484	Aaq24484
56.0	21	3	AAA11510	Aaai1510	Human dys	c 620	11.2	56.0	28	2	AAZ89041	Aaz89041
56.0	21	3	AAA36965	Aaa36965	Human dys	c 621	11.2	56.0	28	3	AAZ88940	Aaz88940
56.0	21	4	AAF96280	Aaf96280	Human gen	c 622	11.2	56.0	28	4	AAF84420	Aaf84420
56.0	21	4	AAF69892	Aaf69892	COXI pro	c 623	11.2	56.0	28	6	ABK66654	Abk66654
56.0	21	6	ABK65613	Abk65613	Human sin	c 624	11.2	56.0	28	7	ABZ83529	Abz83529
56.0	21	8	ADA49835	Ada49835	Human mit	c 625	11.2	56.0	29	2	AAV44979	Aav44979
56.0	22	3	AAAG6698	Aaa66698	Rice cyto	c 626	11.2	56.0	29	2	AAV08884	Aav08884
56.0	23	5	AA13607	Aad13607	H(A12-M)d	c 627	11.2	56.0	30	2	AAQ45423	Aaq45423
56.0	23	6	AA142661	Aal42661	Rice seed	c 628	11.2	56.0	30	2	AAQ45423	Aaq45423
56.0	24	2	AAQ42195	Aaq42195	HCV c33c	c 629	11.2	56.0	30	4	AAQ1054	Aat71054
56.0	24	2	AAQ72292	Aaq72292	Serotonin	c 630	11.2	56.0	31	2	AAQ26644	Aad02644
56.0	24	6	ABQ00673	Abq00673	Oligonucl	c 631	11.2	56.0	31	2	AAQ27962	Aax27962
56.0	24	6	ABQ11635	Abq11635	Oligonucl	c 632	11.2	56.0	31	2	AAA73997	Aaa73997
56.0	24	6	ABQ05307	Abq05307	Oligonucl	c 633	11.2	56.0	31	2	AAZ39516	Aaz39516
56.0	24	6	ABQ11594	Abq11594	Oligonucl	c 634	11.2	56.0	31	3	AAA95630	Aaa95630
56.0	24	6	ABQ05348	Abq05348	Oligonucl	c 635	11.2	56.0	31	4	AAI30885	Aai30885
56.0	24	6	ABT03574	Abt03574	Human Cux	c 636	11.2	56.0	31	5	AAI41247	Aal41247
56.0	24	7	ABV77502	Abv77502	A. margin	c 637	11.2	56.0	31	6	AAI41237	Aal41237
56.0	25	4	AA44581	Aaf44581	Mouse DSS	c 638	11.2	56.0	31	7	ABX93832	Abx93832
56.0	25	6	AA562207	Aae62207	Porcine r	c 639	11.2	56.0	31	7	ACD43814	Acd43814
56.0	25	6	AA562205	Aae62205	Porcine r	c 640	11.2	56.0	32	2	AAQ47881	Aaq47881
56.0	25	6	ABN13457	Abn13457	Human GDM	c 641	11.2	56.0	32	6	ABV73854	Abv73854
56.0	25	6	ABN13463	Abn13463	Human GDM	c 642	11.2	56.0	33	2	AAV15834	Aav15834
56.0	25	6	ABN13464	Abn13464	Human GDM	c 643	11.2	56.0	33	4	AAH75497	Aah75497
56.0	25	6	ABN13462	Abn13462	Human GDM	c 644	11.2	56.0	33	6	ABL60571	Ab160571
56.0	25	6	ABN13458	Abn13458	Human GDM	c 645	11.2	56.0	34	4	AAF81222	Aaf81222
56.0	25	6	ABN13460	Abn13460	Human GDM	c 646	11.2	56.0	34	6	AAI42418	Aal42418
56.0	25	6	ABN13461	Abn13461	Human GDM	c 647	11.2	56.0	34	6	ABN88048	Abn88048
56.0	25	6	ABN13459	Abn13459	Human GDM	c 648	11.2	56.0	34	9	ADC54184	Adc54184
56.0	25	6	ABN13456	Abn13456	Human GDM	c 649	11.2	56.0	35	3	AAQ35855	Aaa35855
56.0	25	6	ABN13465	Abn13465	Human GDM	c 650	11.2	56.0	36	3	AAZ39031	Aaz39031
56.0	25	6	ABX72713	Abx72713	Cryptococ	c 651	11.2	56.0	37	3	AAI66269	Aai66269
56.0	25	6	ABX72706	Abx72706	Cryptococ	c 652	11.2	56.0	37	4	AAI66269	Aai66269
56.0	25	6	ABQ13130	Abq13130	Oligonucl	c 653	11.2	56.0	38	2	AAV58260	Aav58260
56.0	25	6	ABQ13171	Abq13171	Oligonucl	c 654	11.2	56.0	38	5	AAI5541	Aai5541
56.0	25	6	ABV92440	Abv92440	Human POS	c 655	11.2	56.0	38	5	AAI5542	Aai5542
56.0	25	8	ACI30309	Aci30309	Human mic	c 656	11.2	56.0	39	2	AAQ38124	Aaq38124
56.0	25	8	ACI00641	Aci00641	Human mic	c 657	11.2	56.0	40	4	AAQ84460	Aac84460
56.0	25	8	ACK06224	Ack06224	Human mic	c 658	11.2	56.0	40	8	ACC85304	Acc85304
56.0	25	8	ACI44890	Aci44890	Human mic	c 659	11.2	56.0	41	3	AAA77202	Aaa77202
56.0	25	8	ACI09083	Aci09083	Human mic	c 660	11.2	56.0	41	4	AAQ84467	Aac84467
56.0	25	8	ACI84783	Aci84783	Human mic	c 661	11.2	56.0	41	5	AAQ80122	Aaf80122
56.0	25	8	ACI84782	Aci84782	Human mic	c 662	11.2	56.0	41	6	ABL40246	Ab140246
56.0	25	8	ACI96776	Aci96776	Human mic	c 663	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI36129	Aci36129	Human mic	c 664	11.2	56.0	41	6	ABT08105	Abt08105
56.0	25	8	ACI95679	Aci95679	Human mic	c 665	11.2	56.0	41	6	ABT08105	Abt08105
56.0	25	8	ACK05421	Ack05421	Human mic	c 666	11.2	56.0	41	6	ABT08105	Abt08105
56.0	25	8	ACI02211	Aci02211	Human mic	c 667	11.2	56.0	41	6	ABZ47750	Abz47750
56.0	25	8	ACK06920	Ack06920	Human mic	c 668	11.2	56.0	41	6	ABZ45155	Abz45155
56.0	25	8	ACI83951	Aci83951	Human mic	c 669	11.2	56.0	41	6	ABZ47781	Abz47781
56.0	25	8	ACI75696	Aci75696	Human mic	c 670	11.2	56.0	41	6	ABZ45186	Abz45186
56.0	25	8	ACI32391	Aci32391	Human mic	c 671	11.2	56.0	41	6	ABZ50686	Abz50686
56.0	25	8	ACI02256	Aci02256	Human mic	c 672	11.2	56.0	41	7	ABA05074	Ab05074
56.0	25	8	ACI60399	Aci60399	Human mic	c 673	11.2	56.0	42	2	ABZ25674	Abz25674
56.0	25	8	ACK19877	Ack19877	Human mic	c 674	11.2	56.0	44	4	AA855339	Aat855339
56.0	25	8	ACI72680	Aci72680	Human mic	c 675	11.2	56.0	44	4	AAQ06072	Aad06072
56.0	25	8	ACK03261	Ack03261	Human mic	c 676	11.2	56.0	44	4	AAQ62004	Aaf62004
56.0	25	8	ACI32570	Aci32570	Human mic	c 677	11.2	56.0	45	4	AAQ84414	Aaf84414
56.0	25	8	ACK03391	Ack03391	Human mic	c 678	11.2	56.0	45	4	AAQ84413	Aaf84413
56.0	25	8	ACH52395	Ach52395	DNA targe	c 679	11.2	56.0	47	3	AAZ66572	Aaz66572
56.0	25	8	ACH62756	Ach62756	DNA targe	c 680	11.2	56.0	47	3	AAZ66343	Aaz66343
56.0	25	8					11.2	56.0	48	2	AAZ25648	Aax25648

56.0	48	4	AA140776	AA140776 5' PCR pr	c 754	11	55.0	20	2	AAZ03662	Aaz03662
56.0	49	6	ABL51371	Ab151371 Mouse pho	755	11	55.0	20	2	AAX96025	Aax96025
56.0	50	4	AA134028	Aal34028 Human SNP	c 756	11	55.0	20	3	AAa71387	Aaa71387
56.0	50	4	AA134411	Aal34411 Human SNP	757	11	55.0	20	4	AAc67719	Aac67719
56.0	50	4	AA131517	Aal31517 Human SNP	758	11	55.0	20	6	ABN83208	Abn83208
56.0	50	4	AA131754	Aal31754 Human SNP	759	11	55.0	20	6	ABD39528	Abd39528
56.0	50	4	AA131755	Aal31755 Human SNP	c 760	11	55.0	20	6	ABS52091	Abs52091
56.0	50	4	AAH70677	Aah70677 Human cer	c 761	11	55.0	20	6	ABs52083	Abes52083
56.0	50	4	AAH76766	Aaf76766 T flavus	762	11	55.0	20	6	ABO75982	Abot75982
56.0	50	6	ABZ07347	Abz07347 Human leu	763	11	55.0	20	6	AA143887	Aa143887
56.0	50	6	ABZ01635	Abz01635 Human leu	764	11	55.0	20	7	AAU50868	Aau50868
56.0	50	6	ABZ08003	Abz08003 Human leu	765	11	55.0	20	7	ACC49247	Acc49247
56.0	50	6	ABZ05012	Abz05012 Human leu	c 766	11	55.0	20	8	ABT19438	Abt19438
56.0	50	8	ADA21055	Ada21055 Codon-opt	c 767	11	55.0	20	8	ACC99693	Acc99693
56.0	50	8	ADA21083	Ada21083 Codon-opt	768	11	55.0	21	2	AAT86480	Aat86480
56.0	51	3	AAA77291	Aaa77291 Human clo	769	11	55.0	22	3	AAY50457	Aay50457
56.0	51	4	AA129407	Aal29407 Human SNP	770	11	55.0	22	6	ABL58459	Ab158459
56.0	51	4	AA131137	Aal31137 Human SNP	771	11	55.0	22	7	ACA61738	Acc61738
56.0	51	4	AA128244	Aal28244 Human SNP	772	11	55.0	22	9	ADB66806	Adb66806
56.0	51	4	AA176324	Aai76324 Human sil	773	11	55.0	23	2	AAT40438	Aat40438
56.0	51	4	AA176325	Aai76325 Human sil	774	11	55.0	23	2	AXX81852	Axx81852
56.0	51	6	AAH90461	Aah90461 Human clo	775	11	55.0	23	3	AAZ88927	Aaz88927
56.0	51	6	ABA82897	Abas2897 Human pro	c 776	11	55.0	23	3	AAa87966	Aaa87966
56.0	51	6	AA167894	Aai67894 Reverse o	777	11	55.0	23	7	ABT21539	Abt21539
56.0	51	6	AA167894	Aai67894 Reverse o	778	11	55.0	24	2	AAV14051	Aav14051
56.0	53	4	AAH74871	Aah74871 Oligonuc	c 779	11	55.0	24	4	AAH27936	Aah27936
56.0	53	4	AAH74871	Aah74871 Oligonuc	c 780	11	55.0	24	5	AAI12647	Aai12647
56.0	53	6	ABA99040	Abas9040 Kpn-BB'-X	c 781	11	55.0	24	6	ABT08330	Abt08330
56.0	53	7	ADA48045	Aad48045 AtTB reco	c 782	11	55.0	24	6	ABQ03485	Abq03485
56.0	53	8	ACF06160	Acf06160 Nucleic a	c 783	11	55.0	24	6	ABA95103	Abas95103
56.0	54	2	AA644481	Aax644481 Rabbit st	784	11	55.0	24	6	ABR95103	Abra95103
56.0	54	2	AAZ06778	Aaz06778 PCR prime	c 785	11	55.0	24	6	ABT188589	Abt188589
56.0	54	3	AAZ61088	Aaz61088 Forward p	786	11	55.0	25	2	AXX01263	Axx01263
56.0	54	3	AAZ61088	Aaz61088 Forward p	c 787	11	55.0	25	3	AAY50505	Aay50505
56.0	54	3	AAZ73934	Aaz73934 Gpp Glu(G	c 788	11	55.0	25	6	ABs55623	Abes55623
56.0	56	3	AAZ58962	Aaz58962 Primer fo	789	11	55.0	25	7	ABZ37305	Abz37305
56.0	56	3	AAZ58962	Aaz58962 Primer fo	790	11	55.0	25	7	ABZ37259	Abz37259
56.0	57	2	AAQ22693	Aaq22693 Gal alpha	791	11	55.0	25	8	ACT183971	Act183971
56.0	57	3	AAZ52452	Aaz52452 Human I-k	c 792	11	55.0	25	8	ACT177426	Act177426
56.0	57	4	AAH50027	Aah50027 Bacterial	793	11	55.0	25	8	ACI40266	Act40266
56.0	57	6	ABL51346	Ab151346 Human pho	c 794	11	55.0	25	8	ACT02709	Act02709
56.0	58	6	ABR86543	Abk86543 PCR prime	795	11	55.0	25	8	ACI38244	Act38244
56.0	59	3	AAZ90146	Aaz90146 PCR prime	796	11	55.0	25	8	ACI63359	Act63359
56.0	59	5	AAZ82659	Aaz82659 Primer us	797	11	55.0	25	8	ACI89300	Act89300
56.0	60	2	AAZ31935	Aat31935 RIP14-2 c	798	11	55.0	25	8	ACT08603	Act08603
56.0	60	2	AAV54568	Aav54568 GFP-bearl	c 799	11	55.0	25	8	ACI51740	Act51740
56.0	60	2	AAZ89224	Aaz89224 Sense pri	c 800	11	55.0	25	8	ACT172890	Act172890
56.0	60	3	AAZ39408	Aaz39408 Human tra	801	11	55.0	25	8	ACK26915	Act26915
56.0	60	6	ABN40965	Abn40965 Human spl	802	11	55.0	25	8	ACI39822	Act39822
56.0	60	6	ABN43418	Abn43418 Human spl	803	11	55.0	25	8	ACI39802	Act39802
56.0	60	6	ABN38688	Abn38688 Human spl	804	11	55.0	25	8	ACK16388	Act16388
56.0	60	6	ABN44193	Abn44193 Human spl	805	11	55.0	25	8	ACK09986	Act09986
56.0	60	6	ABN35520	Abn35520 Human spl	806	11	55.0	25	8	ACK06083	Act06083
56.0	60	6	ABN319793	Abn319793 Human spl	807	11	55.0	25	8	ACT01511	Act01511
56.0	60	6	ABN47129	Abn47129 Human spl	808	11	55.0	25	8	ACT127896	Act127896
56.0	60	6	ABN35928	Abn35928 Human spl	c 809	11	55.0	25	8	ACK04844	Act04844
56.0	60	6	ABN39401	Abn39401 Human spl	c 810	11	55.0	25	8	ACK04844	Act04844
56.0	60	6	ABN36165	Abn36165 Human spl	811	11	55.0	25	8	ACT184573	Act184573
56.0	60	6	ABN33072	Abn33072 Human spl	812	11	55.0	25	8	ACT162323	Act162323
56.0	60	6	ABN39300	Abn39300 Human spl	813	11	55.0	25	8	ACT166136	Act166136
56.0	60	6	ABN50630	Abn50630 Human spl	814	11	55.0	25	8	ACT194039	Act194039
56.0	60	6	ABN38748	Abn38748 Human spl	815	11	55.0	25	8	ACK04077	Act04077
56.0	60	6	ABN46473	Abn46473 Human spl	c 816	11	55.0	25	8	ACK04077	Act04077
55.0	17	2	AAQ06859	Aaq06859 Sequence	817	11	55.0	25	8	ACT151741	Act151741
55.0	17	2	AAA22909	Aaa22909 Integrin	c 818	11	55.0	25	8	ACH52389	Ach52389
55.0	17	2	AAA22910	Aaa22910 Integrin	c 819	11	55.0	25	8	ACH53320	Ach53320
55.0	17	2	AAA22911	Aaa22911 Integrin	c 820	11	55.0	25	8	ACH53464	Ach53464
55.0	17	7	ABT38399	Abt38399 Tumour su	c 821	11	55.0	25	8	ACH53338	Ach53338
55.0	18	2	AAZ41165	Aaz41165 Human G-a	c 822	11	55.0	25	9	ADC53865	Adc53865
55.0	18	2	AAZ19536	Aaz19536 Human G-a	823	11	55.0	25	9	ADD94046	Add94046
55.0	18	6	ABK68847	Abk68847 PCR prime	824	11	55.0	26	2	AAV80399	Aav80399
55.0	18	7	ACC43590	Acc43590 Probe use	825	11	55.0	26	2	AAV68616	Aav68616
55.0	20	2	AAAT08229	Aat08229 p193, PCR	c 826	11	55.0	26	3	AAc666157	Aac666157



55.0	26	6	AB565327	Ab565327 A. thalia	900	11	55.0	45	7	ACA58031	Aca58031
55.0	27	2	AAV94296	AAv94296 Mouse IL-	901	11	55.0	45	7	ACA71758	Aca71758
55.0	27	2	AAV94355	AAv94355 Mouse IL-	902	11	55.0	45	7	ABX92398	Abx92398
55.0	27	2	AAV83628	AAv83628 PCR prime	903	11	55.0	45	7	ACA66139	Aca66139
55.0	27	4	AAF30904	AAf30904 Yeast HMG	904	11	55.0	45	8	ADA24699	Ada24699
55.0	27	7	ABX33943	Abx33943 Human int	905	11	55.0	45	8	ACD29740	Acd29740
55.0	28	4	AAH20878	Aah20878 Tobacco p	906	11	55.0	45	8	ADA12360	Ada12360
55.0	29	2	AAQ24564	AAq24564 NANBH pep	907	11	55.0	45	8	ACD29155	Acd29155
55.0	29	2	AAQ64062	AAq64062 Anti-canc	908	11	55.0	45	9	ADB73666	Adb73666
55.0	30	2	AAT00205	Aat00205 Thrombin	909	11	55.0	45	9	ADB76382	Adb76382
55.0	30	2	AAT18017	Aat18017 Chemokine	910	11	55.0	45	9	ADC43808	Adc43808
55.0	30	2	AAT98806	Aat98806 Primer 63	911	11	55.0	45	9	ADC61568	Adc61568
55.0	30	2	AAT65532	Aat65532 Oligonucl	912	11	55.0	45	9	ADC63532	Adc63532
55.0	30	2	AAT63002	Aat63002 c-mpl rec	913	11	55.0	45	9	ADC66632	Adc66632
55.0	30	2	AAV55444	AAv55444 Primer 12	914	11	55.0	45	9	ADC68756	Adc68756
55.0	30	4	AAF70757	AAf70757 Thrombin	915	11	55.0	45	9	ADC68216	Adc68216
55.0	30	6	AD34667	Ad34667 PCR prime	916	11	55.0	45	9	ADC67881	Adc67881
55.0	30	6	AA94552	AA94552 Rice XB3	917	11	55.0	45	9	ADC41201	Adc41201
55.0	31	2	AAQ80843	AAq80843 MHC I reg	918	11	55.0	45	9	ADC67256	Adc67256
55.0	31	2	AAT59839	Aat59839 Regulator	919	11	55.0	45	9	ADC62192	Adc62192
55.0	31	4	AAI31136	Aai31136 Human sin	920	11	55.0	45	9	ADC53863	Adc53863
55.0	31	4	AAI29843	Aai29843 Human sin	921	11	55.0	45	9	ADC41825	Adc41825
55.0	31	6	AAI42078	Aai42078 Human Glu	922	11	55.0	45	9	ADE45194	Ade45194
55.0	31	6	ABS64553	Ab64553 Human K+a	923	11	55.0	45	9	ADE35248	Ade35248
55.0	31	6	ABS64526	Ab64526 Human K+a	924	11	55.0	45	9	ADL16362	Adl16362
55.0	31	6	ABS64541	Ab64541 Human K+a	925	11	55.0	45	9	ADD72977	Add72977
55.0	31	7	ACD43786	Acd43786 Human gen	926	11	55.0	45	9	ADD72335	Add72335
55.0	32	2	AAV66474	AAv66474 PCR prime	927	11	55.0	45	9	ADE16986	Ade16986
55.0	32	2	AAQ45872	AAq45872 CMV ampli	928	11	55.0	45	10	ADE48494	Ade48494
55.0	33	6	AK50198	AK50198 Acid phos	929	11	55.0	45	10	ADE89595	Ade89595
55.0	33	7	ABX13121	Abx13121 Rat volta	C 930	11	55.0	47	3	AAZ65844	Aaz65844
55.0	35	1	AA60031	Aan60031 Sequence	C 931	11	55.0	47	4	AAH88310	Aah88310
55.0	35	3	AAV31803	AAv31803 Human cyt	C 932	11	55.0	48	7	ACD55114	Acd55114
55.0	35	3	AA75439	AA75439 PCR prime	C 933	11	55.0	50	2	ACD55264	Acd55264
55.0	35	3	AA70686	AA70686 CMV IE ge	934	11	55.0	50	2	AA76096	Aat76096
55.0	35	5	AAH45499	Aah45499 PCR prime	935	11	55.0	50	2	AA76096	Aat76096
55.0	35	8	AA42077	Aad42077 CMV IE pr	936	11	55.0	50	3	AA33350	Aaa33350
55.0	35	8	ACA62309	Ac62309 PCR prime	937	11	55.0	50	3	AAF19472	Aaf19472
55.0	35	9	AA60101	Aad60101 CMV genom	938	11	55.0	50	6	ABZ02684	Abz02684
55.0	36	2	AAT08949	Aat08949 Reverse p	939	11	55.0	50	6	ABZ04864	Abz04864
55.0	36	2	AAV66305	AAv66305 3' PCR pr	C 940	11	55.0	50	6	ABZ04775	Abz04775
55.0	36	2	AAV32680	AAv32680 Delta thi	941	11	55.0	50	6	ABZ07384	Abz07384
55.0	36	2	AAV52688	AAv52688 HGV rever	942	11	55.0	50	6	ABZ00264	Abz00264
55.0	36	2	AAV16496	AAv16496 PCR prime	C 943	11	55.0	50	6	ABZ03945	Abz03945
55.0	36	2	AAV02543	AAv02543 USS856134	944	11	55.0	50	6	ABZ95166	Abz95166
55.0	36	2	AAV82239	AAv82239 Hepatitis	945	11	55.0	50	7	ABQ80025	Abq80025
55.0	36	8	ACC78362	Acc78362 Bag-1 DNA	C 946	11	55.0	51	3	AA77280	Aaa77280
55.0	37	3	AA71618	Aaa71618 Shuttle v	947	11	55.0	51	4	AAI31657	Aai31657
55.0	38	9	AD19639	Ad19639 Oreochrom	948	11	55.0	51	4	AAI30798	Aai30798
55.0	39	2	AAQ70222	AAq70222 HTLV1 pep	949	11	55.0	51	4	AAI76332	Aai76332
55.0	40	2	AA792660	Aat792660 BNLFI1 gen	950	11	55.0	51	4	AAI76786	Aai76786
55.0	40	6	AA227751	Aad227751 HPV3 wil	951	11	55.0	51	4	AAI75196	Aai75196
55.0	41	8	AC42033	Act42033 Aspergill	C 952	11	55.0	51	4	AAI76994	Aai76994
55.0	42	6	AAI41023	Aai41023 Sense PCR	C 953	11	55.0	51	4	AAI76995	Aai76995
55.0	42	8	ACC84885	Acc84885 S. antibi	954	11	55.0	51	4	AAI75197	Aai75197
55.0	43	6	ABZ49419	Abz49419 Human UDP	955	11	55.0	51	4	AAH79615	Aah79615
55.0	44	6	ABA01121	Ab01121 HBV prime	C 956	11	55.0	51	4	AAH80006	Aah80006
55.0	44	7	ABZ37310	Abz37310 URE adapt	C 957	11	55.0	51	5	ABL00588	Ab100588
55.0	44	7	ABZ37312	Abz37312 URE adapt	C 958	11	55.0	51	5	ABL00199	Ab100199
55.0	44	7	ABZ37309	Abz37309 URE adapt	C 959	11	55.0	52	5	AA84164	Aac84164
55.0	44	7	ABZ37319	Abz37319 URE adapt	960	11	55.0	52	7	ACD95182	Acd95182
55.0	44	7	ABZ37311	Abz37311 URE adapt	961	11	55.0	53	2	AAQ98133	Aaq98133
55.0	44	7	ABZ37321	Abz37321 URE adapt	C 962	11	55.0	53	7	ACD94369	Acd94369
55.0	44	7	ABZ37322	Abz37322 URE adapt	C 963	11	55.0	53	8	AA57536	Aad57536
55.0	44	7	ABZ37320	Abz37320 URE adapt	C 964	11	55.0	53	8	AA57540	Aad57540
55.0	44	7	ACC79259	Acc79259 Hepatitis	C 965	11	55.0	54	2	AAI9719	Aai9719
55.0	45	2	AAZ34026	Aaz34026 Human PRO	966	11	55.0	54	6	AAK99828	Aak99828
55.0	45	3	AA88529	Aaa88529 PRO540 hy	967	11	55.0	55	2	AAZ22253	Aaz22253
55.0	45	3	AA78702	Aac78702 Human PRO	968	11	55.0	57	6	ABK17232	Abk17232
55.0	45	4	AA91594	Aac91594 Human PRO	969	11	55.0	57	7	ACD93496	Acd93496
55.0	45	7	ACD42559	Acd42559 Novel hum	C 970	11	55.0	58	2	AAQ8076	Aaq8076
55.0	45	7	ACA63594	Aca63594 Novel hum	971	11	55.0	58	3	AAZ39001	Aaz39001
55.0	45	7			972	11	55.0	58	4	AA02515	Aad02515

55.0 58 4 AAD02507  
 55.0 58 5 AAH74651  
 55.0 58 6 AAS19340  
 55.0 58 6 AAL41026  
 55.0 59 2 AAV84664  
 55.0 60 6 ABN46615  
 55.0 60 6 ABN40542  
 55.0 60 6 ABN41690  
 55.0 60 6 ABN58812  
 55.0 60 6 ABN48282  
 55.0 60 6 ABN36290  
 55.0 60 6 ABN32535  
 55.0 60 6 ABN41141  
 55.0 60 6 ABN41378  
 55.0 60 6 ABN34235  
 55.0 60 6 ABN58555  
 55.0 60 6 ABN37680  
 55.0 60 6 ABN40893  
 55.0 60 6 ABN58749  
 55.0 60 6 ABN32303  
 55.0 60 6 ABN58956  
 55.0 60 6 ABN49924  
 55.0 60 6 ABN35175  
 55.0 60 6 ABN35938  
 55.0 60 6 ABN38311  
 55.0 60 6 ABN41092  
 55.0 60 6 ABN43683

## ALIGNMENTS

Standard; DNA; 20 BP.

2 (first entry)

PCR primer SEQ ID NO:7.

carcinoembryonic antigen; adenocarcinoma; oesophagus;  
 PCR primer; ss.

ss.

L-Al.

2.

2; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 the lung comprising conducting a PCR amplification on a DNA sample in  
 a mixture.

page 33; 141pp; English.

The invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 mixture in first and second amplification stages, each with one  
 or more cycles comprising denaturing, annealing and elongating steps  
 along with a step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is cond  
 CC different reaction conditions from that of the first amplifica  
 CC to modulate the relative rate of production of the first ampli  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) an  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of meta  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use i  
 CC automated PCR system. (M1) is useful for detecting malignancie  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio  
 CC decreases the time it takes to carry out a PCR reaction. The p  
 CC sequence represents a PCR primer for human CEA (carcinoembryon  
 CC antigen), which is used in an example from the present inventi  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 1 ATCCTGTGCTCCACGGGTT 20  
 |||||  
 Db 1 ATCCTGTGCTCCACGGGTT 20  
 |||||

## RESULT 2

ADE13859

ID ADE13859 standard; DNA; 47 BP.

XX AC ADE13859;

XX XX 29-JAN-2004 (first entry)

XX CEA(6D)-1,2 related oligonucleotide SEQ ID NO:22.

XX carcinoembryonic antigen; CEA; CEA(6D)-1; 2; cytostatic; vacci  
 KW tumour antigen; immunotherapy; ss.

XX Synthetic.

XX WO2003085087-A2.

XX PD 16-OCT-2003.

XX PF 09-APR-2003; 2003WO-US010916.

XX PR 09-APR-2002; 2002US-0372972P.

XX XX (AVET) AVENTIS PASTEUR LTD.

PA (THER-) THERION BIOLOGICS INC.

XX Parrington M, Zhang L, Rovinski B, Gritz LR, Greenhalgh T;

XX WPI; 2003-877029/81.

XX New isolated DNA molecule comprising the carcinoembryonic antic  
 PT 1,2 sequence, useful for diagnosing, preventing and treating ca  
 PT determining the effectiveness of a chemotherapeutic or other th  
 PT regimen.

XX Disclosure; SEQ ID NO 22; 56pp; English.

XX The present invention describes an isolated DNA molecule compri  
 CC carcinoembryonic antigen (CEA) (6D)-1,2 sequence of 2106 bp (se  
 CC ADE13861), or its fragment. Also described: (1) an expression v  
 CC comprising the nucleic acid sequence CEA(6D)-1,2, or its fragme  
 CC (1) in a pharmaceutical carrier; and (3) preventing or treating  
 CC comprising administering to a host the expression vector of (1)  
 CC 1,2 has cytostatic activity, and can be used in vaccines. The C  
 CC nucleic acid and target polypeptide are useful for diagnosing,  
 CC and treating cancer, predicting prognosis, or determining the  
 CC effectiveness of a chemotherapeutic or other treatment regimen.

vector may be used for the insertion and expression of CEA (6D) c acid encoding tumour antigens for the immunotherapeutic use of cancer. The target polypeptides are useful in generating used in screening assays or for immunotherapy. The present presents an oligonucleotide which is given in the tion of the present invention.

BP; 9 A; 16 C; 12 G; 10 T; 0 U; 0 Other;

ilarity 95.0%; Score 19; DB 9; Length 47;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CCTTGCTCCTCCACGGGT 19

CCTTGCTCCTCCACGGGT 47

andard; DNA; 17 BP.

(first entry)

onucleotide associated with tumour suppression, SEQ ID 1490.

viricide; neuroprotective; nootropic; neuroleptic; murine; resion; tumour reversion; apoptosis; virus resistance; se; tumour; cell degeneration; cancer; Alzheimer's disease; ia; ss.

S.

6-A2.

; 2002WO-IB004210.

; 2001FR-00011979.

ECULAR ENGINES LAB.

Amson R, Tuijnder M;

33167/31.

d nucleic acid, useful for treating viral diseases associated and cell degeneration, also related polypeptides, antibodies cted cells.

Page 205; 738pp; French.

invention relates to murine oligonucleotides (ACC62754- which are associated with tumour suppression, tumour apoptosis and virus resistance. The oligonucleotides are 1) as probes and primers for detecting, identifying, and/or amplifying nucleic acid, e.g. as one component of a in vitro as (anti)sense reagents; and (2) for production of polypeptides. The oligonucleotides are useful for preparation uicids for prevention and/or treatment of viral diseases that erised by development of tumours or cell degeneration, Y cancer but also Alzheimer's disease and schizophrenia

BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

ilarity 75.0%; Score 15; DB 7; Length 17;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CCTTGCTCCTCCAC 15

DB 2 ATCCTTGCTCCTCCAC 16

RESULT 4

ACI58088

ID ACI58088 standard; DNA; 25 BP.

XX

AC ACI58088;

XX 13-OCT-2003 (first entry)

XX

DE Human microarray DNA oligonucleotide SEQ ID NO 58079.

XX EST; ss; probe; expressed sequence tag; microarray; gene expres

KW genetic variation; biallelic marker; polymorphism; human;

KW cross-species comparison.

XX

OS Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567553/53.

XX New array of nucleic acid probes, useful for in situ hybridizat

PT Southern, Northern or dot-blot hybridization to identify or det

PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 58079; 9pp; English.

CC The invention discloses a microarray comprising a plurality of acid probes including one of 2,018,500 fully defined sequences, perfect match, perfect mismatch, antisense match or antisense m

CC Also disclosed is a method of gene expression analysis. The arr

CC in monitoring gene expression levels by hybridisation to a DNA

CC in analysis of genetic variation or in hybridisation of tag-lab

CC compounds. The nucleic acid probes are specifically designed fo

CC of at least one target sequence. The method of analysis compris

CC hybridising at least one or more nucleic acids to at least two

CC nucleic acid probes and detecting the hybridisation. The nuclei

CC probes are attached to a solid support. The analysis comprises

CC gene expression levels, identifying biallelic markers or polym

CC or family members of a gene and a cross-species comparison. Eac

CC nucleic acids further comprises a tag sequence. The array of nu

CC probes is useful in in situ hybridisation, in Southern, Norther

CC blot hybridisation to identify or detect the sequence or specif

CC mutations of any gene, in mapping the 5' termini of mRNA molecu

CC primer extensions or in screening cDNA or genomic libraries or

CC for additional subclones containing segments of DNA that have b

CC isolated and previously sequenced. The sequence presented is on

CC nucleic acid probes incorporated in the microarray. Note: The s

CC data for this patent can also be obtained in electronic format

CC from USPTO at seqdata.uspto.gov/sequence.html

XX

SQ Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 8; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 ATCCTTGCTCCTCCAC 15

3 ATCCTTGCTCCTCCAC 17

DB

XX SQ Sequence 20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 7; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
QY 1 ATCCTGTCTCCACGGG 18  
||||| ||||| |||||  
DB 3 ATCCTGTCTCCACGGG 20  
RESULT 6  
ACD02563/c  
ID ACD02563 standard; DNA; 20 BP.  
XX  
AC ACD02563;  
DT  
XX 31-JUL-2003 (first entry)  
XX  
DE Novel human zsig37 sequencing primer ZC13650.  
XX  
KW Blood flow; vasodilation; wound repair; platelet inhibition; t  
KW vascular occlusion; ischaemic reperfusion injury; microvascula  
KW adipocyte complement related protein; intestinal strangulation  
KW angioplasty; coronary artery bypass graft; endarterectomy; an  
KW anastomosis; stroke; cardiopulmonary bypass ischaemia; inflam  
KW myocardial infarction; percutaneous transluminal angioplasty;  
KW post-trauma vasospasm; prostatic biomaterial; fibroblast recu  
KW wound retraction; human; zsig37; primer; ss; sequencing; PCR.  
XX  
OS Homo sapiens.  
XX  
XX US2003022838-A1.  
XX  
PD 30-JAN-2003.  
XX  
XX 25-JUN-2002; 2002US-00180762.  
XX  
XX 19-FEB-1999; 99US-00253604.  
XX 22-NOV-1999; 99US-00444794.  
XX 17-FEB-2000; 2000US-00506855.  
XX 19-JUL-2000; 2000US-00619740.  
XX  
XX (SHEP/) SHEPPARD P O.  
XX (LASS/) LASSER G W.  
XX (BISH/) BISHOP P D.  
XX  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX  
XX WPI; 2003-456304/43.  
XX  
XX Promoting blood flow or inducing vasodilation within vasculat  
XX mammal, or pacifying damaged collagenous tissues or pacifying  
XX prostatic biomaterial, by administering adipocyte complement r  
XX protein.  
XX  
XX Example 1; Page 24; 46pp; English.  
XX  
XX The invention relates to a method of promoting blood flow or ir  
XX vasodilation within the vasculature of a mammal, pacifying dam  
XX collagenous tissues or surface of prostatic biomaterial, media  
XX repair, inhibiting platelet adhesion, activation or accretion,  
XX vascular occlusion, protecting ischaemic myocardium from reper  
XX injury or mediating tumour metastasis, comprising administering  
XX complement related protein. The method is useful for promoting  
XX within the vasculature of a mammal, where the mammal suffers fr  
XX vascular injury, where the injury is due to vascular reconstruct  
XX comprises angioplasty, coronary artery bypass graft, endartere  
XX microvascular repair or anastomosis of a vascular graft, or the  
XX due to trauma, stroke or aneurysm. The method is useful for pac  
XX damaged collagenous tissues within a mammal, where the damaged  
XX collagenous tissues are due to injury associated with ischaemic  
XX

standard; DNA; 20 BP.  
3 (first entry)  
SNP analysis PCR primer, #39.  
; primer; ss; asthma; bronchial hyperresponsiveness;  
; truction; chronic bronchial inflammation;  
rial disease; asthma-associated gene; AAGA; allele-specific;  
leotide polymorphism; SNP; genetic profile; gene therapy;  
gene therapy; adult distress respiratory syndrome;  
structive pulmonary; chronic bronchitis; dyspnea.  
as.  
40-A2.  
3.  
2; 2002WO-EP007847.  
1; 2001US-0305649P.  
VARTIS AG.  
VARTIS-ERFINDUNGEN VERW GES MEH.  
IV WAKE FOREST HEALTH SCI.  
JKSUNIV GRONINGEN.  
PA, Meyers DA, Postma DS, Blecker ER;  
239359/23.  
f whether a subject has or is at risk of developing a disease  
zed by bronchial hyperresponsiveness, comprises determining the  
or bioactivity level of an asthma-associated gene.  
Page 27; 70pp; English.  
ion discloses a method for determining a disease (e.g asthma)  
sed by bronchial hyperresponsiveness, or the risk of developing  
ay obstruction or chronic bronchial inflammation. Asthma is a  
rial disease, so discovery of the asthma susceptibility genes  
fy the fundamental mechanisms behind asthma. One such gene is  
-associated gene, AAGA. Also disclosed is an allele-specific  
lignucleotide probe capable of detecting a polymorphism, an  
ynucleotide, and encoded polypeptide, which is a variant o  
ated with bronchial hyperresponsiveness and methods for  
omically selecting a therapy to be administered to an  
having asthma, comprising determining an AAGA genetic profile  
ing the individual's genetic profile to an AAGA genetic  
profile, monitoring the effectiveness of treatment (e.g. gene  
antisense gene therapy) of a subject and identifying a  
which binds to or modulates the activity of AAGA. The  
ide, polypeptide encoded by it, antibody to the polypeptide,  
nucleotide, is useful for preparing a medicament for treating  
characterised by bronchial hyperresponsiveness, or inflammatory  
ive airways diseases, e.g. adult distress respiratory  
chronic obstructive pulmonary, chronic bronchitis or dyspnea.  
is useful for prognosing, diagnosing or confirming that a  
s subject has a genetic defect which causes or contributes to  
ilar disease or disorder, for ascertaining an individual's  
on to develop bronchial responsiveness and for customising a  
c the individual according to the individual's genetic profile.  
es presented in ABX98968-ABX99053 and ABX99064-ABX99066 are  
s which were used to amplify sequences used in human AAGA  
struction and primers used to analyse AAGA single nucleotide  
ms (SNPs)

The injury comprises trauma injury, ischaemia, intestinal an, or injury associated with pre- and post-establishment of The mammal suffers from cardiopulmonary bypass ischaemia and a, myocardial infarction, or post-trauma vasospasm. The post-spasm comprises stroke, percutaneous transluminal angioplasty, my, accidental vascular trauma or surgical-induced vascular method is useful for pacifying the surface of a prostatic for use in association with a mammal, where the surface of ic biomaterial is coated with collagen or collagen fragments, brin or fibronectin. The method is useful for mediating wound in a mammal, where the method enhances progression in wound progression in wound healing comprises reduction in a, reduction in fibroblast recruitment, wound retraction, or n infection. The method is useful for inhibiting platelet ctivation or accretion. The method is useful for minimising clusion by increasing patency time in a patient in need of the The method is useful for inducing vasodilation within the of a mammal. The method is useful for protecting ischemic from reperfusion injury. The method is useful for mediating stasis. The present sequence represents the human adipocyte related protein zsig37 DNA sequencing primer

BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

74.0%; Score 14.8; DB 7; Length 20;

ilarity 88.9%; Pred. No. 2.7e+03; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGTTT 20

|||||||

TTGTCTCTCCACGGTTT 3

andard; DNA; 20 BP.

(first entry)

zsig37 sequencing primer ZC13651.

vasodilation; wound repair; platelet inhibition; tumour; clusion; ischaemic reperfusion injury; microvascular repair; mplement related protein; intestinal strangulation; trauma; ; coronary artery bypass graft; endarterectomy; aneurysm; ; stroke; cardiopulmonary bypass ischaemia; inflammation; infarction; percutaneous transluminal angioplasty; infection; vasospasm; prostatic biomaterial; fibroblast recruitment; ction; human; zsig37; primer; ss; sequencing; PCR.

3.

1-A1.

2002US-00180762.

99US-00253604.

99US-00444794.

2000US-00506855.

2000US-00619740.

PPARD P O.

SER G W.

TOP P D.

Lasser GW, Bishop PD;

6304/43.

Promoting blood flow or inducing vasodilation within vasculatur mammal, or pacifying damaged collagenous tissues or pacifying s prostatic biomaterial, by administering adipocyte complement re protein.

Example 1; Page 23; 46pp; English.

The invention relates to a method of promoting blood flow or in vasodilation within the vasculature of a mammal, pacifying dama collagenous tissues or surface of prostatic biomaterial, mediat repair, inhibiting platelet adhesion, activation or accretion, vascular occlusion, protecting ischaemic myocardium from reper injury or mediating tumour metastasis, comprising administering complement related protein. The method is useful for promoting within the vasculature of a mammal, where the mammal suffers fr vascular injury, where the injury is due to vascular reconstruc comprises angioplasty, coronary artery bypass graft, endarterec microvascular repair or anastomosis of a vascular graft, or the due to trauma, stroke or aneurysm. The method is useful for pac damaged collagenous tissues within a mammal, where the damaged collagenous tissues are due to injury associated with ischaemia reperfusion. The injury comprises trauma injury, ischaemia, int strangulation, or injury associated with pre- and post-establis blood flow. The mammal suffers from cardiopulmonary bypass isch recesitation, myocardial infarction, or post-trauma vasospasm. trauma vasospasm comprises stroke, percutaneous transluminal an endarterectomy, accidental vascular trauma or surgical-induced trauma. The method is useful for pacifying the surface of a pro biomaterial for use in association with a mammal, where the sur the prostatic biomaterial is coated with collagen or collagen f gelatin, fibrin or fibronectin. The method is useful for mediat repair within a mammal, where the method enhances progression i healing and progression in wound healing comprises reduction i inflammation, reduction in fibroblast recruitment, wound retrac reduction in infection. The method is useful for inhibiting pia adhesion, activation or accretion. The method is useful for min vascular occlusion by increasing patency time in a patient in n treatment. The method is useful for inducing vasodilation withi vasculature of a mammal. The method is useful for protecting is myocardium from reperfusion injury. The method is useful for me tumour metastasis. The present sequence represents the human ad complement related protein zsig37 DNA sequencing primer

Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 7; Length 20;

Best Local Similarity 88.9%; Pred. No. 2.7e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCTCTCCACGGTTT 20

|||||||

Db 1 CTTTGTCTCTCCACGGTTT 18

RESULT 8

ABX04524/c

ID ABX04524 standard; DNA; 20 BP.

XX AC ABX04524;

XX DT 13-JAN-2003 (first entry)

XX DE Human adipose complement related protein zsig37 primer ZC13650.

XX KW Human; ss; primer; adipocyte complement related protein; zsig37;

chromosome 17q25.2; blood flow; vulnerable; antibacterial; vasot

anticoagulant; immunosuppressive; damaged collagenous tissue;

complement activation; thrombosis; trauma; ischaemia; reperfus

intestinal strangulation; cardiopulmonary bypass ischaemia;

myocardial infarction; post-trauma vasospasm; stroke;

percutaneous transluminal angioplasty; endarterectomy;

accidental vascular trauma; surgical-induced vascular trauma;

haemostasis; wound healing; antimicrobial.

ns.  
B1.  
2.  
0; 2000US-00506855.  
9; 99US-00253604.  
9; 99US-00444794.  
MOGENETICS INC.  
O, Lasser GW, Bishop PD;  
038245/03.  
blood flow within the vasculature of a mammal, comprises  
ing a pharmaceutical formulation comprising zsig37 proteins.  
Col 43; 39pp; English.  
ion relates to promoting blood flow within the vasculature of a  
prises administering to the mammal an amount of a  
ical formulation that comprises an adipocyte complement related  
sig37, having residues 26-281 of a sequence appearing as  
Also included is a method of pacifying damaged collagenous  
thin a mammal, comprising administering to the mammal an amount  
rnaceutical formulation cited above, which achieves  
on of the damaged collagenous tissues by inhibiting complement  
or by reducing thrombosis formation. The method is useful in  
blood flow within the vasculature of a mammal by reducing  
ic and complement activity, and in pacifying damaged  
s surfaces (e.g. in trauma, ischaemia, reperfusion, intestinal  
ion, cardiopulmonary bypass ischaemia, myocardial infarction,  
a vasospasm, stroke, percutaneous transluminal angioplasty,  
omy, accidental vascular trauma or surgical- induced vascular  
re zsig37 polypeptide, polynucleotide, and an anti-zsig37  
re useful as inhibitors of haemostasis and immune function, in  
wound healing, and for antimicrobial applications. The human  
sig37 is located on chromosome 17q25.2. The present sequence is  
sed to sequence cDNA encoding zsig37  
J BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
nilarity 74.0%; Score 14.8; DB 7; Length 20;  
Conservative 88.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTGTCTCTCCACGGGTT 20  
|||||  
TTGTCTCTCCACGGGTT 3  
-andard; DNA; 20 BP.  
3 (first entry)  
see complement related protein zsig37 primer ZC13651.  
primer; adipocyte complement related protein; zsig37;  
17q25.2; blood flow; vulnery; antibacterial; vasotropic;  
ant; immunosuppressive; damaged collagenous tissue;  
activation; thrombosis; trauma; ischaemia; reperfusion;  
strangulation; cardiopulmonary bypass ischaemia;  
infarction; post-trauma vasospasm; stroke;  
as transluminal angioplasty; endarterectomy;  
vascular trauma; surgical-induced vascular trauma;  
KW haemostasis; wound healing; antimicrobial.  
XX Homo sapiens.  
XX US6448221-B1.  
XX 10-SEP-2002.  
XX 17-FEB-2000; 2000US-00506855.  
XX 19-FEB-1999; 99US-00253604.  
XX 22-NOV-1999; 99US-00444794.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX WPI; 2003-038245/03.  
XX Promoting blood flow within the vasculature of a mammal, compr  
PT administering a pharmaceutical formulation comprising zsig37 p  
XX Example 1; Col 43; 39pp; English.  
XX The invention relates to promoting blood flow within the vascu  
CC mammal, comprises administering to the mammal an amount of a  
CC pharmaceutical formulation that comprises an adipocyte complem  
CC protein, zsig37, having residues 26-281 of a sequence appearin  
CC ABG99070. Also included is a method of pacifying damaged colla  
CC tissues within a mammal, comprising administering to the mamma  
CC of the pharmaceutical formulation cited above, which achieves  
CC pacification of the damaged collagenous tissues by inhibiting  
CC activation or by reducing thrombosis formation. The method is  
CC promoting blood flow within the vasculature of a mammal by red  
CC thrombogenic and complement activity, and in pacifying damaged  
CC collagenous surfaces (e.g. in trauma, ischaemia, reperfusion,  
CC strangulation, cardiopulmonary bypass ischaemia, myocardial in  
CC post-trauma vasospasm, stroke, percutaneous transluminal angio  
CC endarterectomy, accidental vascular trauma or surgical- induce  
CC trauma). The zsig37 polypeptide, polynucleotide, and an anti-z  
CC antibody are useful as inhibitors of haemostasis and immune fu  
CC modulating wound healing, and for antimicrobial applications.  
CC Gene for zsig37 is located on chromosome 17q25.2. The present  
CC a primer used to sequence cDNA encoding zsig37  
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 7; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
QY 3 CTTGTCTCTCCACGGGTT 20  
Db 1 CTTGTCTCTCCACGGGTT 18  
RESULT 10  
ADCO1943/c  
ID ADC01943 standard; DNA; 20 BP.  
XX ADC01943;  
XX 18-DEC-2003 (first entry)  
XX Human zsig37 cDNA sequencing primer #11.  
XX Human; zsig37; ss; chromosome 17q25.2; vascular occlusion; vasc  
KW adipocyte complement related protein; vascular injury;  
KW vascular reconstruction; trauma; stroke; aneurysm; plaque rupt  
KW vasculature; diabetes; atherosclerosis; blood flow; vasorelaxa  
KW tranquiliser; vulnery; cerebroprotective; antiatherosclerotic  
KW sequencing; primer.

35.  
31.  
3.  
); 2000US-00619740.  
); 99US-00253604.  
); 99US-00444794.  
); 2000US-00506855.  
MOGENETICS INC.  
); Lasser GW, Bishop PD;  
'07011/67.  
vascular occlusion or inducing vasodilation within the  
of a mammal, by administering an adipocyte complement related  
protein, zsig37 that promotes blood flow.  
SEQ ID NO 15; 44pp; English.  
on relates to a method for minimising vascular occlusion or  
inducing vasodilation within a mammal, involving administering a  
formulation comprising an adipocyte complement related protein, zsig37.  
The method is useful for minimising vascular occlusion and inducing  
vasodilation in a mammal suffering from acute vascular injury which may  
be due to plaque rupture, trauma, stroke or aneurysm. The  
vascular injury is due to plaque rupture, degradation of the v  
complications associated with diabetes and atherosclerosis.  
Administration of the formulation promotes blood flow or elicit  
vasorelaxant response. This sequence represents a primer used to  
sequence the human zsig37 polypeptide of the invention.  
BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
74.0%; Score 14.8; DB 9; Length 20;  
Similarity 88.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 2; Indels 0;  
Gaps 0;  
TTGTCTCTCCACGGGTT 20  
TTGTCTCTCCACGGGTT 3  
andard; DNA; 20 BP.  
(first entry)  
7 cDNA sequencing primer #8.  
37; ss; chromosome 17q25.2; vascular occlusion; vasodilation;  
complement related protein; vascular injury;  
construction; trauma; stroke; aneurysm; plaque rupture;  
diabetes; atherosclerosis; blood flow; vasorelaxant;  
x; vulnary; cerebroprotective; antiatherosclerotic;  
primer.  
s.  
1.  
); 2000US-00619740.  
); 99US-00253604.

PR 22-NOV-1999; 99US-00444794.  
PR 17-FEB-2000; 2000US-00506855.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX WPI; 2003-707011/67.  
XX Minimizing vascular occlusion or inducing vasodilation within  
PT vasculature of a mammal, by administering an adipocyte comple  
PT protein, zsig37 that promotes blood flow.  
XX Example 1; SEQ ID NO 12; 44pp; English.  
XX The invention relates to a method for minimising vascular occl  
CC inducing vasodilation within a mammal, involving administering  
CC formulation comprising an adipocyte complement related protein  
CC The method is useful for minimising vascular occlusion and ind  
CC vasodilation in a mammal suffering from acute vascular injury  
CC be due to vascular reconstruction, trauma, stroke or aneurysm.  
CC vascular injury is due to plaque rupture, degradation of the v  
CC complications associated with diabetes and atherosclerosis.  
CC Administration of the formulation promotes blood flow or elicit  
CC vasorelaxant response. This sequence represents a primer used  
CC cDNA encoding the human zsig37 polypeptide of the invention.  
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;  
SQ Query Match 74.0%; Score 14.8; DB 9; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
Oy 3 CCTGTCTCTCCACGGGTT 20  
Db 1 CTTGTCTCTCCACGGGTT 18  
RESULT 12  
AAD59886  
ID AAD59886 standard; DNA; 20 BP.  
XX AAD59886;  
AC AAD59886;  
XX 18-DEC-2003 (first entry)  
DT 18-DEC-2003 (first entry)  
XX ZC13651 oligo used to identify human zsig37 DNA.  
KW Adipocyte complement related protein; collagenous surface pacif  
KW wound healing; tumour metastasis; gene therapy; thrombogenic; f  
KW Acip; zsig37; ss.  
XX Homo sapiens.  
XX US2003144208-A1.  
XX 31-JUL-2003.  
XX 07-FEB-2003; 2003US-00360186.  
XX 19-FEB-1999; 99US-00253604.  
PR 22-NOV-1999; 99US-00444794.  
PR 17-FEB-2000; 2000US-00506855.  
PR 19-JUL-2000; 2000US-00619740.  
XX (SHEP/) SHEPPARD P O.  
PA (LASS/) LASSER G W.  
PA (BISH/) BISHOP P D.  
XX Sheppard PO, Lasser GW, Bishop PD;  
WPI; 2003-755532/71.  
XX

blood flow within the vasculature of a mammal, comprising an adipocyte complement related protein to reduce blood flow and complement activity within the vasculature.

Page 24; 48pp; English.

ion relates to a method of promoting blood flow within the vasculature of a mammal. The method involves administering an adipocyte complement related protein (Acpr) to the mammal to reduce thrombogenic activity within the vasculature. Methods and compositions are useful in promoting blood flow within the vasculature of a mammal, in pacifying collagenous surfaces, in modulating blood flow or mediating tumour metastasis. The invention is also directed to a gene therapy. The present sequence is an oligo used to identify an adipocyte complement related protein homologue (zsig37) DNA

20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Similarity 74.0%; Score 14.8; DB 9; Length 20;

Conservative 88.9%; Pred. No. 2.7e+03; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20

TTGTCTCTCCACGGTT 18

Standard; DNA; 20 BP.

3 (first entry)

Oligo used to identify human zsig37 DNA.

complement related protein; collagenous surface pacification; gene therapy; tumour metastasis; gene therapy; thrombogenic; human; 37; ss.

ss.

38-A1.

3.

3; 2003US-00360186.

3; 99US-00253604.

3; 99US-00444794.

3; 2000US-00506855.

3; 2000US-00619740.

3PPARD P O.

3SER G W.

3SHOP F D.

3; Lasser GW, Bishop PD;

755532/71.

blood flow within the vasculature of a mammal, comprising an adipocyte complement related protein to reduce blood flow and complement activity within the vasculature.

Page 24; 48pp; English.

ion relates to a method of promoting blood flow within the vasculature of a mammal. The method involves administering an adipocyte complement related protein (Acpr) to the mammal to reduce thrombogenic activity within the vasculature. Methods and compositions are useful in promoting blood flow within the

CC vasculature of a mammal, in pacifying collagenous surfaces, in  
CC wound healing or mediating tumour metastasis. The invention is  
CC useful in gene therapy. The present sequence is an oligo used  
CC human adipocyte complement related protein homologue (zsig37)

XX Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match

Best Local Similarity 74.0%; Score 14.8; DB 9; Length 20;

Matches 16; Conservative 88.9%; Pred. No. 2.7e+03;

Indels 0;

QY 3 CTTGTCTCTCCACGGTT 20

DB 20 CTTGTCTCTCCACGGTT 3

RESULT 14

ACK19038

ID ACK19038 standard; DNA; 25 BP.

XX ACK19038;

XX ACK19038;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 119019.

XX EST; ss; probe; expressed sequence tag; microarray; gene expres  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

OS Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization  
PT Southern, Northern or dot-blot hybridization to identify or del  
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 119019; 9pp; English.

CC The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense  
CC Also disclosed is a method of gene expression analysis. The ar  
CC in monitoring gene expression levels by hybridisation to a DNA  
CC in analysis of genetic variation or in hybridisation of tag-lab  
CC compounds. The nucleic acid probes are specifically designed fo  
CC of at least one target sequence. The method of analysis compris  
CC hybridising at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridisation. The nucle  
CC probes are attached to a solid support. The analysis compris  
CC gene expression levels, identifying biallelic markers or polym  
CC or family members of a gene and a cross-species comparison. Ea  
CC nucleic acids further comprises a tag sequence. The array of n  
CC probes is useful in in situ hybridisation, in Southern, Northern  
CC blot hybridisation to identify or detect the sequence or specifi  
CC mutations of any gene, in mapping the 5' termini of mRNA molec  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b  
CC isolated and previously sequenced. The sequence presented is or  
CC nucleic acid probes incorporated in the microarray. Note: The i



his patent can also be obtained in electronic format directly at seqdata.uspto.gov/sequence.html

BP; 1 A; 7 C; 7 G; 10 T; 0 U; 0 Other;

ilarity 74.0%; Score 14.8; DB 8; Length 25;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTGCTCTCCACGGT 19  
||||| |||||  
CTGTGCTCTCCACGGT 24

andard; DNA; 38 BP.

(first entry)

3 cDNA PCR forward primer ZnRING.

-3; tumour necrosis factor receptor-associated factor 3;  
AF-3; delta221 TRAF-3; immunosuppressive; antiarthritic;  
cal; antiinflammatory; antianaemic; antipsoriatic;  
c; antithyroid; antitumour; anti-HIV; antibacterial;  
ophthalmological; antiallergic; antiatherosclerotic;  
neuroprotective; haemostatic; CD40 signalling inhibitor;  
y; necrosis factor kappaB activator; autoimmune disease;  
disease; allergy; PCR primer; ss.

S.

-Al.

; 200WO-US006503.

; 99US-00268544.

V COLUMBIA NEW YORK.

Van Eynhoven W;

87425/55.

necrosis factor (TNF) receptor-associated factor deletion  
r identifying an agent that inhibits CD-40 mediated cellular  
od for inhibiting e.g. rheumatoid arthritis and diabetes

Page 166; 170pp; English.

sequence is a PCR primer which was used in the isolation and  
ation of tumour necrosis factor receptor (TNF)-associated  
RAF-3) cDNA clones from the D1.1 Jurkat T cell line. TRAF-3  
cluding delta130 and delta221 TRAF-3 deletion isoforms, are  
inhibiting activation of a CD40 ligand on a wide range of  
ing B cells, fibroblasts, endothelial cells, epithelial  
ls, basophils, macrophages, Reed-Steinberg cells, dendritic  
l cells or smooth muscle cells expressing CD40 on the cell  
e proteins are also useful for treating conditions associated  
iated intracellular signalling, such as organ rejection as a  
ransplantation or an immune response after receiving gene  
may be useful for treating an CD40-dependent immune response  
suffering from an autoimmune disease such as rheumatoid  
myasthenia gravis, systemic lupus erythematosus, Grave's  
topathic thrombocytopenia purpura, haemolytic anaemia,  
litis, a drug-induced autoimmune disease (drug-induced  
iasis or hyper immunoglobulin (Ig)E syndrome. The proteins

CC may also be used to treat an immune response associated with a  
CC infectious disease such as Reiter's syndrome, spondyloarthritis  
CC disease, human immunodeficiency virus (HIV) infection, syphilis  
CC tuberculosis. They may be used to treat an allergic response,  
CC atherosclerosis, reperfusion injury and chronic inflammatory a  
CC diseases such as vasculitis, scleroderma or multiple sclerosis  
XX

SQ Sequence 38 BP; 11 A; 9 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 4.2e-03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCCTGTCTCTCCACGG 17  
||||| |||||  
DB 32 TACTTGCTCTCCACGG 17

RESULT 16

AAA95963/c

ID AAA95963 standard; DNA; 38 BP.

XX AC AAA95963;

XX 19-JAN-2001 (first entry)

1.8 kb TRAF-3 cDNA forward primer 5'CRAF-EST2(186).F.

Human; TRAF-3; tumour necrosis factor receptor-associated facto  
delta130 TRAF-3; delta221 TRAF-3; immunosuppressive; antiarthr  
dermatological; antiinflammatory; antianaemic; antipsoriatic;  
antidiabetic; antithyroid; antitumour; anti-HIV; antibacterial;  
uropathic; ophthalmological; antiallergic; antiatherosclerotic;  
vasotropic; neuroprotective; haemostatic; CD40 signalling inhib  
gene therapy; necrosis factor kappaB activator; autoimmune dise  
infectious disease; allergy; 3'-RACE primer; ss.

XX OS Homo sapiens.

XX PN WO2000053629-A1.

XX PD 14-SEP-2000.

XX PF 10-MAR-2000; 2000WO-US006503.

XX PR 11-MAR-1999; 99US-00268544.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Lederman S, Van Eynhoven W;

XX DR WPI; 2000-587425/55.

PT Novel tumor necrosis factor (TNF) receptor-associated factor de  
PT isoforms for identifying an agent that inhibits CD-40 mediated  
PT signaling and for inhibiting e.g. rheumatoid arthritis and diab  
PT mellitus.

XX Example 2; Page 59; 170pp; English.

CC The present sequence is a primer which was used to generate a 1  
CC tumour necrosis factor receptor (TNF)-associated factor 3 (TRAF  
CC clone by 3'-RACE. TRAF-3 isoforms, including delta130 and delta  
CC deletion isoforms, are useful for inhibiting activation of a CD  
CC on a wide range of cells including B cells, fibroblasts, endothe  
CC cells, epithelial cells, T cells, basophils, macrophages, Reed-  
CC cells, dendritic cells, renal cells or smooth muscle cells expri  
CC CD40 on the cell surface. The proteins are also useful for treat  
CC conditions associated with CD40-mediated intracellular signalin  
CC as organ rejection as a result of transplantation or an immune  
CC after receiving gene therapy. It may be useful for treating an (c  
CC dependent immune response in patients suffering from an autoimmu  
CC disease such as rheumatoid arthritis, myasthenia gravis, system:

mus, Grave's disease, idiopathic thrombocytopenia purpura, anaemia, diabetes mellitus, a drug-induced autoimmune disease (lupus), psoriasis or hyper immunoglobulin (Ig)E syndrome. ns may also be used to treat an immune response associated with disease such as Reiter's syndrome, spondyloarthritis, Lyme disease, immunodeficiency virus (HIV) infection, syphilis or is. They may be used to treat an allergic response, rosis, reperfusion injury and chronic inflammatory autoimmune uch as vasculitis, scleroderma or multiple sclerosis

8 BP; 11 A; 8 C; 13 G; 6 T; 0 U; 0 Other;

72.0%; Score 14.4; DB 3; Length 38;

milarity 93.8%; Pred. No. 4.2e+03; Length 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTGTCTCTCCACGG 17

ACTGTCTCTCCACGG 17

-andard; DNA; 25 BP.

1 (first entry)

array DNA oligonucleotide SEQ ID NO 76558.

robe; expressed sequence tag; microarray; gene expression; iation; biallelic marker; polymorphism; human; es comparison.

is.

.0-A1.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

;

.67953/53.

of nucleic acid probes, useful for in situ hybridization, in northern or dot-blot hybridization to identify or detect the specific mutations of any gene.

Q ID NO 76558; 9pp; English.

on discloses a microarray comprising a plurality of nucleic including one of 2,018,500 fully defined sequences, or its ch, perfect mismatch, antisense match or antisense mismatch. sed is a method of gene expression analysis. The array is used ng gene expression levels by hybridisation to a DNA library, of genetic variation or in hybridisation of tag-labelled The nucleic acid probes are specifically designed for analysis one target sequence. The method of analysis comprises at least one or more nucleic acids to at least two or more d probes and detecting the hybridisation. The nucleic acid ion levels, identifying biallelic markers or polymorphisms, members of a gene and a cross-species comparison. Each of the ds further comprises a tag sequence. The array of nucleic acid seful in in situ hybridisation, in Southern, Northern or dot- isation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molec CC primer extensions or in screening cDNA or genomic libraries or CC for additional subclones containing segments of DNA that have CC isolated and previously sequenced. The sequence presented is o CC nucleic acid probes incorporated in the microarray. Note: The CC data for this patent can also be obtained in electronic format CC from USPTO at segdata.uspto.gov/sequence.html

XX Sequence 25 BP; 8 A; 7 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 25;

Best Local Similarity 84.2%; Pred. No. 5.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTCTCTCCACGGTT 20

Db 25 TCCGTCTCTCCACGGCTT 7

RESULT 18

AAF84148

ID AAF84148 standard; DNA; 36 BP.

XX AAF84148;

XX 07-SEP-2001 (first entry)

Human novel betal-like subunit cDNA amplifying 3' primer SCNIB

XX Sodium channel; sensory neurone specific channel; betal-like s

KW SNS; therapeutic; pain; analgesic; PCR primer; ss.

XX Homo sapiens.

XX WO200144293-A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 2000WO-GB004802.

XX 17-DEC-1999; 99GB-00029970.

XX (GLAX ) GLAXO GROUP LTD.

XX Plumpton M, Powell AJ, Sanseau P;

XX WPI; 2001-398-29/42.

XX Novel sub-unit for voltage-gated sodium channel proteins for pr

XX agents useful for treating pain.

XX Example; Page 8; 31pp; English.

XX The invention provides a novel betal-like sub-unit for voltage-

XX sodium ion channel polypeptide, specifically a sensory neurone

XX channel (SNS) subunit. The novel betal-like subunit is useful f

XX producing a therapeutic agent which is useful treating pain in

XX The subunit can be expressed by standard recombinant methodolog

XX Sequences AAF84147-48 represent PCR primers for amplifying the

XX novel sodium channel betal-like subunit cDNA fragment

XX Sequence 36 BP; 6 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

Query Match

71.0%; Score 14.2; DB 4; Length 36;

Best Local Similarity 84.2%; Pred. No. 5.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0;

Qy 1 ATCCTTCTCTCCACGGTT 19

Db 6 ATCCTTCTCTCCACGGTT 24

RESULT 19

standard; DNA; 33 BP.

(revised)  
(first entry)

probe CMV.GB.20.

ure; amplifier; hybridisation; assay; detection; CMV;  
irus; solution phase; comb-type branched polynucleotide;  
extension; binding site; ligation; template; linker; ss.

1.

; 92WO-US011170.

; 91US-00813590.

RON CORP.

Shen L, Urdea MS;

27341/28.

for detection of cytomegalovirus - in a solution phase  
oridisation assay.

pe 63; 71pp; English.

amplified soln. phase nucleic acid sandwich hybridisation  
ys two multimers: (1) an amplifier probe having a first  
that binds to CMV and a second segment (B\*) that hybridises to  
lifier multimer having a first segment (B\*) that hybridises to  
(B) and fifteen iterations of a segment (C), wherein segment  
s to three labeled oligonucleotides. CMV amplifier probes are  
345840-74. CMV capture probes are given in AAQ45875-84. Each  
robe contained, in addition to the sequences complementary to a  
ences, the 5' extension given in AAQ45885, complementary to a  
he amplifier multimer. Each capture probe contained, in  
the sequences complementary to the CMV sequences, a  
sequence given in AAQ45886, complementary to the DNA bound to  
ase. (Updated on 25-MAR-2003 to correct PN field.)

BP; 5 A; 11 C; 8 G; 7 T; 0 U; 2 Other;

larity 70.0%; Score 14; DB 2; Length 33;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TGTCCTCCAG 16

|||||

TGTCCTCCAG 31

standard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 54313.

be; expressed sequence tag; microarray; gene expression;  
ation; biallelic marker; polymorphism; human;  
s comparison.

XX Homo sapiens.  
OS US2003104410-A1.  
PN 05-JUN-2003.  
PD 15-MAR-2002; 2002US-00098263.  
XX 16-MAR-2001; 2001US-0276759P.  
PF (AFFY-) AFFYMETRIX INC.  
PR Mittmann MP;  
XX WPI; 2003-567953/53.  
XX New array of nucleic acid probes, useful for in situ hybridizat  
Southern, Northern or dot-blot hybridization to identify or det  
sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 54313; 9pp; English.

The invention discloses a microarray comprising a plurality of  
acid probes including one of 2,018,500 fully defined sequences,  
perfect match, perfect mismatch, antisense match or antisense m  
Also disclosed is a method of gene expression analysis. The arr  
in monitoring gene expression levels by hybridisation to a DNA  
in analysis of genetic variation or in hybridisation of tag-lab  
compounds. The nucleic acid probes are specifically designed fo  
of at least one target sequence. The method of analysis compris  
hybridising at least one or more nucleic acids to at least two  
nucleic acid probes and detecting the hybridisation. The nuclei  
probes are attached to a solid support. The analysis comprises  
gene expression levels, identifying biallelic markers or polymo  
or family members of a gene and a cross-species comparison. Eac  
nucleic acids further comprises a tag sequence. The array of nu  
probes is useful in situ hybridisation, in Southern, Northern  
blot hybridisation to identify or detect the sequence or specifi  
mutations of any gene, in mapping the 5' termini of mRNA molecu  
primer extensions or in screening cDNA or genomic libraries or  
for additional subclones containing segments of DNA that have b  
isolated and previously sequenced. The sequence presented is on  
nucleic acid probes incorporated in the microarray. Note: The s  
data for this patent can also be obtained in electronic format  
from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 1 A; 8 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 8; Length 25;

Best Local Similarity 88.2%; Pred. No. 7.9e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTGTCTCCACGGT 20

Db 1 CTGTCTCCACGGT 17

RESULT 21

ABN35794

ID ABN35794 standard; DNA; 60 BP.

XX ABN35794;

AC XX

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:854

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS

XX

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

257383/30.

ucleotide libraries comprising oligonucleotides which  
y hybridize to mRNAs transcribed from a transcription unit of a  
eul for detecting tissue-, pathology-, and developmental-  
enes.

SEQ ID NO 8542; 47pp; English.

t invention describes oligonucleotide libraries for detecting  
RNAs that populate a (sub-)transcriptome, where the (sub-  
ome comprises messenger RNAs transcribed from multiple  
ion units that populate a genome. The library comprises several  
ptides, each capable of hybridising selectively to a set of  
RNAs transcribed from a given transcription unit of the genome,  
les one or more messenger RNA splice variants. The  
ptide libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
rely characterising the corresponding transcriptome, and in  
RNA transcripts and splice variants of human or animal  
mes. The libraries may also be used as specialised mini  
:o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
ology-specific genes such as those genes only expressed in  
issue under a specific pathological condition; to detect  
:al specific genes; and to detect RNA transcripts and splice  
: a transcriptome of a patient suffering from a particular  
ABN2753 to ABN59589 represent oligonucleotide sequences from  
s and mice, which are used in the exemplification of the  
ention N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

) BP; 11 A; 22 C; 7 G; 20 T; 0 U; 0 Other;

69.0%; Score 13.8; DB 6; Length 60;

ilarity 88.2%; Pred. No. 8.2e+03;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTGTGCTCCACGG 17

|||||

CCTGTGCTCTCTGG 36

andard; DNA; 24 BP.

) (first entry)

rotein primer 2.

immunogenic; active immunization; primer; ss.

.lomavirus.

v2.

XX 04-NOV-1999.  
PD  
XX 30-APR-1999; 99WO-DE001331.  
PF  
XX 30-APR-1998; 98DE-01019476.  
PR  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA  
XX Gissmann L, Jochmus I;  
PI  
XX WPI; 2000-023362/02.  
DR  
XX Immunogenic protein with altered biological function, useful f  
immunization.  
PT  
XX Example 1; Page 28; 33pp; German.  
PS  
XX This invention describes the construction of a novel polypepti  
CC immunogenic and altered biological function of a protein, wher  
CC polypeptide has regions of the protein of about 10-40 amino ac  
CC different order. The polypeptide, or its DNA, is useful for ac  
CC immunization without cross-reactivity and problems associated  
CC biological function of the protein. AAZ24131-ZZ4143 represent  
CC used in the construction of the peptides of the invention  
XX Sequence 24 BP; 10 A; 3 C; 10 G; 1 T; 0 U; 0 Other;  
SQ  
Query Match 68.0%; Score 13.6; DB 3; Length 24;  
Best Local Similarity 80.0%; Pred. No. 9.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;  
QY 1 ATCCTGTGCTCCACGGTT 20  
|||||  
Db 21 ATCCTGCTCTCTGGTT 2  
|||||  
RESULT 23  
AAK99483/c  
ID AAK99483 standard; DNA; 24 BP.  
XX  
AC AAK99483;  
XX  
DT 27-JUN-2002 (first entry)  
XX  
DE Lipophilin C cDNA sense PCR primer P14.  
XX  
KW Immunogenic epitope; hormonally regulated organ; malignant tum  
KW Lipophilin; human; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1..24  
FT /\*tag= a  
FT /bound moiety= "Lipophilin C cDNA nucleotides 1  
FT /note= "Bound to nucleotides 107-130 of Lipophi  
XX  
PN US2002034739-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 07-JUL-1998; 98US-00110716.  
XX  
PR 07-JUL-1998; 98US-00110716.  
XX  
PA (LEHR/) LEHRER R I.  
PA (ZHAO/) ZHAO C.  
PA (GLAS/) GLASGOW B J.  
XX  
PI Lehrer RI, Zhao C, Glasgow BJ;  
XX WPI; 2002-338922/37.  
DR

ving the sequence of human lipophilin A, B and C are with carcinomas of hormonally regulated organs and are useful nosis and prognosis of various cancers.

Fig 3; 22pp; English.

on relates to a peptide comprising the amino acid sequences of hlin A, B, or C or its allelic variant or fragment comprising e immunogenic epitope, which is purified and isolated, and may terminal acylated and/or C-terminal amidated or be a fusion lecles of the invention are used in the diagnosis and f malignant tumours associated with hormonally regulated as uterus, ovary, prostate, testis, breast, kidney and s polynucleotide sequence represents a PCR primer of c DNA of the invention

BP; 8 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

ilarity 68.0%; Score 13.6; DB 6; Length 24;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCTGTCCTCCACGGGTT 20

|||||  
CCATGTCCTCCACGGAGTT 2

andard; DNA; 24 BP.

(first entry)

peptide-related coding sequence #2.

de; human; central nervous system disorder; disorder; heart disease; kidney disease; urinary disease;

S.

Location/Qualifiers

1..24

/\*tag= a

/partial

/product= "Novel human peptide-related peptide #2"

/note= "No start or stop codon given"

6-Al.

; 2003WO-JP0000597.

; 2002JP-00017591.

; 2002JP-00107045.

EDA CHEM IND LTD.

90 T, Murakami Y, Miyajima N;

18362/58.

46724.

de for screening for treatments for central nervous system ulatory, heart, kidney and urinary disorders.

ge 104; 124pp; Japanese.

on comprises the amino acid and coding sequence of a novel

CC human peptide. The human peptide of the invention is useful for  
CC central nervous system disorders, circulatory disorders, heart  
CC kidney disease and urinary disease. The present DNA sequence er  
CC human peptide of the invention.

XX Sequence 24 BP; 8 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 9; Length 24;

Best Local Similarity 80.0%; Pred. No. 9.7e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

Qy 1 ATCCTTCCTCCACGGGTT 20

|||||  
22 ATCCTTCCTCCACTAGCT 3

RESULT 25

ABX90062/c

ID ABX90062 standard; DNA; 30 BP.

XX AC ABX90062;

XX DT 30-APR-2003 (first entry)

XX S. aureus detecting microarray probe #49.

DE Probe; detection; genotyping; cell status; chromosomal resistan  
XX array; ss.

XX OS Staphylococcus aureus.

XX PN DE10117857-Al.

XX PD 24-OCT-2002.

XX PF 10-APR-2001; 2001DE-01017857.

XX PR 10-APR-2001; 2001DE-01017857.

XX PA (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.

XX PI Ellinger T, Ehrlich R, Wagenhaus A, Ermantraut E;

XX DR WPI; 2003-069801/07.

XX PT Detecting specific interactions between molecular targets and p  
XX useful for determining genotypic and physiological status of ce  
XX attaching an adaptable adapter to the target.

XX Example 3; Page 17; 25pp; German.

XX This invention describes a novel method for detecting the speci  
XX interaction between a target sequence, especially a nucleic aci  
XX probe on an array, in which adapter molecules are fixed to the  
XX forming a continuous sequence. Labelling of the target is indep  
XX mediated by interaction of the adapter molecule with a label. T  
XX is used to investigate the genotypic and physiological status o  
XX e.g. to detect chromosomal resistance genes in Staphylococcus a  
XX method provides a modular, specific and sensitive system for qu  
XX or qualitative detection of a specific target. It provides effi  
XX homogeneous and parallel labeling of a target, before, during o  
XX interaction with the probe array, and both DNA and RNA can be l  
XX The detection signal may be amplified and only low concentratio  
XX label (particularly 0.1-1 micro M) are used, so non-specific si  
XX minimised. ABX9954-ABX90005 & ABX90014-ABX90082 represent prob  
XX the method described in the disclosure of the invention

XX Sequence 30 BP; 12 A; 2 C; 13 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 7; Length 30;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

CCCTGTCTCTCCACGGGTT 20  
|||||  
CCCTGTCTCTCCACGGT 5

standard; DNA; 32 BP.

(first entry)

protegerin gene 3' Bam HI PCR primer.

oprotegerin; OPG; osteopathic; cytostatic; gene therapy;  
genesis inhibition; multiple myeloma; Paget's disease;  
osteoporosis; secondary osteopetrosis; osteopaenia;  
hyperparathyroidism; PCR primer; ss.

is.

9-A1.

2000WO-US023755.  
99US-0151415P.

FOUND MEDICAL EDUCATION RES.

Riggs BL, Khosla S, Russel ST;

65890/27.

or preventing osteoclastic overactivity in a mammal, involves  
pluripotent mammalian cells genetically altered with a  
d molecule encoding osteoprotegerin.

Page 32; 73pp; English.

sequence was used to amplify the osteoprotegerin (OPG) gene  
in example illustrating an invention relating to a method for  
or preventing osteoclastic overactivity in a mammal. The  
olives contacting pluripotent mammalian cells with a composition  
a nucleic acid molecule encoding osteoprotegerin, its variant  
ally active fragment to yield genetically altered mammalian  
introducing the cells into the mammal to alter  
genesis. The composition is useful for inhibiting or  
osteoclastic overactivity in a mammal having multiple myeloma,  
metastatic lesions, hypercalcaemia, involutional osteoporosis,  
osteopetrosis, Paget's disease, refractory hyperparathyroidism  
nia, especially osteolytic lesions, and for introducing  
nucleic acid into unfractionated bone marrow cells of a mammal

BP; 6 A; 9 C; 8 G; 9 T; 0 U; 0 Other;

68.0%; Score 13.6; DB 5; Length 32;  
similarity 80.0%; Pred. No. 9.8e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCCTGTCTCTCCACGGGTT 20  
|||||  
CCCTATATCATCCATGGGAT 28

standard; DNA; 20 BP.

DT 16-APR-2003 (first entry)  
XX  
DE Multiplex group PCR primer #186.  
XX  
KW Racing potential; horse; grandpaternal DNA; over-represented; l  
KW grandmother; performance; progeny horse; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200292851-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 15-MAY-2002; 2002WO-GB002273.  
XX  
PR 15-MAY-2001; 2001GB-00011886.  
XX  
PA (ANIM-) ANIMAL HEALTH TRUST.  
PA (BRHO-) BRITISH HORSERACING BOARD.  
XX  
PI Birns MW, Swinburne JE;  
XX  
DR WPI; 2003-129314/12.  
XX  
XX Determining the racing potential of a horse comprises measuring  
PT grandpaternal or grandmaternal DNA from the selected grandmothe  
PT over-represented in the genome of the horse.  
XX  
PS Example 2; Page 24; 49pp; English.  
XX  
CC The invention relates to a novel method for determining racing  
CC of a horse. The method comprises measuring: whether grandpatern  
CC over-represented in the genome of the horse; or in the case whe  
CC the grandmothers was selected for breeding on the basis of raci  
CC performance, whether grandmaternal DNA from the selected grand  
CC over-represented in the genome of the horse which indicates the  
CC horse has good racing potential. The method of the invention is  
CC for determining the racing potential of a horse or for obtaini  
CC progeny horse with good racing potential. This polynucleotide  
CC represents a PCR primer used in the detection method of over-  
CC representation of DNA from male grandparents of the invention  
XX  
SQ Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 67.0%; Score 13.4; DB 7; Length 20;  
Best Local Similarity 93.3%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
QY 1 ATCCTTGTCCTCCAC 15  
DB 20 ATCCTTGTCCTCCAC 6  
RESULT 28  
ACI58089  
ID ACI58089 standard; DNA; 25 BP.  
XX  
AC ACI58089;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 58080.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expres  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.

09:38:25 2004

us-10-090-326-7.max.rng

: 2002US-00098263.

: 2001US-0276759P.

QNETRIX INC.

;

67953/53.

f nucleic acid probes, useful for in situ hybridization, in orthern or dot-blot hybridization to identify or detect the specific mutations of any gene.

Q ID NO 58080; 9pp; English.

on discloses a microarray comprising a plurality of nucleic including one of 2,018,500 fully defined sequences, or its ch, perfect mismatch, antisense match or antisense mismatch. sed is a method of gene expression analysis. The array is used ng gene expression levels by hybridisation to a DNA library, of genetic variation or in hybridisation of tag-labelled. The nucleic acid probes are in hybridisation of tag-labelled one target sequence. The method of analysis comprises at least one or more nucleic acids to at least two or more i probes and detecting the hybridisation. The nucleic acid attached to a solid support. The analysis comprises monitoring sion levels, identifying biallelic markers or polymorphisms, nbers of a gene and a cross-species comparison. Each of the ds further comprises a tag sequence. The array of nucleic acid sful in in situ hybridisation, in Southern, Northern or dot- isation to identify or detect the sequence or specific f any gene, in mapping the 5' termini of mRNA molecules by sions or in screening cDNA or genomic libraries or subclones al subclones containing segments of DNA that have been i previously sequenced. The sequence presented is one of the i probes incorporated in the microarray. Note: The sequence is patent can also be obtained in electronic format directly at seqdata.uspto.gov/sequence.html

BP; 4 A; 8 C; 4 G; 9 T; 0 U; 0 Other;

67.0%; Score 13.4; DB 8; Length 25;

ilarity 93.3%; Pred. No. 1.2e+04;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CTTGTCTCTCCAC 15

|||||

CTTGTCTCCACC 17

andard; DNA; 31 BP.

(first entry)

a nucleotide polymorphism (SNP) COL7A1 9.

quence; genotype; disease; forensic; paternity testing; aotide polymorphism; SNP; ss.

s.

Location/Qualifiers

replace(16,T)

/\*tag= a

/standard\_name= "single nucleotide polymorphism"

-A2.

PD 13-SEP-2001.

XX 07-MAR-2001; 2001WO-US007268.

XX 07-MAR-2000; 2000US-0187510P.

XX 22-MAY-2000; 2000US-0206129P.

XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-522952/57.

XX Nucleic acid molecules from the human genome which include poly

PT sites, useful in methods for predicting the presence, absence o

PT of a particular phenotype or disorder (e.g. diabetes) associate

PT particular genotype.

XX Claim 1; Page 86; 145pp; English.

XX The invention relates to the identification of nucleic acid mol

CC (AA129513-AA13114) from the human genome which include polymor

CC of individuals were resequenced and single nucleotide polymorph

CC (SNPs) in these genes discovered. The method is useful for pred

CC presence, absence or severity of a particular phenotype or diso

CC diabetes) associated with a particular genotype. The nucleic ac

CC containing the polymorphic sites may be useful in forensics and

CC testing

XX Sequence 31 BP; 6 A; 12 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 4; Length 31;

Best Local Similarity 93.3%; Pred. No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CTTGTCTCTCCACGG 17

|||||

Db 24 CTTGTCTCTCCACGG 10

RESULT 30

ABZ02460

ID ABZ02460 standard; DNA; 50 BP.

XX AC ABZ02460;

XX DT 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 2451.

XX TV; leukocyte; gene expression profiling; allograft rejection;

XX atherosclerosis; congestive heart failure; systemic lupus eryth

XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infectio

XX ss.

XX Homo sapiens.

XX WO200257414-A2.

XX 25-JUL-2002.

XX 22-OCT-2001; 2001WO-US047856.

XX 20-OCT-2000; 2000US-0241994P.

XX 08-JUN-2001; 2001US-0296764P.

XX (BIOC-) BIOCARDIA INC.

XX Wohlgenuth J, Fry K, Matouk G, Altman P, Prentice J, Phill:

XX Ly N, Woodward R, Quatermous T, Johnson P;

XX WPI; 2002-636525/68.

for leukocyte expression profiling, diagnosing a disease, or (the rate of) progression of a disease, e.g. atherosclerosis or heart failure, comprises diagnostic oligonucleotides.

age 405; Opp; English.

ion relates to a system for detecting gene expression, which one or two isolated DNA molecules that detect expression of a gene corresponds to any of 8143 oligonucleotides (ABZ08152) each having 50 base pairs (bp). The system is useful for gene expression profiling. It is particularly useful for a disease, monitoring (rate of) progression of a disease, therapeutic outcome, determining prognosis for a patient, disease complications in an individual or monitoring response in an individual. The diseases include cardiac allograft kidney allograft rejection, liver allograft rejection, rosacea, congestive heart failure, systemic lupus erythematosus, arthritis, osteoarthritis or cytomegalovirus infection.

0 BP; 6 A; 14 C; 12 G; 18 T; 0 U; 0 Other;

milarity 67.0%; Score 13.4; DB 6; Length 50;  
Conservative 93.3%; Pred. No. 1.2e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGTCCTCCACGGGT 19  
|||||||  
TGTCCTCCACGGGT 25

standard; DNA; 20 BP.

1 (first entry)

rogen receptor alpha search PCR primer 75.

endent transcriptional factor; oestrogen receptor; ER;  
coid receptor protein; GR; mineralocorticoid receptor protein;  
some proliferator-activated receptor protein; PPAR;  
ne receptor protein; PR; pregnane X receptor protein; PXR;  
mone receptor protein; TR; vitamin D receptor protein; VDR;  
ation; ERalpha; breast cancer; PCR primer; probe; ss.

ns.

7-Al.

1.

0; 2000WO-JP008553.  
9; 99JP-00348022.  
9; 99JP-00370667.  
0; 2000JP-00207011.  
0; 2000JP-00220508.  
0; 2000JP-00234053.  
0; 2000JP-00235460.  
0; 2000JP-00235461.  
0; 2000JP-00235463.

MITOMO CHEM CO LTD.

Ohe N, Satoh H;

367866/38.

endent transcriptional factors, nucleic acids encoding them and  
rising them and a specified reporter gene, useful for screening

PT agents for the treatment of breast cancer.

XX  
PS Example 9; Page 231; 276pp; English.

XX  
PS The present invention relates to ligand dependent transcriptional  
CC including oestrogen receptor (ER) alpha and beta protein, gluc  
CC receptor protein (GR), mineralocorticoid receptor protein (MR)  
CC peroxisome proliferator-activated receptor protein (PPAR), prc  
CC receptor protein (PR), pregnane X receptor protein (PXR), thyr  
CC receptor protein (TR) and vitamin D receptor protein (VDR), th  
CC acids encoding them and cells comprising them and a specified  
CC gene for the ligand dependent transcriptional factor. These pr  
CC useful in the modulation of ligand dependent transcriptional f  
CC activity. The cells, mutant ERalpha and the polynucleotide enc  
CC may be used in assays for qualitatively analysing an activity  
CC transactivation of a reporter gene by a test ERalpha, for scre  
CC mutant ligand dependent transcriptional factors, for evaluat  
CC activity for transactivation of a reporter gene by a test ERal  
CC for screening a compound useful for treating a disorder of a m  
CC ERalpha, especially breast cancer

XX SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTCTCTCCACGGGT 19  
|||||  
DB 20 TCCTTCTCTCCACGGGT 3

RESULT 32

AAQ21480/c  
ID AAQ21480 standard; DNA; 22 BP.

XX AC AAQ21480;

XX 25-MAR-2003 (revised)

DT 01-JUN-1992 (first entry)

XX CTP synthetase gene mutation-specific probe #3.

DE MDR; chemotherapy; PCR; cytosine triphosphate synthetase;

XX splice acceptor site; ss.

XX Synthetic.

XX

PH Key Location/Qualifiers

FT misc\_difference 11

FT /\*tag= a

FT /note= "mutation"

XX WO9201811-A.

XX PD 06-FEB-1992.

XX 25-JUL-1990; 90GB-00016287.

XX 25-JUL-1990; 90GB-00016287.

XX 11-APR-1991; 91US-00682975.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX Meuth M;

XX WPI; 1992-064967/08.

XX

XX Assay method for CTP synthetase mutation(s) - utilising polymers;

XX reaction to reveal the presence of the multiple drug resistance

XX indicative of a mutation.

XX Example 2; Page 28; 46pp; English.

PS



was purified from white blood cells of patients with acute or solid tumour cells. The DNA or cDNA (reverse transcribed) was amplified using the PCR technique (see e.g. AAQ23749-primers designed to amplify regions potentially containing mutations). The critical mutation can then be detected in the product using a mutation-specific probe. This probe is end-labeled then hybridised to a slot or dot blot. (Updated on 25-MAR-01)

BP; 9 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

ilarity 66.0%; Score 13.2; DB 2; Length 22;

Conservative 83.3%; Pred. No. 1.5e+04;

CTGTGCTCCACGGT 19

TAATGCTCCACGGT 3

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 119020.

obe; expressed sequence tag; microarray; gene expression;

ation; biallelic marker; polymorphism; human; es comparison.

S.

O-Al.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

;

67953/53.

f nucleic acid probes, useful for in situ hybridization, in orthern or dot-blot hybridization to identify or detect the specific mutations of any gene.

Q ID NO 119020; 9pp; English.

on discloses a microarray comprising a plurality of nucleic including one of 2,018,500 fully defined sequences, or its ch, perfect mismatch, antisense match or antisense mismatch. sed is a method of gene expression analysis. The array is used ng gene expression levels by hybridisation to a DNA library, of genetic variation or in hybridisation of tag-labelled. The nucleic acid probes are specifically designed for analysis one target sequence. The method of analysis comprises at least one or more nucleic acids to at least two or more d probes and detecting the hybridisation. The nucleic acid attached to a solid support. The analysis comprises monitoring sion levels, identifying biallelic markers or polymorphisms, embers of a gene and a cross-species comparison. Each of the ds further comprises a tag sequence. The array of nucleic acid seful in in situ hybridization, in Southern, Northern or dot- isation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molec  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have  
CC isolated and previously sequenced. The sequence presented is o  
CC nucleic acid probes incorporated in the microarray. Note: The  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX

SQ Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 8; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

OY 2 TCCTTGCTCCACGGT 19

Db 7 TCCTTGCTCCACGGT 24

RESULT 34

AAT31832/c

ID AAT31832 standard; DNA; 30 BP.

XX AAT31832;

AC AAT31832;

XX 11-JAN-1997 (first entry)

XX Primer for amplifying HPV E7 protein fragment coding region.

XX Human papilloma virus; E6; E7; deletion mutant; HPV; immune res

KW humoral immune response; cellular immune response; vaccine; ss.

XX Synthetic.

XX WO9619496-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-AU000868.

XX 20-DEC-1994; 94AU-00000157.

XX (CSLC-) CSL LTD.

XX (UYQU) UNIV QUEENSLAND.

XX Edwards SJ, Cox J, Webb EA, Frazer I;

XX WPI; 1996-309518/31.

XX Vaccine variants of human papilloma virus antigens - contain va  
E6 and/or E7 protein, pref. deletion mutants, and are used to t  
prevent HPV infection.

XX Example 3; Page 13; 37pp; English.

XX A variant of the human papilloma virus (HPV) E6 or E7 protein w  
elicits a humoral and/or cellular immune response against HPV c  
in vaccines against HPV or to treat HPV infection. The variant  
preferably a deletion mutant comprising at least half, and pref  
-thirds of full length E6 or E7 protein starting from the N- or  
terminal, or is a full length E6 moiety fused to a full length  
CC The variant optionally has a linkage moiety and a foreign prote  
peptide which facilitates the purification of, and enhances the  
immunogenicity of, the fusion protein. Two primers (AAT31829, A  
were used to amplify the 198 C-terminal bases of the HPV E7 pro  
for its use in an E6/E7 fusion construct

SQ Sequence 30 BP; 9 A; 4 C; 14 G; 3 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 2; Length 30;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

TCCTTGCTCTCCACGGG 18  
|||||  
TCCTCTCTCTCCCGGG 3

tandard; DNA; 32 BP.

6 (first entry)

primer #2.

thelial cell protein; cerebral arteriole smooth muscle cell;  
protein; collateral cerebrovascular circulation; human;  
cular disease; intracerebral haemorrhage; aneurysm; migraine;  
id haemorrhage; intracerebral atherosclerosis; lipohyalinosis;  
's disease; subcortical arteriopathic encephalopathy; therapy;  
isease; blood brain barrier; brain oedema formation; primer;  
cle cell; radioimmunoassay; polymerase chain reaction; PCR;  
rk-A; ss.

A1.

5.

5; 95WO-US005659.

4; 94US-00239889.

3 DEV FOUND.

Alam NA, Alam SS;

103939/51.

ilo: dalton protein secreted by brain endothelial cells -  
cerebral arteriole smooth muscle cell proliferation and is  
improving cerebral collateral cerebrovascular circulation.

Page 12; 33pp; English.

ad AAT02497 represent amplification primers for a 200 bp region  
brain trk-A gene. The amplified fragment encodes the  
lar domain of the neurotrophic protein. The peptide encoded by  
ied sequence was used to isolate a 67 kDa brain endothelial  
in. This protein stimulates proliferation of cerebral arteriole  
le cells. The protein can be used in the regulation of the  
ion of cerebral arteriole smooth muscle cells, and can be  
ad to improve collateral cerebrovascular circulation in humans.  
be used to treat cerebrovascular diseases which result from  
ion of fragile brain vessels due to the under- or over-  
of the protein. These include intracerebral haemorrhage,  
id haemorrhage due to aneurysms, migraine, intracerebral  
osis, lipohyalinosis, Bingwanger's disease or subcortical  
ic encephalopathy, Moyamoya disease and impairment of the  
ic barrier with brain oedema formation. Oligonucleotides can be  
to inhibit the production of this protein. These  
ptides are preferably triplex forming or antisense. The  
ptides can be used to treat diseases which involve increased  
le cell proliferation from overproduction of the protein. The  
f these diseases can be measured by measuring the serum  
ion of the protein by radioimmunoassay

2 BP; 5 A; 12 C; 5 G; 10 T; 0 U; 0 Other;

ilarity 66.0%; Score 13.2; DB 2; Length 32;

ilarity 83.3%; Pred. No. 1.5e+04;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCCTTGCTCTCCACGGG 18  
|||||  
Db 15 ATCCTTGCTCTCCACGGG 32

RESULT 36

ABA95667/C

ID ABA95667 standard; DNA; 41 BP.

XX

AC ABA95667;

XX

DT 25-MAR-2002 (first entry)

XX

DE Human splicing protein 10.56 probe #2.

XX

KW Human; splicing protein 10.56; cytostatic; haemostatic; viruci  
KW immunomodulatory; antiinflammatory; gene therapy; tumour; haem  
KW HIV infection; immunological disease; inflammation; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200192315-A1.

XX

PD 06-DEC-2001.

XX

PF 21-MAY-2001; 2001WO-CN000828.

XX

PR 24-MAY-2000; 2000CN-00115832.

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-090028/12.

XX

PT Human splicing protein 10.56 and encoding polynucleotide, used  
PT diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.

XX

PS Example 6; Page 20; 34pp; English.

XX

CC The present invention relates to human splicing protein 10.56  
CC AAM48273). The protein and its coding sequence are useful in t  
CC diagnosis and treatment of malignant tumours, haemopathy, HIV  
CC immunological diseases and various inflammations. The present  
CC a probe, which was used in an example from the present inventi

XX

SQ Sequence 41 BP; 8 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 41;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGGG 18

Db 27 AGCCTTGCTCTCTAGG 10

RESULT 37

AAL54343/C

ID AAL54343 standard; DNA; 41 BP.

XX

AC AAL54343;

XX

DT 27-MAR-2003 (first entry)

XX

DE Human sigma receptor 11-55 protein probe 1.

XX

KW Human sigma receptor 11.55; DNA recombination; psychogenic dise  
KW heart-originating asthma; acute poisoning; morphine analgesic;  
KW progesterone dysfunction; probe; ss.

```

d.
.
.
: 2001CN-00105190.
: 2001CN-00105190.
WINDOW GENE DEV INC SHANGHAI.
: Y;
00517/01.
tide-human sigma receptor 11.55 and polynucleotide for
ch polypeptide.
Page 19 (Disclosure); 3lpp; Chinese.
invention relates to a novel kind of polypeptide, human sigma
.55, polynucleotides for encoding this polypeptide and a DNA
on process to produce the polypeptide. The present invention
ses the method of applying the polypeptide in treating various
uch as psychogenic disease, heart-originating asthma, acute
used by morphine analgesic and progesterone dysfunction. The
ention also discloses the antagonist resisting the polypeptide
ation effect. The present invention also discloses the
of the polynucleotides for encoding human sigma receptor
polynucleotide sequence represents a probe of the human sigma
.55 protein of the invention
BP; 6 A; 13 C; 17 G; 5 T; 0 U; 0 Other;
66.0%; Score 13.2; DB 7; Length 41;
ilarity 83.3%; Pred. No. 1.5e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
TTGTCTCTCCACGGGTT 20
| | | | | | | | | |
TCGTCTCTCCACAGGCT 9
andard; DNA; 47 BP.
(first entry)
elated biallelic marker SEQ ID NO:1000.
e; biallelic marker; high density disequilibrium map;
; haplotype; phenotype; polymorphic base; genotyping;
; hybridisation; identification; characterisation; diagnosis;
eotide polymorphism; SNP; ds.
s.
Location/Qualifiers
replace(24,T)
/*tag= a
/standard_name= "single nucleotide polymorphism"
2.
.
: 99WO-IB000822.

```

---

```

PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
XX
PA (BEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density diseq
PT map of the human genome.
XX
PS Claim 1; Page 444; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the
CC invention, which contain a polymorphic base at position 24 of t
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplificat
CC primers for the biallelic markers. The biallelic markers of the
CC have a variety of uses: they can be used for high density mappi
CC human genome, and in complex association studies and haplotypir
CC which are useful in determining the genetic basis for disease s
CC Compositions and methods of the invention can also be useful fo
CC identification of the targets for the development of pharmaceut
CC agents and diagnostic methods, as well as the characterisation
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other trea
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3
CC 3367, are not actually given a sequence in the Sequence Listing
CC present invention
XX
SQ Sequence 47 BP; 12 A; 13 C; 6 G; 16 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 3; Length 47;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;
QY 2 TCCTTGTCCTCCACGGGT 19
| | | | | | | | | |
Dd 2 TCCTTCTCTCGAAGGGT 19
| | | | | | | | | |
RESULT 39
AAF89887/c
ID AAF89887 standard; DNA; 48 BP.
XX
XX AAF89887;
XX
XX 23-JUL-2001 (first entry)
XX
XX PCR primer for human nuclear regulatory factor-1 (NRF-1) cDNA.
XX mitochondrial function; mitochondrial biogenesis; UCP gene; NRF
XX uncoupling protein gene; PGC gene; nuclear regulatory factor ge
XX peroxisome proliferator-activated receptor gamma coactivator ge
XX PPAR-gamma coactivator gene; type 2 diabetes mellitus; PCR prim
XX Homo sapiens.
XX OS
XX WO200135096-A2.
XX PN
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US031119.
XX
XX 10-NOV-1999; 99US-0164533P.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Clevenger W, Becker DK, Grako KA;
XX WPI; 2001-335965/35.
XX
XX Treating a disease associated with altered mitochondrial functi
PT

```

betes mellitus, involves administering an agent that increases  
ial mass in cells of the individual.

Page 146; 184pp; English.

s AARE9886-88 were used to amplify epitope-tagged human nuclear factor-1 (NRF-1) cDNA. The amplified sequence was used in the invention. The specification describes a method for disease associated with altered mitochondrial function. The invention describes administering an agent that increases mitochondrial mitochondrial function, in cells of the individual. The invention describes mitochondrial biogenesis by induction of a peroxisome  $\alpha$ -activated receptor gamma (PPAR-gamma) coactivator gene (PGC-1) uncoupling protein gene (UCP gene), and/or a nuclear regulatory gene (NRF gene). The agents are useful for treating a disease with altered mitochondrial function such as diabetes, e.g., diabetes mellitus.

8 BP; 18 A; 7 C; 16 G; 7 T; 0 U; 0 Other;

66.0%; Score 13.2; DB 5; Length 48;  
milarity 83.3%; Pred. No. 1.5e+04;

Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
--------------	----	------------	----	--------	----	------	----

CCTTGTCCTCCACGGGT 19  
||||| ||||| ||||| |||||  
CCTTGTACTCCATGGAT 6

tandard; DNA; 60 BP.

2 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:16879.

se; rat; splice transcript; detection; RNA transcript;  
 iant; transcriptome; oligonucleotide library; ss.

ns.

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faiqler S;

257383/30-

nucleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a gene for detecting tissue-, pathology-, and developmental-genes.

SEQ ID NO 16879; 47pp; English.

that invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, and one or more messenger RNA splice variants. The

oligonucleotide libraries are useful for detecting mRNAs from biological sample, in expression profiling studies, in qualitative and quantitative characterising the corresponding transcriptome, detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised libraries to detect transcripts of a sub-transcriptome under a biological or pathological state, and so allowing the detection of - and pathology-specific genes such as those genes only expressed specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and variants of a transcriptome of a patient suffering from a part disorder. ABN27253 to ABN5989 represent oligonucleotide sequences, humans and mice, which are used in the exemplification of present invention. N.B. The sequence data for this patent did part of the printed specification, but was obtained in electro directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match	66.0%;	Score 13.2;	DB 6;	Length 60;
Best Local Similarity	83.3%;	Pred. No. 1.5e+04;		
Matches 15;	Conservative	0;	Mismatches 3;	Indels 0;

QY 2 TCCTTGTTCTCCACGGT 19  
|||  
Db 33 TCCTTGTTCTCTATGGT 16

RESULT 41

ABN35011/C

ID ABN35011 standard; DNA; 60 BP.

XX

AC ABN35011;

DT 15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:7

Human; mouse; rat; splice transcript; detection; RNA transcript splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

AA 07-FEB-2002. PD

20-JUL-2001: 2001WO-IB001903.

28-JUL-2000: 2000US-0221607P-

0Z-MAY-2001; 200105-0287724P.  
FR  
XX

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription genome, useful for detecting tissue-, pathology-, and development specific genes.

PS Example 1; SEQ ID NO 7759; 47bp; English.

The present invention describes oligonucleotide libraries for ( ) messenger RNAs that populate a (sub-)transcriptome, where the ( ) transcriptome comprises messenger RNAs transcribed from multi- transcription units that populate a genome. The library comprises oligonucleotides, each capable of hybridising selectively to a messenger RNAs transcribed from a given transcription unit of a ( ) which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from ( )

sample, in expression profiling studies, in qualitatively or  
 ely characterising the corresponding transcriptome, and in  
 NA transcripts and splice variants of human or animal  
 mes. The libraries may also be used as specialised mini  
 o detect transcripts of a sub-transcriptome under a particular  
 or pathological state, and so allowing the detection of tissue  
 logy-specific genes such as those genes only expressed in  
 sue under a specific pathological condition; to detect  
 al specific genes; and to detect RNA transcripts and splice  
 a transcriptome of a patient suffering from a particular  
 BN27253 to ABN59589 represent oligonucleotide sequences from  
 s and mice, which are used in the exemplification of the  
 ention. N.B. The sequence data for this patent did not form  
 printed specification, but was obtained in electronic format  
 om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 18 A; 12 C; 20 G; 10 T; 0 U; 0 Other;

66.0%; Score 13.2; DB 6; Length 60;  
 ilarity 83.3%; Pred. No. 1.5e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTGTCTCCACGGGT 19  
 ||||| |||||  
 CTTGCTTCACTGGT 3

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:10055.

e; rat; splice transcript; detection; RNA transcript;  
 ant; transcriptome; oligonucleotide library; ss.

S.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

37383/30.

cleotide libraries comprising oligonucleotides which  
 hybridize to mRNAs transcribed from a transcription unit of a  
 ful for detecting tissue-, pathology-, and developmental-  
 nes.

SEQ ID NO 10055, 47pp; English.

invention describes oligonucleotide libraries for detecting  
 NAs that populate a (sub-)transcriptome, where the (sub-  
 me comprises messenger RNAs transcribed from multiple  
 on units that populate a genome. The library comprises several  
 tides, each capable of hybridising selectively to a set of  
 NAs transcribed from a given transcription unit of the genome,  
 es one or more messenger RNA splice variants. The  
 tide libraries are useful for detecting mRNAs from a  
 sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome,  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcripts. The libraries may also be used as specialised  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC biological or pathological state, and so allowing the detection  
 CC - and pathology-specific genes such as those genes only expressed  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and  
 CC variants of a transcriptome of a patient suffering from a part;  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequer  
 CC rats, humans and mice, which are used in the exemplification of  
 CC present invention. N.B. The sequence data for this patent did r  
 CC part of the printed specification, but was obtained in electron  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

Sequence 60 BP; 20 A; 11 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 60;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 3 CTTGTCTCTCCACGGGTT 20  
 ||||| |||||  
 Db 23 CTTGTCTCTCCACGGGTT 6

RESULT 43

AAV71103

ID AAV71103 standard; DNA; 35 BP.

AC AAV71103;

XX

DT 05-FEB-1999 (first entry)

XX

PCR primer used to amplify the dnaE gene of Thermus thermophilu  
 Alpha subunit; DNA Polymerase III-type enzyme; chromosomal repl  
 DNA amplification; DNA sequencing; dnaE gene; PCR primer; ss.

XX

OS Synthetic.

OS Thermus thermophilus.

PN WO9845452-A2.

XX

PD 15-OCT-1998.

XX

PF 08-APR-1998; 98WO-US006921.

XX

PR 08-APR-1997; 97US-00823407.

XX

PA (UYRQ ) UNIV ROCKEFELLER.

XX

PI Yurieva O, Kuriyan J, Odonnell ME, Jeruzalmi D;

XX

WPI; 1998-594486/50.

XX

PT New isolated DNA Polymerase III-type enzymes - used to develop  
 for the amplification and sequencing of DNA, particularly by PC  
 Example 10; Page 79; 153pp; English.

XX

CC PCR primers AAV71102-03 were used to amplify the dnaE gene of T  
 CC thermophilus. This gene encodes the alpha subunit of the T. the  
 CC DNA Polymerase III-type enzyme (DP3). DP3 functions as a chromo  
 CC replicase, and is a holoenzyme. The products can be used for DN  
 CC amplification and sequencing. They can provide faster and longe  
 CC production in PCR, and higher quality of DNA sequencing ladders  
 CC compared to other DNA polymerases

XX

Sequence 35 BP; 4 A; 7 C; 12 G; 8 T; 0 U; 4 Other;

XX

Query Match 65.0%; Score 13; DB 2; Length 35;

Best Local Similarity 76.5%; Pred. No. 1.9e+04;

Conservative 2; Mismatches 2; Indels 0; Gaps 0;

TCTTGTCTCCACGG 17  
||||| :  
TCTTGTCTCSAGSG 22

standard; DNA; 35 BP.

0 (first entry)

ermophilus dnaE PCR primer #4.

ase III; dnaE gene; alpha subunit; thermostable;  
sis; speed; accuracy; processivity; frameshift; holoenzyme;  
exonuclease; proofreading; PCR; primer; ss.

ermophilus.

Al.

9.

8; 98WO-US007070.

8; 98WO-US007070.

IV ROCKEFELLER.

Kuriyan J, O'donnell ME, Jeruzalmi D;

611306/52.

Y50014.

ed thermostable DNA polymerase III-type enzyme, used  
ly for the amplification and sequencing of nucleic acids.

; Page 79; 156pp; English.

nce represents *Thermus thermophilus* dnaE PCR primer #4, used  
r #3 (AAZ30923) to amplify a portion of the *thermus*  
us dnaE gene. The dnaE gene encodes the alpha subunit of a  
mostable DNA polymerase holoenzyme which corresponds to DNA  
III (Pol III) of *E. coli*. Pol III-type enzymes have a high  
ty (>50 kb) and rapid rate of synthesis (750 nucleotides/s).  
sists of 18 subunits of 10 different types. The DNA polymerase  
a catalytic unit and consists of the alpha (DNA polymerase),  
"-5' exonuclease) and theta subunits. The beta subunit  
clamp") is ring-shaped and encircles DNA and slides along it  
aring the Pol III holoenzyme to the template. It is the beta  
ich is responsible for the high processivity and speed. The  
lex (composed of gamma, delta, delta', chi and psi subunits) is  
loader" which couples ATP hydrolysis to assembly of beta  
and DNA. A dimer of the tau subunit acts as a "macromolecular  
, holding together molecules of core polymerase and one  
f gamma complex, forming the Pol III\* subassembly. Two beta  
ociate with the two cores within Pol III\* to form the  
s capable of replicating both strands of duplex DNA  
usly. The *Thermus thermophilus* Pol III-type enzyme can be used  
ar cloning techniques such as PCR (polymerase chain reaction).  
t limitations of enzymes previously used in PCR are that they  
to synthesize extended lengths of nucleotides, and in the  
f Tag (*Thermus aquaticus*) polymerase, the lack of 3'-5'  
e activity and the subsequent inability to excise misinserted  
s (proofreading)

5 BP; 4 A; 7 C; 12 G; 8 T; 0 U; 4 Other;

Query Match 65.0%; Score 13; DB 2; Length 35;  
Best Local Similarity 76.5%; Pred. No. 1.9e+04;  
Matches 13; Conservative 2; Mismatches 2; Indels 0;

QY 1 ATCCTTGTCTCCACGG 17  
||||| :  
Db 6 ATCCTTGTCTCSAGSG 22

RESULT 45

ACC54203/c

ID ACC54203 standard; DNA; 17 BP.

XX ACC54203;

DT 27-JUN-2003 (first entry)

XX Human tumour suppressor sequence #2970.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppress  
KW tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.

XX Homo sapiens.

XX FR2826373-AL.

XX 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Tuijnder M, Telerman A, Amson R;

XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression,  
PT apoptosis or virus resistance are useful to diagnose and treat  
PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 726; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence ass  
CC with tumour suppression or regression, apoptosis or virus resi  
CC invention relates to these sequences or sequences having at le  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences.  
CC invention is used to diagnose or treat viral disease or diseas  
CC characterized by development of tumour cells or cellular degen

XX Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 7; Length 17;  
Best Local Similarity 87.5%; Pred. No. 2.2e-04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTGTGCTCTCCACGGT 19  
||||| :  
Db 17 CTGTGCTCTCCACAGAT 2

Search completed: February 29, 2004, 09:03:07  
Job time : 201.649 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

cleic search, using sw model

February 29, 2004, 08:44:24 ; Search time 37.6623 Seconds  
(without alignments)  
294.698 Million cell updates/sec

US-10-090-326-7

20  
1 atccgtgtctccacgggtt 20

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

682709 segs, 277475446 residues

hits satisfying chosen parameters: 874574

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Issued Patents NA: \*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
74.0	20	3	US-09-118-408-12	Sequence 12, Appl
74.0	20	3	US-09-118-408-15	Sequence 15, Appl
74.0	20	4	US-09-506-855-12	Sequence 12, Appl
74.0	20	4	US-09-506-855-15	Sequence 15, Appl
74.0	20	4	US-09-911-176B-12	Sequence 12, Appl
74.0	20	4	US-09-911-176B-15	Sequence 15, Appl
74.0	20	4	US-09-619-740-12	Sequence 12, Appl
74.0	20	4	US-09-619-740-15	Sequence 15, Appl
74.0	20	4	US-09-506-852-12	Sequence 12, Appl
74.0	20	4	US-09-506-852-15	Sequence 15, Appl
72.0	38	4	US-09-268-544B-2	Sequence 2, Appl
70.0	33	1	US-08-138-608-44	Sequence 44, Appl
67.0	29	4	US-08-891-292A-5	Sequence 5, Appl
67.0	29	4	US-08-891-292A-7	Sequence 7, Appl
67.0	29	4	US-09-927-737C-5	Sequence 5, Appl
67.0	29	4	US-09-927-737C-7	Sequence 7, Appl
66.0	30	3	US-08-860-165-8	Sequence 8, Appl
66.0	30	4	US-09-358-645-8	Sequence 8, Appl
66.0	30	4	US-09-359-382-8	Sequence 8, Appl
66.0	32	1	US-08-239-889A-2	Sequence 2, Appl
66.0	32	5	PCT-US95-05659-2	Sequence 2, Appl
66.0	47	4	US-09-422-978-1000	Sequence 1000, Ap
66.0	55	4	US-09-621-976-13666	Sequence 13666, A
64.0	28	2	US-08-859-998-991	Sequence 991, App
64.0	28	4	US-09-225-928-991	Sequence 991, App
64.0	28	4	US-09-225-201B-991	Sequence 991, App
64.0	45	1	US-08-440-103-12	Sequence 12, Appl

28	12.8	64.0	45	1	US-08-440-542-12	Sequence
29	12.8	64.0	45	1	US-08-231-368-12	Sequence
30	12.8	64.0	45	1	US-08-440-210-12	Sequence
31	12.8	64.0	45	4	US-09-046-604-12	Sequence
C 32	12.8	64.0	57	4	US-09-313-294A-4232	Sequence
C 33	12.6	63.0	27	1	US-08-758-306-1196	Sequence
C 34	12.6	63.0	41	1	US-08-356-405-12	Sequence
35	12.6	63.0	45	4	US-08-162-597-6	Sequence
36	12.6	63.0	45	4	US-09-770-949-6	Sequence
37	12.6	63.0	52	2	US-08-883-795A-21	Sequence
C 38	12.4	62.0	36	4	US-09-769-863-4	Sequence
C 39	12.2	61.0	21	4	US-09-079-812E-8	Sequence
C 40	12.2	61.0	31	1	US-08-477-877B-3	Sequence
C 41	12.2	61.0	31	1	US-08-472-281A-3	Sequence
C 42	12.2	61.0	31	2	US-08-477-985B-3	Sequence
C 43	12.2	61.0	32	1	US-08-347-792-23	Sequence
C 44	12.2	61.0	32	1	US-08-431-357-23	Sequence
C 45	12.2	61.0	32	5	PCT-US95-15353-23	Sequence
C 46	12.2	61.0	37	1	US-08-273-362-1	Sequence
C 47	12.2	61.0	45	3	US-08-484-686B-63	Sequence
C 48	12.2	61.0	45	3	US-08-463-160B-63	Sequence
C 49	12.2	61.0	45	5	PCT-US91-02568-4	Sequence
C 50	12.2	61.0	51	4	US-09-529-279-44	Sequence
C 51	12.2	61.0	51	4	US-10-158-895-44	Sequence
52	12.2	61.0	51	4	US-09-443-199C-957	Sequence
C 53	12.2	61.0	51	4	US-09-443-199C-1042	Sequence
C 54	12.2	61.0	56	2	US-08-883-795A-5	Sequence
55	12	60.0	24	1	US-08-095-162-14	Sequence
56	12	60.0	24	1	US-08-294-434-15	Sequence
57	12	60.0	24	1	US-08-457-166-15	Sequence
58	12	60.0	24	1	US-08-470-220A-14	Sequence
59	12	60.0	24	2	US-08-595-868C-19	Sequence
60	12	60.0	24	3	US-08-967-374-14	Sequence
61	12	60.0	24	3	US-08-927-128-11	Sequence
62	12	60.0	24	3	US-09-139-819A-19	Sequence
63	12	60.0	24	4	US-09-505-991-14	Sequence
64	12	60.0	24	4	US-09-750-913-19	Sequence
65	12	60.0	24	5	PCT-US93-06591-15	Sequence
66	12	60.0	24	5	PCT-US95-15800-5	Sequence
67	12	60.0	27	3	US-08-513-974B-186	Sequence
68	12	60.0	28	1	US-08-328-314-8	Sequence
69	12	60.0	28	1	US-08-731-045-8	Sequence
70	12	60.0	28	4	US-09-475-947A-111	Sequence
C 71	12	60.0	38	4	US-09-367-777-15	Sequence
C 72	12	60.0	38	4	US-09-367-777-19	Sequence
73	12	60.0	57	4	US-09-097-055B-12	Sequence
74	12	60.0	57	4	US-09-097-055B-60	Sequence
75	11.8	59.0	20	3	US-08-488-145-11	Sequence
76	11.8	59.0	20	3	US-08-475-470A-20	Sequence
77	11.8	59.0	20	4	US-09-596-938-11	Sequence
78	11.8	59.0	20	4	US-09-780-045-34	Sequence
79	11.8	59.0	20	4	US-08-723-303-20	Sequence
C 80	11.8	59.0	25	4	US-09-551-305C-7	Sequence
81	11.8	59.0	30	3	US-09-130-663-9	Sequence
82	11.8	59.0	30	3	US-08-913-842-37	Sequence
83	11.8	59.0	30	3	US-09-432-335-9	Sequence
84	11.8	59.0	30	4	US-09-614-022-9	Sequence
C 85	11.8	59.0	44	1	US-08-306-546C-9	Sequence
C 86	11.8	59.0	44	2	US-08-530-524A-9	Sequence
87	11.8	59.0	45	2	US-08-761-277A-73	Sequence
88	11.8	59.0	47	4	US-09-641-638-898	Sequence
C 89	11.8	59.0	47	4	US-09-422-978-2678	Sequence
C 90	11.8	59.0	60	1	US-08-424-788-14	Sequence
91	11.6	58.0	20	4	US-09-658-688A-18	Sequence
92	11.6	58.0	21	4	US-09-182-024A-3	Sequence
C 93	11.6	58.0	22	4	US-09-297-369A-9	Sequence
94	11.6	58.0	22	2	US-08-859-998-1145	Sequence
C 95	11.6	58.0	27	3	US-08-856-331-18	Sequence
96	11.6	58.0	27	4	US-09-225-928-1145	Sequence
97	11.6	58.0	27	4	US-09-225-201B-1145	Sequence
C 98	11.6	58.0	27	4	US-09-418-830-6	Sequence
99	11.6	58.0	27	4	US-09-622-166A-6	Sequence
100	11.6	58.0	28	1	US-07-780-973-2	Sequence

58.0	28	2	US-08-899-324-14	Sequence 14, Appl	c 174	11.2	56.0	20	1	US-08-714-626-8	Sequenc
58.0	28	3	US-08-852-824-11	Sequence 11, Appl	175	11.2	56.0	20	2	US-08-478-178A-67	Sequenc
58.0	28	3	US-08-329-892B-14	Sequence 14, Appl	176	11.2	56.0	20	2	US-08-488-177-67	Sequenc
58.0	30	4	US-09-402-317-5	Sequence 5, Appl	177	11.2	56.0	20	2	US-08-481-072A-67	Sequenc
58.0	32	1	US-07-780-973-12	Sequence 12, Appl	178	11.2	56.0	20	2	US-08-664-336-67	Sequenc
58.0	32	1	US-07-780-973-13	Sequence 13, Appl	c 179	11.2	56.0	20	2	US-08-922-169-8	Sequenc
58.0	33	1	US-08-461-731-4	Sequence 4, Appl	180	11.2	56.0	20	2	US-08-481-066A-67	Sequenc
58.0	33	2	US-09-002-072B-4	Sequence 4, Appl	181	11.2	56.0	20	3	US-09-313-930-7	Sequenc
58.0	33	3	US-09-314-199-4	Sequence 4, Appl	182	11.2	56.0	20	4	US-08-829-637A-67	Sequenc
58.0	33	4	US-09-314-198-4	Sequence 4, Appl	183	11.2	56.0	20	4	US-10-025-139-67	Sequenc
58.0	34	1	US-08-361-337-33	Sequence 33, Appl	c 184	11.2	56.0	20	4	US-09-747-391-94	Sequenc
58.0	35	1	US-07-780-973-3	Sequence 3, Appl	185	11.2	56.0	20	5	PCT-US95-04852-8	Sequenc
58.0	37	1	US-09-050-739-25	Sequence 25, Appl	186	11.2	56.0	21	1	US-08-219-842-53	Sequenc
58.0	43	1	US-07-780-973-8	Sequence 8, Appl	c 187	11.2	56.0	21	1	US-08-219-842-86	Sequenc
58.0	47	1	US-09-422-978-3710	Sequence 3710, Ap	188	11.2	56.0	21	1	US-08-451-096-53	Sequenc
58.0	48	1	US-08-753-054-10	Sequence 10, Appl	c 189	11.2	56.0	21	1	US-08-451-096-86	Sequenc
58.0	48	4	US-08-720-565-15	Sequence 15, Appl	190	11.2	56.0	21	3	US-08-413-740A-14	Sequenc
58.0	51	3	US-08-785-247-17	Sequence 17, Appl	191	11.2	56.0	21	4	US-09-382-552-227	Sequenc
58.0	51	4	US-09-443-199C-831	Sequence 831, App	192	11.2	56.0	21	5	PCT-US95-04063-14	Sequenc
58.0	57	3	US-09-470-618-5	Sequence 5, Appl	193	11.2	56.0	24	1	US-08-411-913-3	Sequenc
58.0	57	3	US-09-364-862-5	Sequence 5, Appl	c 194	11.2	56.0	24	2	US-08-031-538-35	Sequenc
58.0	57	4	US-09-724-916A-25	Sequence 25, Appl	c 195	11.2	56.0	25	4	US-09-946-678-14	Sequenc
58.0	57	4	US-09-724-916A-26	Sequence 26, Appl	c 196	11.2	56.0	25	4	US-09-946-678-21	Sequenc
58.0	60	4	US-08-172-332-3	Sequence 3, Appl	c 197	11.2	56.0	25	4	US-09-866-108A-13448	Sequenc
58.0	16	4	US-09-531-000-24	Sequence 24, Appl	c 198	11.2	56.0	25	4	US-09-866-108A-13449	Sequenc
58.0	18	4	US-07-758-282B-191	Sequence 191, App	c 199	11.2	56.0	25	4	US-09-866-108A-13450	Sequenc
58.0	18	4	US-09-758-282B-196	Sequence 196, App	c 200	11.2	56.0	25	4	US-09-866-108A-13451	Sequenc
58.0	20	3	US-09-280-799-60	Sequence 60, Appl	c 201	11.2	56.0	25	4	US-09-866-108A-13452	Sequenc
58.0	20	4	US-09-658-688A-19	Sequence 19, Appl	c 202	11.2	56.0	25	4	US-09-866-108A-13453	Sequenc
58.0	21	4	US-09-216-393B-255	Sequence 255, App	c 203	11.2	56.0	25	4	US-09-866-108A-13454	Sequenc
58.0	24	3	US-08-150-900-33	Sequence 33, Appl	c 204	11.2	56.0	25	4	US-09-866-108A-13455	Sequenc
58.0	26	3	US-08-702-665A-17	Sequence 17, Appl	c 205	11.2	56.0	25	4	US-09-866-108A-13456	Sequenc
58.0	28	3	US-09-150-900-34	Sequence 34, Appl	c 206	11.2	56.0	25	4	US-09-866-108A-13457	Sequenc
58.0	30	1	US-09-150-900-35	Sequence 35, Appl	c 207	11.2	56.0	28	2	US-08-859-998-742	Sequenc
58.0	30	1	US-08-321-613-3	Sequence 3, Appl	c 208	11.2	56.0	28	4	US-09-225-928-742	Sequenc
58.0	30	3	US-09-150-900-36	Sequence 36, Appl	c 209	11.2	56.0	28	4	US-09-225-201B-742	Sequenc
58.0	30	4	US-09-170-496D-116	Sequence 116, App	c 210	11.2	56.0	28	4	US-09-530-685A-26	Sequenc
58.0	30	4	US-09-364-425B-25	Sequence 25, Appl	c 211	11.2	56.0	29	1	US-08-846-012A-6	Sequenc
58.0	31	4	US-09-635-872A-49	Sequence 49, Appl	c 212	11.2	56.0	29	2	US-09-100-297-6	Sequenc
58.0	31	4	US-09-636-077A-49	Sequence 49, Appl	c 213	11.2	56.0	30	4	US-09-794-529B-23	Sequenc
58.0	31	4	US-09-636-060C-49	Sequence 49, Appl	c 214	11.2	56.0	30	4	US-09-794-517A-23	Sequenc
58.0	31	4	US-09-986-552-49	Sequence 49, Appl	c 215	11.2	56.0	30	4	US-09-011-645B-23	Sequenc
58.0	32	3	US-09-150-900-37	Sequence 37, Appl	c 216	11.2	56.0	30	4	US-09-794-832-23	Sequenc
58.0	33	2	US-08-343-923-11	Sequence 11, Appl	c 217	11.2	56.0	31	2	US-08-942-423-54	Sequenc
58.0	36	1	US-08-021-623C-1	Sequence 1, Appl	c 218	11.2	56.0	31	2	US-08-694-869-8	Sequenc
58.0	36	1	US-08-021-623C-14	Sequence 14, Appl	c 219	11.2	56.0	31	3	US-09-502-831-8	Sequenc
58.0	36	1	US-08-021-623C-16	Sequence 16, Appl	c 220	11.2	56.0	31	4	US-09-349-546-8	Sequenc
58.0	36	4	US-09-403-752A-14	Sequence 14, Appl	c 221	11.2	56.0	31	4	US-09-889-914B-5	Sequenc
58.0	39	1	US-08-225-989-10	Sequence 10, Appl	c 222	11.2	56.0	32	3	US-08-606-505B-40	Sequenc
58.0	39	1	US-08-570-923-10	Sequence 10, Appl	c 223	11.2	56.0	32	3	US-09-616-990-40	Sequenc
58.0	39	1	US-08-580-014-10	Sequence 10, Appl	c 224	11.2	56.0	32	4	US-09-479-479-14	Sequenc
58.0	39	3	US-09-079-785-10	Sequence 10, Appl	c 225	11.2	56.0	32	4	US-09-297-851-14	Sequenc
58.0	39	4	US-09-628-126-10	Sequence 10, Appl	c 226	11.2	56.0	33	3	US-08-884-324-24	Sequenc
58.0	42	1	US-08-753-054-12	Sequence 12, Appl	c 227	11.2	56.0	34	4	US-09-718-034-5	Sequenc
58.0	47	4	US-09-641-638-900	Sequence 900, App	c 228	11.2	56.0	38	1	US-07-829-954-3	Sequenc
58.0	47	4	US-09-422-978-3692	Sequence 3692, Ap	c 229	11.2	56.0	39	5	PCT-US92-06821A-107	Sequenc
58.0	49	1	US-08-014-723-8	Sequence 8, Appl	c 230	11.2	56.0	39	5	PCT-US92-06821A-107	Sequenc
58.0	49	1	US-08-110-011A-8	Sequence 8, Appl	c 231	11.2	56.0	41	4	US-09-443-199C-885	Sequenc
58.0	49	1	US-08-361-873A-3	Sequence 3, Appl	c 232	11.2	56.0	46	4	US-09-377-885A-16	Sequenc
58.0	60	4	US-09-339-913B-8	Sequence 8, Appl	c 233	11.2	56.0	46	4	US-09-377-885A-17	Sequenc
58.0	60	4	US-09-339-904A-8	Sequence 8, Appl	c 234	11.2	56.0	47	4	US-09-641-638-921	Sequenc
58.0	60	4	US-08-769-062B-8	Sequence 8, Appl	c 235	11.2	56.0	47	4	US-09-422-978-43	Sequenc
58.0	60	4	US-09-344-002B-8	Sequence 8, Appl	c 236	11.2	56.0	47	4	US-09-422-978-2093	Sequenc
58.0	60	4	US-09-559-565C-8	Sequence 8, Appl	c 237	11.2	56.0	47	4	US-08-891-271-29	Sequenc
58.0	60	4	US-09-693-350-8	Sequence 8, Appl	c 238	11.2	56.0	48	3	US-08-755-587-201	Sequenc
58.0	60	4	US-09-693-389-8	Sequence 8, Appl	c 239	11.2	56.0	50	3	US-09-390-867A-42	Sequenc
58.0	60	4	US-09-559-671A-8	Sequence 8, Appl	c 240	11.2	56.0	50	3	US-09-548-260-42	Sequenc
58.0	60	4	US-09-339-926A-8	Sequence 8, Appl	c 241	11.2	56.0	51	4	US-09-443-199C-974	Sequenc
58.0	17	4	US-09-866-108A-8556	Sequence 8556, Ap	c 242	11.2	56.0	54	1	US-08-390-850-1097	Sequenc
58.0	17	4	US-09-866-108A-8557	Sequence 8557, Ap	c 243	11.2	56.0	54	1	US-08-435-634-1097	Sequenc
58.0	18	3	US-09-339-964-35	Sequence 35, Appl	c 244	11.2	56.0	54	1	US-08-435-634-1097	Sequenc
58.0	18	4	US-09-422-978-5304	Sequence 5304, Ap	c 245	11.2	56.0	54	4	US-09-256-000-25	Sequenc
58.0	19	2	US-08-117-952-533	Sequence 533, App	c 246	11.2	56.0	54	4	US-09-479-645A-179	Sequenc



56.0	56	4	US-09-007-288E-133	Sequence 133, App	320	10.8	54.0	17	4	US-09-371-772B-3137	Sequence
56.0	56	4	US-08-893-911A-3	Sequence 3, Appli	321	10.8	54.0	18	2	US-09-205-922-26	Sequence
56.0	58	3	US-08-755-587-202	Sequence 202, App	C 322	10.8	54.0	18	3	US-08-881-450A-12	Sequence
56.0	59	4	US-09-007-288E-84	Sequence 84, Appl	C 323	10.8	54.0	18	4	US-09-475-947A-260	Sequence
56.0	60	2	US-08-372-652-15	Sequence 15, Appl	324	10.8	54.0	19	3	US-09-215-221-43	Sequence
56.0	60	5	PCT-US95-16311-15	Sequence 15, Appl	C 325	10.8	54.0	20	1	US-08-531-556-70	Sequence
55.0	18	2	US-09-205-922-76	Sequence 76, Appl	C 326	10.8	54.0	20	1	US-08-472-416-70	Sequence
55.0	20	3	US-09-428-584-39	Sequence 39, Appl	C 327	10.8	54.0	20	3	US-09-286-904-68	Sequence
55.0	20	4	US-09-702-327-62	Sequence 62, Appl	C 328	10.8	54.0	20	3	US-09-418-640-50	Sequence
55.0	20	4	US-09-198-452A-5351	Sequence 5351, Ap	C 329	10.8	54.0	20	4	US-09-360-545-71	Sequence
55.0	21	3	US-08-840-767-21	Sequence 21, Appl	330	10.8	54.0	20	4	US-09-640-101-68	Sequence
55.0	22	4	US-09-358-383C-19	Sequence 19, Appl	C 331	10.8	54.0	20	4	US-09-255-154D-21	Sequence
55.0	23	3	US-09-222-817-17	Sequence 17, Appl	332	10.8	54.0	20	4	US-09-780-045-33	Sequence
55.0	23	3	US-09-050-559C-28	Sequence 28, Appl	333	10.8	54.0	20	4	US-09-780-045-107	Sequence
55.0	24	3	US-08-041-185-15	Sequence 15, Appl	C 334	10.8	54.0	22	4	US-09-363-243-13	Sequence
55.0	27	1	US-08-758-306-822	Sequence 822, App	C 335	10.8	54.0	23	1	US-08-741-406-13	Sequence
55.0	27	1	US-08-758-306-940	Sequence 940, App	C 336	10.8	54.0	23	3	US-08-544-381B-233	Sequence
55.0	27	1	US-09-023-731-20	Sequence 20, Appl	C 337	10.8	54.0	23	3	US-08-544-381B-234	Sequence
55.0	27	4	US-08-851-062-6	Sequence 6, Appli	C 338	10.8	54.0	23	3	US-09-024-472-13	Sequence
55.0	30	1	US-08-219-012-31	Sequence 31, Appl	C 339	10.8	54.0	25	1	US-08-362-706A-9	Sequence
55.0	30	3	US-08-687-421-219	Sequence 219, App	C 340	10.8	54.0	25	2	US-08-859-998-687	Sequence
55.0	31	4	US-08-793-381A-4	Sequence 4, Appli	341	10.8	54.0	25	3	US-09-522-494-39	Sequence
55.0	31	1	US-08-480-525-10	Sequence 10, Appl	342	10.8	54.0	25	3	US-09-522-494-40	Sequence
55.0	31	5	PCT-US94-06422-10	Sequence 10, Appl	C 343	10.8	54.0	25	4	US-09-549-608-9	Sequence
55.0	32	1	US-08-688-649-13	Sequence 13, Appl	C 344	10.8	54.0	25	4	US-09-225-928-687	Sequence
55.0	33	1	US-08-138-608-38	Sequence 38, Appl	C 345	10.8	54.0	25	4	US-09-225-201B-687	Sequence
55.0	35	3	US-08-928-881-23	Sequence 23, Appl	C 346	10.8	54.0	25	4	US-09-306-653-7	Sequence
55.0	35	4	US-09-543-921-23	Sequence 23, Appl	C 347	10.8	54.0	25	4	US-09-621-275-14	Sequence
55.0	35	4	US-09-266-014-10	Sequence 10, Appl	C 348	10.8	54.0	26	2	US-08-859-998-1262	Sequence
55.0	35	4	US-09-491-759-23	Sequence 23, Appl	C 349	10.8	54.0	26	4	US-09-225-928-1262	Sequence
55.0	36	1	US-08-466-033-261	Sequence 261, App	C 350	10.8	54.0	26	4	US-09-225-201B-1262	Sequence
55.0	36	1	US-08-444-733-261	Sequence 261, App	C 351	10.8	54.0	26	4	US-09-602-586-8	Sequence
55.0	36	2	US-08-464-134-261	Sequence 261, App	C 352	10.8	54.0	26	4	US-09-602-586-15	Sequence
55.0	36	2	US-08-461-361-261	Sequence 261, App	C 353	10.8	54.0	26	4	US-09-602-586-30	Sequence
55.0	36	2	US-08-485-910-261	Sequence 261, App	354	10.8	54.0	26	4	US-09-602-586-37	Sequence
55.0	39	1	US-08-066-961-22	Sequence 22, Appl	C 355	10.8	54.0	26	4	US-09-561-579A-8	Sequence
55.0	39	1	US-08-034-153D-9	Sequence 9, Appli	C 356	10.8	54.0	26	4	US-09-561-579A-15	Sequence
55.0	40	2	US-08-628-422-36	Sequence 36, Appl	357	10.8	54.0	26	4	US-09-561-579A-30	Sequence
55.0	44	3	US-08-666-354A-5	Sequence 5, Appli	C 358	10.8	54.0	26	4	US-09-561-579A-37	Sequence
55.0	47	4	US-09-422-978-2917	Sequence 2917, Ap	C 359	10.8	54.0	27	2	US-08-389-423-6	Sequence
55.0	51	4	US-09-443-199C-963	Sequence 963, App	C 360	10.8	54.0	27	3	US-08-776-251-8	Sequence
55.0	53	1	US-08-429-181-43	Sequence 43, Appl	361	10.8	54.0	27	4	US-09-189-028-6	Sequence
55.0	53	1	US-08-164-388-43	Sequence 43, Appl	C 362	10.8	54.0	28	3	US-08-993-008A-1	Sequence
55.0	58	3	US-09-061-702-12	Sequence 12, Appl	C 363	10.8	54.0	28	4	US-09-534-407-40	Sequence
55.0	58	3	US-08-860-038-15	Sequence 15, Appl	C 364	10.8	54.0	28	4	US-09-999-201B-40	Sequence
55.0	58	4	US-09-580-923-15	Sequence 15, Appl	C 365	10.8	54.0	28	4	US-09-698-154-5	Sequence
55.0	59	4	US-09-424-712-3	Sequence 3, Appli	C 366	10.8	54.0	31	3	US-08-544-381B-167	Sequence
55.0	60	3	US-07-602-848E-12	Sequence 12, Appl	C 367	10.8	54.0	32	1	US-08-619-724-4	Sequence
54.0	14	3	US-08-544-381B-235	Sequence 235, App	C 368	10.8	54.0	32	1	US-08-619-724-6	Sequence
54.0	15	1	US-08-311-462-3	Sequence 3, Appli	C 369	10.8	54.0	32	3	US-09-522-494-55	Sequence
54.0	15	1	US-08-311-462-12	Sequence 12, Appl	370	10.8	54.0	32	5	PCT-US95-04094-11	Sequence
54.0	15	2	US-08-434-354-3	Sequence 3, Appli	C 371	10.8	54.0	35	1	US-08-530-492-94	Sequence
54.0	15	2	US-08-434-354-12	Sequence 12, Appl	C 372	10.8	54.0	35	3	US-08-906-517-94	Sequence
54.0	17	1	US-08-179-738-23	Sequence 23, Appl	C 373	10.8	54.0	36	3	US-09-440-001-3	Sequence
54.0	17	1	US-08-281-940-4	Sequence 4, Appli	C 374	10.8	54.0	36	4	US-08-983-035A-20	Sequence
54.0	17	1	US-08-281-940-35	Sequence 35, Appl	C 375	10.8	54.0	36	4	US-08-983-035A-23	Sequence
54.0	17	1	US-08-308-638-3	Sequence 3, Appli	C 376	10.8	54.0	36	4	US-09-605-685-3	Sequence
54.0	17	1	US-08-373-124A-182	Sequence 182, App	C 377	10.8	54.0	38	4	US-09-564-805-156	Sequence
54.0	17	1	US-08-373-124A-184	Sequence 184, App	C 378	10.8	54.0	39	1	US-08-966-961-27	Sequence
54.0	17	1	US-08-435-628-182	Sequence 182, App	C 379	10.8	54.0	40	1	US-08-443-957-11	Sequence
54.0	17	1	US-08-435-628-184	Sequence 184, App	C 380	10.8	54.0	40	2	US-08-628-422-35	Sequence
54.0	17	2	US-08-710-134-4	Sequence 4, Appli	C 381	10.8	54.0	42	3	US-08-908-643C-30	Sequence
54.0	17	2	US-08-710-134-35	Sequence 35, Appl	C 382	10.8	54.0	43	1	US-08-437-538-11	Sequence
54.0	17	2	US-08-485-885-4	Sequence 4, Appli	C 383	10.8	54.0	45	1	US-08-443-957-34	Sequence
54.0	17	2	US-08-485-885-35	Sequence 35, Appl	C 384	10.8	54.0	45	2	US-08-470-939-25	Sequence
54.0	17	2	US-08-628-145-23	Sequence 23, Appl	C 385	10.8	54.0	45	2	US-08-356-786-13	Sequence
54.0	17	3	US-08-544-381B-243	Sequence 243, App	C 386	10.8	54.0	45	5	PCT-US96-09452-25	Sequence
54.0	17	3	US-09-215-221-41	Sequence 41, Appl	C 387	10.8	54.0	47	4	US-09-345-882-41	Sequence
54.0	17	4	US-08-584-040-7327	Sequence 7327, Ap	C 388	10.8	54.0	47	4	US-09-345-882-62	Sequence
54.0	17	4	US-08-584-040-7328	Sequence 7328, Ap	C 389	10.8	54.0	47	4	US-09-422-978-690	Sequence
54.0	17	4	US-09-270-140A-46	Sequence 46, Appl	C 390	10.8	54.0	47	4	US-09-422-978-919	Sequence
54.0	17	4	US-09-270-140A-47	Sequence 47, Appl	391	10.8	54.0	47	4	US-09-422-978-3644	Sequence
54.0	17	4	US-09-371-772B-3136	Sequence 3136, Ap	C 392	10.8	54.0	47	6	5510256-6	Patent No

54.0	49	4	US-09-306-653-1	Sequence 1, Appli	C 466	10.6	53.0	28	1	US-08-434-823-4	Sequenc
54.0	49	4	US-09-621-275-8	Sequence 8, Appli	C 467	10.6	53.0	28	1	US-08-457-366-4	Sequenc
54.0	49	5	PCT-US91-02568-35	Sequence 35, Appl	C 468	10.6	53.0	28	1	US-07-695-472B-22	Sequenc
54.0	50	1	US-08-171-389-511	Sequence 511, App	C 469	10.6	53.0	28	2	US-08-465-609-1	Sequenc
54.0	50	1	US-08-123-936-511	Sequence 511, App	C 470	10.6	53.0	28	3	US-08-646-861-28	Sequenc
54.0	50	2	US-08-475-228A-511	Sequence 511, App	C 471	10.6	53.0	28	3	US-09-176-320-3	Sequenc
54.0	50	3	US-08-482-080A-511	Sequence 511, App	C 472	10.6	53.0	28	4	US-09-106-375-22	Sequenc
54.0	50	4	US-09-357-487B-29	Sequence 29, Appl	C 473	10.6	53.0	29	4	US-09-562-069-3	Sequenc
54.0	50	4	US-09-354-947-511	Sequence 511, App	C 474	10.6	53.0	30	1	US-08-219-013-35	Sequenc
54.0	50	5	PCT-US93-12388-511	Sequence 511, App	C 475	10.6	53.0	30	1	US-08-186-229-24	Sequenc
54.0	54	1	US-08-390-850-1045	Sequence 1045, Ap	C 476	10.6	53.0	30	2	US-08-470-124-24	Sequenc
54.0	54	1	US-08-435-634-1045	Sequence 1045, Ap	C 477	10.6	53.0	30	3	US-08-467-023-198	Sequenc
54.0	55	1	US-08-484-686B-24	Sequence 24, Appl	C 478	10.6	53.0	30	3	US-08-687-421-223	Sequenc
54.0	55	3	US-08-463-160B-24	Sequence 8, Appli	C 479	10.6	53.0	30	3	US-08-658-034-4	Sequenc
54.0	55	4	US-09-698-154-8	Sequence 27, Appl	C 480	10.6	53.0	30	4	US-09-123-030-6	Sequenc
54.0	56	2	US-08-537-811-27	Sequence 126, App	C 481	10.6	53.0	30	4	US-09-358-052-4	Sequenc
54.0	57	1	US-08-530-492-126	Sequence 126, App	C 482	10.6	53.0	32	1	US-08-445-050-19	Sequenc
54.0	57	3	US-08-906-517-126	Sequence 18, Appl	C 483	10.6	53.0	32	1	US-08-204-691-19	Sequenc
54.0	57	4	US-09-306-653-18	Sequence 25, Appl	C 484	10.6	53.0	32	3	US-08-875-509-6	Sequenc
54.0	57	4	US-09-621-275-25	Sequence 33, Appl	C 485	10.6	53.0	32	4	US-09-619-334-1	Sequenc
54.0	57	5	PCT-US91-02568-33	Sequence 33, Appl	C 486	10.6	53.0	33	3	US-08-875-509-2	Sequenc
54.0	60	2	US-08-828-008-10	Sequence 10, Appl	C 487	10.6	53.0	33	3	US-07-987-264-19	Sequenc
54.0	60	2	US-08-252-620A-1831	Sequence 1831, Ap	C 488	10.6	53.0	33	4	US-09-472-065A-16	Sequenc
53.0	17	2	US-09-071-845-1831	Sequence 190, App	C 489	10.6	53.0	33	4	US-09-818-780-56	Sequenc
53.0	18	1	US-08-050-073-190	Sequence 17, Appl	C 490	10.6	53.0	34	1	US-08-271-880A-40	Sequenc
53.0	19	3	US-08-369-822C-17	Sequence 17, Appl	C 491	10.6	53.0	34	2	US-08-910-408-40	Sequenc
53.0	19	3	US-08-582-776C-17	Sequence 17, Appl	C 492	10.6	53.0	34	3	US-09-249-215-40	Sequenc
53.0	20	3	US-09-167-921-41	Sequence 41, Appl	C 493	10.6	53.0	34	3	US-09-091-305-4	Sequenc
53.0	20	3	US-08-434-831B-17	Sequence 12, Appl	C 494	10.6	53.0	35	1	US-08-753-054-5	Sequenc
53.0	20	3	US-08-822-516-12	Sequence 8, Appli	C 495	10.6	53.0	36	1	US-08-482-882-57	Sequenc
53.0	20	3	US-08-515-495-8	Sequence 41, Appl	C 497	10.6	53.0	36	1	US-08-483-389-57	Sequenc
53.0	20	3	US-09-323-743-41	Sequence 53, Appl	C 498	10.6	53.0	36	2	US-08-487-113D-57	Sequenc
53.0	20	3	US-09-657-481A-53	Sequence 141, App	C 499	10.6	53.0	36	2	US-08-473-503-57	Sequenc
53.0	20	3	US-09-593-711A-141	Sequence 142, App	C 500	10.6	53.0	36	2	US-08-483-932-57	Sequenc
53.0	20	3	US-09-593-711A-142	Sequence 68, Appl	C 501	10.6	53.0	36	2	US-08-954-333-4	Sequenc
53.0	20	3	US-09-109-663-68	Sequence 12, Appl	C 502	10.6	53.0	36	2	US-08-720-420A-57	Sequenc
53.0	20	4	US-09-142-623-9	Sequence 9, Appli	C 503	10.6	53.0	36	3	US-08-714-017-57	Sequenc
53.0	20	4	US-09-188-452A-2507	Sequence 2507, Ap	C 504	10.6	53.0	36	4	US-08-475-680-57	Sequenc
53.0	20	4	US-08-823-549-69	Sequence 69, Appl	C 505	10.6	53.0	36	4	US-09-147-208-17	Sequenc
53.0	21	1	US-08-379-078-584	Sequence 584, App	C 506	10.6	53.0	36	4	US-09-550-117A-17	Sequenc
53.0	21	4	US-07-974-409C-207	Sequence 207, App	C 507	10.6	53.0	38	2	US-08-464-257-7	Sequenc
53.0	21	4	US-09-194-842A-33	Sequence 33, Appl	C 508	10.6	53.0	38	2	US-08-715-941-10	Sequenc
53.0	21	4	US-09-380-836-51	Sequence 51, Appl	C 509	10.6	53.0	38	2	US-09-062-375-7	Sequenc
53.0	21	5	PCT-US93-00977-207	Sequence 207, App	C 510	10.6	53.0	38	3	US-09-203-796A-7	Sequenc
53.0	22	1	US-08-118-441-22	Sequence 22, Appl	C 511	10.6	53.0	39	2	US-08-254-354-11	Sequenc
53.0	22	3	US-08-338-579A-22	Sequence 22, Appl	C 512	10.6	53.0	39	2	US-08-453-024-4	Sequenc
53.0	22	3	US-09-092-314-7	Sequence 7, Appli	C 513	10.6	53.0	39	3	US-08-070-162-4	Sequenc
53.0	22	5	PCT-US94-09851-22	Sequence 8, Appli	C 514	10.6	53.0	39	5	US-09-475-947A-344	Sequenc
53.0	25	4	US-08-462-509B-8	Sequence 10, Appl	C 515	10.6	53.0	40	4	PCT-US95-06137-11	Sequenc
53.0	25	4	US-08-462-509B-10	Sequence 12, Appl	C 516	10.6	53.0	40	4	US-08-911-393-10	Sequenc
53.0	25	4	US-08-462-509B-12	Sequence 36, Appl	C 517	10.6	53.0	41	3	US-08-480-640A-187	Sequenc
53.0	25	5	PCT-US95-05616-8	Sequence 8, Appli	C 518	10.6	53.0	41	3	US-08-295-802-187	Sequenc
53.0	25	5	PCT-US95-05616-10	Sequence 10, Appl	C 519	10.6	53.0	41	3	US-08-686-968C-75	Sequenc
53.0	25	5	PCT-US95-05616-12	Sequence 12, Appl	C 520	10.6	53.0	41	3	US-08-488-237A-187	Sequenc
53.0	26	1	US-07-832-905B-65	Sequence 65, Appl	C 521	10.6	53.0	41	4	US-08-375-992A-187	Sequenc
53.0	26	2	US-08-700-757-65	Sequence 65, Appl	C 522	10.6	53.0	41	4	US-08-472-679H-187	Sequenc
53.0	26	2	US-08-996-306-6	Sequence 17, Appli	C 523	10.6	53.0	42	1	US-08-225-224-47	Sequenc
53.0	26	2	US-08-747-536-17	Sequence 17, Appl	C 524	10.6	53.0	42	1	US-08-445-050-14	Sequenc
53.0	26	2	US-08-859-998-556	Sequence 556, App	C 525	10.6	53.0	42	1	US-08-204-691-14	Sequenc
53.0	26	3	US-09-338-907-6	Sequence 6, Appli	C 526	10.6	53.0	42	2	US-08-428-257A-55	Sequenc
53.0	26	4	US-09-218-207-6	Sequence 556, App	C 527	10.6	53.0	42	3	US-08-722-258-47	Sequenc
53.0	26	4	US-09-225-928-556	Sequence 556, App	C 528	10.6	53.0	42	3	US-08-724-586-5	Sequenc
53.0	26	4	US-09-225-201B-556	Sequence 1301, Ap	C 529	10.6	53.0	42	3	US-08-421-632-5	Sequenc
53.0	27	3	US-08-985-162-1301	Sequence 1583, Ap	C 530	10.6	53.0	42	4	US-09-932-190-5	Sequenc
53.0	27	3	US-08-985-162-1583	Sequence 267, App	C 531	10.6	53.0	42	5	PCT-US95-04468-47	Sequenc
53.0	27	3	US-08-998-099-267	Sequence 6561, Ap	C 532	10.6	53.0	43	1	US-08-116-388-8	Sequenc
53.0	27	4	US-08-584-040-6561	Sequence 25, Appl	C 533	10.6	53.0	43	1	US-08-445-050-15	Sequenc
53.0	27	4	US-09-585-228-25	Sequence 1301, Ap	C 534	10.6	53.0	43	1	US-08-204-691-15	Sequenc
53.0	27	4	US-09-401-063-1301	Sequence 1583, Ap	C 535	10.6	53.0	44	1	PCT-US94-09318-8	Sequenc
53.0	27	4	US-09-401-063-1583	Sequence 16, Appl	C 536	10.6	53.0	44	1	US-08-375-116A-42	Sequenc
53.0	27	4	US-08-250-740-16		C 537	10.6	53.0	47	4	US-09-422-978-191	Sequenc
53.0	28	1			C 538	10.6	53.0	47	4	US-09-422-978-2656	Sequenc

53.0	47	4	US-09-422-978-2725	Sequence 2725, Ap	612	10.4	52.0	20	4	US-09-997-579-34	Sequence
53.0	47	4	US-09-422-978-3806	Sequence 3806, Ap	c 613	10.4	52.0	21	4	US-08-977-378-18	Sequence
53.0	49	1	US-08-530-492-89	Sequence 89, Appl	614	10.4	52.0	22	1	US-08-379-078-418	Sequence
53.0	49	1	US-08-482-862-72	Sequence 72, Appl	615	10.4	52.0	22	1	US-08-379-078-419	Sequence
53.0	49	1	US-08-483-389-72	Sequence 72, Appl	c 616	10.4	52.0	22	1	US-08-223-902-12	Sequence
53.0	49	1	US-08-487-113D-72	Sequence 72, Appl	617	10.4	52.0	22	1	US-09-101-886B-8	Sequence
53.0	49	2	US-08-473-503-72	Sequence 72, Appl	618	10.4	52.0	22	3	US-09-101-886B-16	Sequence
53.0	49	2	US-08-483-932-72	Sequence 72, Appl	c 619	10.4	52.0	22	3	US-09-101-886B-26	Sequence
53.0	49	2	US-08-720-420A-72	Sequence 72, Appl	c 620	10.4	52.0	22	3	US-09-101-886B-27	Sequence
53.0	49	3	US-08-714-017-72	Sequence 72, Appl	621	10.4	52.0	22	4	US-07-974-409C-31	Sequence
53.0	49	3	US-08-475-680-72	Sequence 72, Appl	622	10.4	52.0	22	4	US-07-974-409C-32	Sequence
53.0	49	3	US-08-906-517-89	Sequence 89, Appl	623	10.4	52.0	22	5	PCT-US93-00977-31	Sequence
53.0	50	1	US-08-171-389-571	Sequence 571, Appl	624	10.4	52.0	22	5	PCT-US93-00977-32	Sequence
53.0	50	1	US-08-207-901-34	Sequence 34, Appl	625	10.4	52.0	23	1	US-07-722-798A-95	Sequence
53.0	50	1	US-08-123-936-571	Sequence 571, Appl	c 626	10.4	52.0	23	3	US-09-456-830-68	Sequence
53.0	50	1	US-08-475-228A-571	Sequence 571, Appl	c 627	10.4	52.0	23	3	US-09-002-285-68	Sequence
53.0	50	2	US-08-999-811-12	Sequence 12, Appl	c 628	10.4	52.0	23	4	US-09-589-477-68	Sequence
53.0	50	3	US-08-482-080A-571	Sequence 12, Appl	c 629	10.4	52.0	24	3	US-09-474-922A-8	Sequence
53.0	50	3	US-09-042-105-12	Sequence 571, Appl	c 630	10.4	52.0	25	1	US-07-722-798A-96	Sequence
53.0	50	4	US-09-354-947-571	Sequence 571, Appl	631	10.4	52.0	25	1	US-08-049-061-36	Sequence
53.0	50	4	US-08-465-968-7	Sequence 7, Appl	c 632	10.4	52.0	25	1	US-08-049-061-38	Sequence
53.0	50	5	PCT-US93-12388-571	Sequence 7, Appl	c 633	10.4	52.0	25	1	US-08-374-144-5	Sequence
53.0	50	5	PCT-US96-09001-4	Sequence 4, Appl	634	10.4	52.0	25	1	US-08-374-144-21	Sequence
53.0	51	4	US-09-648-667-10	Sequence 10, Appl	c 635	10.4	52.0	25	1	US-08-775-164-5	Sequence
53.0	51	4	US-09-443-199C-58	Sequence 58, Appl	636	10.4	52.0	25	1	US-08-775-164-21	Sequence
53.0	51	4	US-09-443-199C-147	Sequence 147, Appl	c 637	10.4	52.0	25	2	US-08-775-609-5	Sequence
53.0	51	4	US-09-443-199C-148	Sequence 148, Appl	638	10.4	52.0	25	2	US-08-775-609-21	Sequence
53.0	51	4	US-09-443-199C-636	Sequence 636, Appl	c 639	10.4	52.0	25	2	US-08-775-607-5	Sequence
53.0	51	4	US-09-443-199C-958	Sequence 958, Appl	640	10.4	52.0	25	2	US-08-775-607-21	Sequence
53.0	51	4	US-09-443-199C-1041	Sequence 1041, Ap	c 641	10.4	52.0	25	2	US-09-866-108A-13458	Sequence
53.0	53	1	US-08-429-181-48	Sequence 48, Appl	c 642	10.4	52.0	25	4	US-09-866-108A-13459	Sequence
53.0	53	1	US-08-164-388-48	Sequence 48, Appl	c 643	10.4	52.0	25	4	US-09-866-108A-13460	Sequence
53.0	54	4	US-09-315-926A-31	Sequence 31, Appl	c 644	10.4	52.0	25	4	US-09-866-108A-13461	Sequence
53.0	54	4	US-09-315-926A-65	Sequence 65, Appl	c 645	10.4	52.0	25	5	PCT-US93-06828-5	Sequence
53.0	55	1	US-08-445-050-18	Sequence 18, Appl	646	10.4	52.0	26	2	US-08-852-806-4	Sequence
53.0	55	1	US-08-204-691-18	Sequence 18, Appl	647	10.4	52.0	26	3	US-09-163-669-4	Sequence
53.0	55	2	US-08-715-941-11	Sequence 11, Appl	c 648	10.4	52.0	26	4	US-09-043-646-5	Sequence
53.0	55	2	US-08-715-941-14	Sequence 14, Appl	649	10.4	52.0	27	2	US-08-853-998-844	Sequence
53.0	56	3	US-08-307-896-8	Sequence 8, Appl	c 650	10.4	52.0	27	3	US-08-513-974B-187	Sequence
53.0	60	1	US-08-424-788-15	Sequence 15, Appl	651	10.4	52.0	27	3	US-09-242-948-7	Sequence
53.0	60	2	US-08-743-130A-25	Sequence 25, Appl	652	10.4	52.0	27	3	US-08-891-292A-2	Sequence
52.0	16	4	US-09-308-683-3	Sequence 3, Appl	653	10.4	52.0	27	4	US-09-225-928-844	Sequence
52.0	17	1	US-08-373-124A-180	Sequence 180, Appl	654	10.4	52.0	27	4	US-09-225-201B-844	Sequence
52.0	17	1	US-08-435-628-180	Sequence 180, Appl	655	10.4	52.0	27	4	US-09-921-737C-2	Sequence
52.0	17	2	US-08-292-620A-1881	Sequence 1881, Ap	656	10.4	52.0	28	2	US-08-981-663-7	Sequence
52.0	17	3	US-09-071-845-1881	Sequence 1881, Ap	657	10.4	52.0	28	2	US-08-859-998-373	Sequence
52.0	17	4	US-08-679-645-680	Sequence 680, Appl	658	10.4	52.0	28	4	US-09-225-928-373	Sequence
52.0	17	4	US-09-866-108A-8558	Sequence 8558, Ap	659	10.4	52.0	28	4	US-09-225-201B-373	Sequence
52.0	17	4	US-09-866-108A-8559	Sequence 8559, Ap	660	10.4	52.0	29	2	US-08-467-603-83	Sequence
52.0	17	4	US-09-866-108A-8560	Sequence 8560, Ap	661	10.4	52.0	29	2	US-08-466-793-83	Sequence
52.0	17	4	US-09-866-108A-8561	Sequence 8561, Ap	662	10.4	52.0	29	2	US-08-491-861A-83	Sequence
52.0	18	1	US-08-369-282-2	Sequence 2, Appl	663	10.4	52.0	29	3	US-08-544-381B-166	Sequence
52.0	18	2	US-09-205-922-85	Sequence 85, Appl	c 664	10.4	52.0	29	3	US-08-920-919A-20	Sequence
52.0	18	3	US-09-474-922A-77	Sequence 77, Appl	c 665	10.4	52.0	29	3	US-09-324-910-10	Sequence
52.0	18	4	US-09-422-978-8353	Sequence 8353, Ap	666	10.4	52.0	29	3	US-09-275-850-160	Sequence
52.0	18	4	PCT-US92-00626-2	Sequence 2, Appl	c 667	10.4	52.0	29	3	US-09-374-671A-85	Sequence
52.0	18	5	US-08-044-618-2	Sequence 32, Appl	668	10.4	52.0	29	3	US-08-303-162A-9	Sequence
52.0	20	1	US-08-148-058A-32	Sequence 32, Appl	669	10.4	52.0	30	1	US-08-123-702-36	Sequence
52.0	20	1	US-08-478-042-32	Sequence 32, Appl	670	10.4	52.0	30	1	US-08-634-060-9	Sequence
52.0	20	1	US-08-645-215-32	Sequence 32, Appl	671	10.4	52.0	30	1	US-08-709-515-9	Sequence
52.0	20	2	US-08-466-604-32	Sequence 47, Appl	672	10.4	52.0	30	1	US-08-078-090-14	Sequence
52.0	20	2	US-08-810-599-47	Sequence 36, Appl	673	10.4	52.0	30	3	US-08-544-381B-161	Sequence
52.0	20	3	US-08-757-438-38	Sequence 3, Appl	c 674	10.4	52.0	30	3	US-08-544-381B-163	Sequence
52.0	20	3	US-09-416-756A-3	Sequence 3, Appl	c 675	10.4	52.0	30	3	US-08-544-381B-164	Sequence
52.0	20	3	US-09-435-296-31	Sequence 84, Appl	c 676	10.4	52.0	30	3	US-08-544-381B-165	Sequence
52.0	20	3	US-09-428-583-84	Sequence 40, Appl	c 677	10.4	52.0	30	4	US-09-342-143-12	Sequence
52.0	20	4	US-09-336-643A-40	Sequence 40, Appl	c 678	10.4	52.0	30	4	US-09-342-143-12	Sequence
52.0	20	4	US-09-702-327-63	Sequence 63, Appl	c 679	10.4	52.0	30	4	US-09-549-564-1	Sequence
52.0	20	4	US-09-302-681-39	Sequence 39, Appl	c 680	10.4	52.0	30	4	US-09-236-268-4	Sequence
52.0	20	4	US-08-626-285-36	Sequence 36, Appl	c 681	10.4	52.0	30	4	US-09-236-268-5	Sequence
52.0	20	4	US-09-425-233-2	Sequence 2, Appl	c 682	10.4	52.0	30	4	US-09-924-439-12	Sequence
52.0	20	4	US-09-422-978-7954	Sequence 7954, Ap	c 683	10.4	52.0	30	4	US-09-390-134B-2	Sequence
52.0	20	4			684	10.4	52.0	30	4		

52.0	31	2	US-08-649-619B-3	Sequence 3, Appli	C 758	10.4	52.0	50	4	US-09-443-199C-632	Sequenc
52.0	32	3	US-08-446-909-4	Sequence 4, Appli	C 759	10.4	52.0	50	4	US-09-443-199C-633	Sequenc
52.0	32	3	US-08-446-911-4	Sequence 4, Appli	C 760	10.4	52.0	51	4	US-09-443-199C-257	Sequenc
52.0	32	4	US-09-420-861-4	Sequence 4, Appli	C 761	10.4	52.0	51	4	US-09-443-199C-258	Sequenc
52.0	32	4	US-09-374-669-4	Sequence 4, Appli	C 762	10.4	52.0	51	4	US-09-443-199C-259	Sequenc
52.0	32	4	US-09-552-709-4	Sequence 4, Appli	C 763	10.4	52.0	51	4	US-09-443-199C-261	Sequenc
52.0	34	1	US-08-102-567-13	Sequence 13, Appl	C 764	10.4	52.0	51	4	US-09-443-199C-631	Sequenc
52.0	34	3	US-08-462-947-13	Sequence 13, Appl	C 765	10.4	52.0	51	4	US-09-443-199C-634	Sequenc
52.0	34	3	US-08-379-452-32	Sequence 32, Appl	C 766	10.4	52.0	52	5	PCT-US91-02568-34	Sequenc
52.0	34	3	US-08-379-452-33	Sequence 33, Appl	C 767	10.4	52.0	53	2	US-08-771-624B-7	Sequenc
52.0	34	3	US-09-409-670-32	Sequence 32, Appl	C 768	10.4	52.0	54	1	US-08-311-486C-1037	Sequenc
52.0	34	3	US-09-409-670-33	Sequence 33, Appl	C 769	10.4	52.0	54	1	US-08-484-686B-12	Sequenc
52.0	37	1	US-08-021-623C-11	Sequence 11, Appl	C 770	10.4	52.0	54	2	US-08-771-624B-5	Sequenc
52.0	38	4	US-09-367-777-9	Sequence 9, Appli	C 771	10.4	52.0	54	2	US-08-771-624B-9	Sequenc
52.0	38	4	US-09-367-777-25	Sequence 25, Appl	C 772	10.4	52.0	54	3	US-08-463-160B-12	Sequenc
52.0	38	4	US-09-367-777-29	Sequence 29, Appl	C 773	10.4	52.0	55	1	US-08-160-670A-11	Sequenc
52.0	38	4	US-09-367-777-33	Sequence 33, Appl	C 774	10.4	52.0	55	4	US-08-956-171B-2854	Sequenc
52.0	39	2	US-08-771-624B-11	Sequence 11, Appl	C 775	10.4	52.0	56	5	PCT-US91-02568-3	Sequenc
52.0	39	3	US-09-052-995-3	Sequence 3, Appli	C 776	10.4	52.0	57	4	US-09-097-055B-48	Sequenc
52.0	39	4	US-09-318-786-4	Sequence 4, Appli	C 777	10.4	52.0	58	3	US-09-097-055B-54	Sequenc
52.0	39	4	US-09-952-572-5	Sequence 5, Appli	C 778	10.4	52.0	58	3	US-09-275-850-263	Sequenc
52.0	40	1	US-08-443-957-24	Sequence 24, Appl	C 779	10.4	52.0	58	4	US-08-956-171B-2914	Sequenc
52.0	40	2	US-08-857-946-80	Sequence 80, Appl	C 780	10.4	52.0	60	3	US-08-870-930-29	Sequenc
52.0	40	3	US-08-831-132-16	Sequence 16, Appl	C 781	10.4	52.0	60	4	US-09-254-968-32	Sequenc
52.0	40	3	US-08-970-740-80	Sequence 80, Appl	C 782	10.2	51.0	15	2	US-08-292-620A-18	Sequenc
52.0	40	3	US-09-416-150-16	Sequence 16, Appl	C 783	10.2	51.0	15	3	US-09-071-845-18	Sequenc
52.0	40	3	US-09-091-814-84	Sequence 84, Appl	C 784	10.2	51.0	16	1	US-07-646-998A-20	Sequenc
52.0	41	1	US-07-931-473B-173	Sequence 173, App	C 785	10.2	51.0	16	1	US-08-094-128A-20	Sequenc
52.0	41	1	US-07-714-131C-173	Sequence 173, App	C 786	10.2	51.0	16	1	US-08-094-128A-32	Sequenc
52.0	41	1	US-08-412-110-173	Sequence 173, App	C 787	10.2	51.0	16	1	US-08-455-674-20	Sequenc
52.0	41	1	US-08-409-442A-173	Sequence 173, App	C 788	10.2	51.0	16	1	US-08-455-674-32	Sequenc
52.0	41	2	US-08-469-609A-173	Sequence 173, App	C 789	10.2	51.0	16	1	US-08-455-992-20	Sequenc
52.0	41	3	US-09-143-190-173	Sequence 173, App	C 790	10.2	51.0	16	1	US-08-455-992-32	Sequenc
52.0	41	4	US-09-502-344-173	Sequence 173, App	C 791	10.2	51.0	16	1	US-08-455-972-32	Sequenc
52.0	42	1	US-08-437-538-14	Sequence 14, Appl	C 792	10.2	51.0	16	1	US-08-455-972-32	Sequenc
52.0	43	1	US-07-931-473B-335	Sequence 335, App	C 793	10.2	51.0	16	1	US-08-741-881-120	Sequenc
52.0	43	1	US-07-714-131C-335	Sequence 335, App	C 794	10.2	51.0	16	1	US-08-739-158-120	Sequenc
52.0	43	1	US-08-412-110-335	Sequence 335, App	C 795	10.2	51.0	16	2	US-08-739-167-120	Sequenc
52.0	43	1	US-08-409-442A-335	Sequence 335, App	C 796	10.2	51.0	16	3	US-08-404-796-120	Sequenc
52.0	43	1	US-08-466-033-260	Sequence 260, App	C 797	10.2	51.0	16	3	US-08-331-869-120	Sequenc
52.0	43	1	US-08-444-733-260	Sequence 260, App	C 798	10.2	51.0	16	3	US-09-121-162-6	Sequenc
52.0	43	2	US-08-469-609A-335	Sequence 335, App	C 799	10.2	51.0	16	4	US-09-350-399-120	Sequenc
52.0	43	2	US-08-464-134-260	Sequence 260, App	C 800	10.2	51.0	16	4	US-09-236-140A-120	Sequenc
52.0	43	2	US-08-461-361-260	Sequence 260, App	C 801	10.2	51.0	16	5	PCT-US92-00652-20	Sequenc
52.0	43	2	US-08-485-910-260	Sequence 260, App	C 802	10.2	51.0	17	1	US-08-306-546C-5	Sequenc
52.0	43	3	US-09-143-190-335	Sequence 335, App	C 803	10.2	51.0	17	1	US-08-257-784A-7	Sequenc
52.0	43	4	US-09-502-344-335	Sequence 335, App	C 804	10.2	51.0	17	2	US-08-530-524A-5	Sequenc
52.0	44	4	US-09-011-143-14	Sequence 14, Appl	C 805	10.2	51.0	17	2	US-08-489-066A-11	Sequenc
52.0	44	4	US-09-302-495-14	Sequence 14, Appl	C 806	10.2	51.0	17	2	US-08-897-340-9	Sequenc
52.0	44	4	US-10-079-616-14	Sequence 14, Appl	C 807	10.2	51.0	17	3	US-08-489-072A-11	Sequenc
52.0	45	3	US-09-164-023-22	Sequence 22, Appl	C 808	10.2	51.0	17	3	US-08-985-162-362	Sequenc
52.0	46	4	US-08-977-378-19	Sequence 19, Appl	C 809	10.2	51.0	17	3	US-08-985-162-363	Sequenc
52.0	47	4	US-09-641-638-853	Sequence 853, App	C 810	10.2	51.0	17	3	US-09-252-329-9	Sequenc
52.0	47	4	US-09-422-978-55	Sequence 55, Appl	C 811	10.2	51.0	17	4	US-08-489-071A-11	Sequenc
52.0	47	4	US-09-422-978-400	Sequence 400, App	C 812	10.2	51.0	17	4	US-09-401-063-362	Sequenc
52.0	47	4	US-09-422-978-1473	Sequence 1473, Ap	C 813	10.2	51.0	17	4	US-09-401-063-363	Sequenc
52.0	47	4	US-09-422-978-2458	Sequence 2458, Ap	C 814	10.2	51.0	17	4	US-09-866-108A-8555	Sequenc
52.0	47	4	US-08-422-978-3111	Sequence 3111, Ap	C 815	10.2	51.0	18	1	US-08-411-796-301	Sequenc
52.0	48	1	US-08-453-924-12	Sequence 12, Appl	C 816	10.2	51.0	18	2	US-08-117-952-729	Sequenc
52.0	48	2	US-08-618-911-10	Sequence 10, Appl	C 817	10.2	51.0	18	3	US-08-471-039-301	Sequenc
52.0	48	4	US-09-761-962A-38	Sequence 38, Appl	C 818	10.2	51.0	18	3	US-08-181-664-28	Sequenc
52.0	48	5	PCT-US94-06079-7	Sequence 7, Appli	C 819	10.2	51.0	18	3	US-08-975-080-2	Sequenc
52.0	50	1	US-08-199-508-35	Sequence 35, Appl	C 820	10.2	51.0	18	4	US-09-283-144-14	Sequenc
52.0	50	4	US-09-073-661-3	Sequence 3, Appli	C 821	10.2	51.0	18	4	US-09-000-286A-23	Sequenc
52.0	50	4	US-09-073-661-5	Sequence 5, Appli	C 822	10.2	51.0	18	4	US-09-000-286A-24	Sequenc
52.0	50	4	US-09-073-661-6	Sequence 6, Appli	C 823	10.2	51.0	18	4	US-08-559-390-301	Sequenc
52.0	50	4	US-09-073-661-7	Sequence 7, Appli	C 824	10.2	51.0	18	5	PCT-US93-11198-301	Sequenc
52.0	50	4	US-09-073-661-8	Sequence 8, Appli	C 825	10.2	51.0	19	4	US-09-475-947A-178	Sequenc
52.0	50	4	US-10-100-785-3	Sequence 3, Appli	C 826	10.2	51.0	19	4	US-09-422-978-6184	Sequenc
52.0	50	4	US-10-100-785-5	Sequence 5, Appli	C 827	10.2	51.0	19	4	US-09-422-978-6968	Sequenc
52.0	50	4	US-10-100-785-6	Sequence 6, Appli	C 828	10.2	51.0	19	4	US-09-422-978-6968	Sequenc
52.0	50	4	US-10-100-785-7	Sequence 7, Appli	C 829	10.2	51.0	20	1	US-08-063-167A-9	Sequenc
52.0	50	4	US-10-100-785-8	Sequence 8, Appli	C 830	10.2	51.0	20	1	US-08-007-997A-9	Sequenc

51.0	20	1	US-08-359-696-4	Sequence 4, Appli	904	10.2	51.0	27	4	US-09-469-211A-8	Sequence
51.0	20	1	US-08-171-718-13	Sequence 13, Appli	905	10.2	51.0	27	5	PCT-US93-11198-300	Sequence
51.0	20	2	US-08-440-740A-9	Sequence 9, Appli	906	10.2	51.0	28	2	US-08-859-998-619	Sequence
51.0	20	2	US-08-785-750-12	Sequence 12, Appli	907	10.2	51.0	28	3	US-08-952-967-12	Sequence
51.0	20	2	US-08-344-155C-9	Sequence 9, Appli	908	10.2	51.0	28	4	US-09-225-928-619	Sequence
51.0	20	2	US-08-904-901-117	Sequence 117, App	909	10.2	51.0	28	4	US-09-225-201B-619	Sequence
51.0	20	2	US-08-982-845B-9	Sequence 9, Appli	910	10.2	51.0	29	1	US-08-219-633-25	Sequence
51.0	20	3	US-08-478-087-13	Sequence 13, Appli	911	10.2	51.0	29	1	US-08-515-236-25	Sequence
51.0	20	3	US-08-291-562-3	Sequence 3, Appli	912	10.2	51.0	29	1	US-08-761-950-25	Sequence
51.0	20	3	US-08-911-525B-9	Sequence 9, Appli	913	10.2	51.0	29	2	US-08-811-492-100	Sequence
51.0	20	3	US-09-197-380-3	Sequence 3, Appli	914	10.2	51.0	29	2	US-08-811-492-101	Sequence
51.0	20	3	US-09-085-759-9	Sequence 9, Appli	915	10.2	51.0	29	3	US-08-632-575B-39	Sequence
51.0	20	3	US-08-733-360A-5	Sequence 5, Appli	916	10.2	51.0	29	3	US-08-344-604-22	Sequence
51.0	20	3	US-09-249-730-117	Sequence 117, App	917	10.2	51.0	29	3	US-09-327-229-31	Sequence
51.0	20	3	US-09-428-696-31	Sequence 31, Appli	918	10.2	51.0	29	4	US-09-199-542B-39	Sequence
51.0	20	3	US-09-128-496-9	Sequence 9, Appli	919	10.2	51.0	29	5	PCT-US95-12608-31	Sequence
51.0	20	3	US-09-280-805-173	Sequence 173, App	920	10.2	51.0	30	2	US-08-545-562A-42	Sequence
51.0	20	3	US-08-916-935-5	Sequence 5, Appli	921	10.2	51.0	30	2	US-08-896-501A-42	Sequence
51.0	20	3	US-09-487-368A-54	Sequence 54, Appli	922	10.2	51.0	30	2	US-08-859-998-446	Sequence
51.0	20	4	US-09-009-490A-9	Sequence 9, Appli	923	10.2	51.0	30	2	US-08-331-081B-14	Sequence
51.0	20	4	US-09-007-097-4	Sequence 82, Appli	924	10.2	51.0	30	2	US-09-161-466-3	Sequence
51.0	20	4	US-09-488-856A-82	Sequence 12, Appli	925	10.2	51.0	30	4	US-09-225-928-446	Sequence
51.0	20	4	US-08-205-337-12	Sequence 33, Appli	926	10.2	51.0	30	4	US-09-684-938-167	Sequence
51.0	20	4	US-09-732-199A-33	Sequence 54, Appli	927	10.2	51.0	30	4	US-09-308-825A-167	Sequence
51.0	20	4	US-09-629-644A-54	Sequence 54, Appli	928	10.2	51.0	30	4	US-09-758-282B-42	Sequence
51.0	20	4	US-09-198-452A-5279	Sequence 5279, Ap	929	10.2	51.0	31	3	US-08-836-329-14	Sequence
51.0	20	4	US-09-578-764A-4	Sequence 4, Appli	930	10.2	51.0	31	4	US-09-508-370A-13	Sequence
51.0	20	4	US-09-249-247-117	Sequence 117, App	931	10.2	51.0	31	5	PCT-US94-06331A-39	Sequence
51.0	20	4	US-09-629-644A-54	Sequence 54, Appli	932	10.2	51.0	32	1	US-08-181-271A-60	Sequence
51.0	20	4	US-09-112-580-175	Sequence 175, App	933	10.2	51.0	32	1	US-08-449-315-60	Sequence
51.0	20	4	US-09-526-193A-103	Sequence 103, App	934	10.2	51.0	32	1	US-08-456-265A-60	Sequence
51.0	20	5	PCT-US93-08101-9	Sequence 9, Appli	935	10.2	51.0	32	1	US-08-455-416-60	Sequence
51.0	20	5	PCT-US96-03965-4	Sequence 4, Appli	936	10.2	51.0	32	1	US-08-455-244-60	Sequence
51.0	21	1	US-08-137-252-4	Sequence 4, Appli	937	10.2	51.0	32	1	US-08-454-876-60	Sequence
51.0	21	1	US-08-079-110A-4	Sequence 4, Appli	938	10.2	51.0	32	1	US-08-632-575B-59	Sequence
51.0	21	1	US-08-196-630A-4	Sequence 4, Appli	939	10.2	51.0	32	2	US-08-457-364-60	Sequence
51.0	21	3	US-08-573-186-4	Sequence 19, Appli	940	10.2	51.0	32	2	US-08-456-262-60	Sequence
51.0	21	3	US-08-913-942-19	Sequence 545, App	941	10.2	51.0	32	2	US-08-456-240-60	Sequence
51.0	21	3	US-08-943-731-545	Sequence 2, Appli	942	10.2	51.0	32	2	US-08-797-689-24	Sequence
51.0	21	3	US-08-406-030A-2	Sequence 114, App	943	10.2	51.0	32	2	US-08-455-736-60	Sequence
51.0	21	4	US-09-382-552-114	Sequence 6, Appli	944	10.2	51.0	32	2	US-08-648-657-11	Sequence
51.0	21	4	US-09-698-286A-6	Sequence 50, Appli	945	10.2	51.0	32	2	US-08-971-217-60	Sequence
51.0	22	4	US-09-431-705-50	Sequence 149, App	946	10.2	51.0	32	2	US-09-350-600-60	Sequence
51.0	22	4	US-08-931-858E-149	Sequence 149, App	947	10.2	51.0	32	3	US-09-199-542B-59	Sequence
51.0	23	3	US-08-981-739-149	Sequence 7, Appli	948	10.2	51.0	32	3	US-09-027-287-17	Sequence
51.0	23	3	US-09-402-817B-7	Sequence 149, App	949	10.2	51.0	32	4	US-09-252-656B-17	Sequence
51.0	23	4	US-09-128-026-149	Sequence 149, App	950	10.2	51.0	32	4	US-03-331-741A-47	Sequence
51.0	23	4	US-09-220-616-149	Sequence 75, Appli	951	10.2	51.0	32	4	US-09-906-234-60	Sequence
51.0	24	4	US-09-019-160-75	Sequence 4, Appli	952	10.2	51.0	32	4	US-09-523-323-17	Sequence
51.0	24	4	US-09-323-873A-4	Sequence 28, Appli	953	10.2	51.0	32	4	US-09-984-186-24	Sequence
51.0	24	4	US-09-181-585-11	Sequence 11, Appli	954	10.2	51.0	32	4	US-08-426-792-7	Sequence
51.0	24	4	US-09-954-560-6	Sequence 6, Appli	955	10.2	51.0	33	1	US-08-454-928-3	Sequence
51.0	24	4	US-08-214-770-17	Sequence 17, Appli	956	10.2	51.0	33	3	US-07-987-264-27	Sequence
51.0	25	1	US-09-140-804-22	Sequence 22, Appli	957	10.2	51.0	33	3	US-09-199-542B-76	Sequence
51.0	25	3	US-09-538-709-369	Sequence 369, App	958	10.2	51.0	33	4	US-09-918-696-3	Sequence
51.0	25	4	US-09-686-838B-22	Sequence 22, Appli	959	10.2	51.0	33	4	US-09-758-282B-161	Sequence
51.0	25	4	US-09-866-108A-13447	Sequence 13447, A	960	10.2	51.0	34	4	US-08-961-083-442	Sequence
51.0	25	5	PCT-US95-02885-17	Sequence 28, Appli	961	10.2	51.0	34	4	US-09-367-293-12	Sequence
51.0	26	3	US-08-911-894-28	Sequence 48, Appli	962	10.2	51.0	34	4	US-08-536-784-442	Sequence
51.0	26	3	US-09-174-437-48	Sequence 25, Appli	963	10.2	51.0	36	2	US-08-684-594-11	Sequence
51.0	26	4	US-09-688-748-25	Sequence 26, Appli	964	10.2	51.0	36	2	US-07-791-931-19	Sequence
51.0	26	4	US-09-688-748-26	Sequence 48, Appli	965	10.2	51.0	36	3	US-08-748-547-8	Sequence
51.0	26	4	US-09-686-055A-48	Sequence 300, App	966	10.2	51.0	39	3	US-09-703-309A-26	Sequence
51.0	27	1	US-08-411-796-300	Sequence 12, Appli	967	10.2	51.0	40	1	US-08-199-507B-47	Sequence
51.0	27	1	US-08-444-792-12	Sequence 12, Appli	968	10.2	51.0	40	1	US-08-346-293-1	Sequence
51.0	27	1	US-08-627-845-7	Sequence 7, Appli	969	10.2	51.0	40	1	US-08-087-772A-10	Sequence
51.0	27	1	US-08-627-845-7	Sequence 300, App	970	10.2	51.0	40	1	US-08-441-828-47	Sequence
51.0	27	3	US-08-471-039-300	Sequence 25, Appli	971	10.2	51.0	40	1	US-08-482-882-63	Sequence
51.0	27	3	US-08-257-584-25	Sequence 300, App	972	10.2	51.0	40	1		
51.0	27	4	US-08-559-390-300	Sequence 13, Appli	973	10.2	51.0	40	1		
51.0	27	4	US-09-379-530B-13		974	10.2	51.0	40	1		
51.0	27	4			975	10.2	51.0	40	1		
51.0	27	4			976	10.2	51.0	40	1		

51.0 40 1 US-08-483-389-63 Sequence 63, Appl  
51.0 40 2 US-08-487-113D-63 Sequence 63, Appl  
51.0 40 2 US-08-473-503-63 Sequence 63, Appl  
51.0 40 2 US-08-483-932-63 Sequence 63, Appl  
51.0 40 2 US-08-720-420A-63 Sequence 63, Appl  
51.0 40 3 US-08-714-017-63 Sequence 63, Appl  
51.0 40 3 US-08-475-680-63 Sequence 63, Appl  
51.0 40 3 US-09-416-050A-49 Sequence 49, Appl  
51.0 40 3 US-09-664-800-49 Sequence 49, Appl  
51.0 40 3 US-09-665-309-49 Sequence 49, Appl  
51.0 40 3 US-09-661-569-49 Sequence 49, Appl  
51.0 41 1 US-07-931-473B-83 Sequence 83, Appl  
51.0 41 1 US-07-977-434-36 Sequence 36, Appl  
51.0 41 1 US-07-714-131C-83 Sequence 83, Appl  
51.0 41 1 US-08-384-490-9 Sequence 9, Appl  
51.0 41 1 US-08-412-110-83 Sequence 83, Appl  
51.0 41 1 US-08-409-442A-83 Sequence 83, Appl  
51.0 41 1 US-08-459-383-9 Sequence 9, Appl  
51.0 41 1 US-08-458-819-36 Sequence 36, Appl  
51.0 41 1 US-08-469-609A-83 Sequence 83, Appl  
51.0 41 3 US-09-143-190-83 Sequence 83, Appl  
51.0 41 4 US-09-502-344-83 Sequence 83, Appl  
51.0 41 5 PCT-US91-07035-36 Sequence 36, Appl  
51.0 42 1 US-08-152-483B-5 Sequence 5, Appl

## ALIGNMENTS

2 Application US/09118408A  
65544

MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/118,408A

NG DATE: 1998-07-17

ICATION NUMBER: 60/053,154

NG DATE: 1997-07-18

Q ID NOS: 47

stSEQ for Windows Version 3.0

rtificial Sequence

MATION: Oligonucleotide ZC13651

2

74.0%; Score 14.8; DB 3; Length 20;  
milarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCCTCCACGGTT 20

TTTTTTTTTTTTTTTT

TTTGTCCTCCACGGTT 18

.5/c

Application US/09118408A

65544

MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/118,408A

NG DATE: 1998-07-17

ICATION NUMBER: 60/053,154

NG DATE: 1997-07-18

Q ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC13650  
US-09-118-408-15

Query Match 74.0%; Score 14.8; DB 3; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCCTCCACGGTT 20

TTTTTTTTTTTTTTTT

Db 20 CTTTGTCCTCCACGGTT 3

## RESULT 3

US-09-506-855-12  
Sequence 12, Application US/09506855  
Patent No. 6448221  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Lasser, Gerald W.  
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
TITLE OF INVENTION: IMMUNE FUNCTION  
FILE REFERENCE: 99-12  
CURRENT APPLICATION NUMBER: US/09/506,855  
CURRENT FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC13651  
US-09-506-855-12

Query Match 74.0%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCCTCCACGGTT 20

TTTTTTTTTTTTTTTT

Db 1 CTTTGTCCTCCACGGTT 18

## RESULT 4

US-09-506-855-15/c  
Sequence 15, Application US/09506855  
Patent No. 6448221  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Lasser, Gerald W.  
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
TITLE OF INVENTION: IMMUNE FUNCTION  
FILE REFERENCE: 99-12  
CURRENT APPLICATION NUMBER: US/09/506,855  
CURRENT FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC13650  
US-09-506-855-15

09:38:26 2004

us-10-090-326-7.max.rni

74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
|||||  
TTGTCTCCACGGGTTT 3

2  
pplication US/09911176B  
8403

ATION:  
eppard, Paul O.  
ENTION: ANTIBODIES THAT BIND AN  
ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
E: 97-30D1  
CATION NUMBER: US/09/911,176B  
G DATE: 2001-07-23  
TION NUMBER: 09/118,408  
DATE: 1998-07-17  
TION NUMBER: 60/053,154  
DATE: 1997-07-18  
ID NOS: 52  
tSEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13651  
2

74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
|||||  
TTGTCTCCACGGGTTT 18

15/c  
Application US/09911176B  
8403

ATION:  
eppard, Paul O.  
ENTION: ANTIBODIES THAT BIND AN  
ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
E: 97-30D1  
CATION NUMBER: US/09/911,176B  
G DATE: 2001-07-23  
TION NUMBER: 09/118,408  
DATE: 1998-07-17  
TION NUMBER: 60/053,154  
DATE: 1997-07-18  
ID NOS: 52  
tSEQ for Windows Version 3.0

rtificial Sequence

ATION: Oligonucleotide ZC13650  
15

74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTCTCCACGGGTT 20

|||||  
20 CTGTCTCTCCACGGTTT 3

RESULT 7

US-09-619-740-12  
; Sequence 12, Application US/09619740  
; Patent No. 6544946  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE  
; FILE REFERENCE: 99-12C3  
; CURRENT APPLICATION NUMBER: US/09/619,740  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/253,604  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/444,794  
; PRIOR FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: 09/506,855  
; PRIOR FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13651  
US-09-619-740-12

Query Match 74.0%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CTGTCTCTCCACGGTTT 20  
|||||  
DB 1 CTGTCTCTCCACGGTTT 18

RESULT 8

US-09-619-740-15/c  
; Sequence 15, Application US/09619740  
; Patent No. 6544946  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE  
; FILE REFERENCE: 99-12C3  
; CURRENT APPLICATION NUMBER: US/09/619,740  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/253,604  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: 09/444,794  
; PRIOR FILING DATE: 1999-11-22  
; PRIOR APPLICATION NUMBER: 09/506,855  
; PRIOR FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13650  
US-09-619-740-15

Query Match 74.0%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

CTTGCTCTCCACGGTTT 20  
|||||  
TTTGCTCTCCACGGTTT 3

2 Application US/09506852  
56499

# MATION:

heppard, Paul O.  
ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
CE: 97-30  
ICATION NUMBER: US/09/506,852  
NG DATE: 2000-02-17  
ICATION NUMBER: 60/053,154  
NG DATE: 1997-07-18  
Q ID NOS: 44  
stSEQ for Windows Version 3.0

## rtificial Sequence

MATION: Oligonucleotide ZC13651

2  
74.0%; Score 14.8; DB 4; Length 20;  
milarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGCTCTCCACGGTTT 20  
|||||  
TTTGCTCTCCACGGTTT 18

5/c  
Application US/09506852  
66499

# MATION:

heppard, Paul O.  
ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
CE: 97-30  
ICATION NUMBER: US/09/506,852  
NG DATE: 2000-02-17  
ICATION NUMBER: 60/053,154  
NG DATE: 1997-07-18  
Q ID NOS: 44  
stSEQ for Windows Version 3.0

## artificial Sequence

MATION: Oligonucleotide ZC13650

5  
74.0%; Score 14.8; DB 4; Length 20;  
milarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGCTCTCCACGGTTT 20  
|||||  
TTTGCTCTCCACGGTTT 3

## -2/c

Application US/09268544B

410710

# MATION:

Jederman, Seth

; APPLICANT: van Eynhoven, Winfried  
; TITLE OF INVENTION: TRAF-3 Deletion Isoforms And Uses Thereof  
; FILE REFERENCE: 0575-58732  
; CURRENT APPLICATION NUMBER: US/09/268,544B  
; CURRENT FILING DATE: 1999-03-11  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Forwar  
; OTHER INFORMATION: Primer or Polymerase Chain Reaction.  
US-09-268-544B-2

Query Match 72.0%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCCTGTCTCTCCACGG 17  
|||||  
DB 32 TACTGTCTCTCCACGG 17  
|||||

## RESULT 12

US-08-138-608-44  
; Sequence 44, Application US/08138608  
; Patent No. 5407795  
; GENERAL INFORMATION:  
; APPLICANT: Kolberg, Janice A.  
; APPLICANT: Shen, Lu-Ping  
; APPLICANT: Urdea, Michael S.  
; TITLE OF INVENTION: CMV PROBES FOR USE IN SOLUTION  
; TITLE OF INVENTION: PHASE SANDWICH HYBRIDIZATION ASSAYS  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/138,608  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/813,590  
; FILING DATE: 23-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. Clotti  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 22300-20236.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-813-5600  
; TELEFAX: 415-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-138-608-44

Query Match 70.0%; Score 14; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;



09:38:26 2004

us-10-090-326-7.max.rni

Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
TTGTCTCCACG 16  
|||||  
TTGTCTCCACG 31

plication US/08891292A  
2892  
ATION:  
arany, Francis  
uo, Jianying  
hanna, Marilyn  
ergstrom, Donald E.  
TION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFERENCES BY  
TION: LIGASE DETECTION REACTION  
E: 19603/457  
3 DATE: 1997-07-10  
TION NUMBER: 60/022,535  
DATE: 1996-07-19  
ID NOS: 96  
tentIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer for  
ATION: PCR or LDR

67.0%; Score 13.4; DB 4; Length 29;  
ilarity 93.3%; Pred. No. 8.6e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCCACG 17  
|||||  
TTGTCTCCACG 28

plication US/08891292A

2892  
ATION:  
arany, Francis  
uo, Jianying  
hanna, Marilyn  
ergstrom, Donald E.  
TION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFERENCES BY  
TION: LIGASE DETECTION REACTION  
E: 19603/457  
ATION NUMBER: US/08/891,292A  
3 DATE: 1997-07-10  
TION NUMBER: 60/022,535  
DATE: 1996-07-19  
ID NOS: 96  
tentIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer for  
ATION: PCR or LDR  
asure  
10)  
ATION: N at position 10 is either A, C, G, or T  
7

Query Match 67.0%; Score 13.4; DB 4; Length 29;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 3 CCTGTCTCCACGG 17  
|||||  
Db 14 CCTGTCTCCACGG 28

RESULT 15

US-09-927-737C-5  
; Sequence 5, Application US/09927737C  
; Patent No. 6576453  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFE  
; FILE REFERENCE: 19603/459  
; CURRENT APPLICATION NUMBER: US/09/927,737C  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/022,535  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-19  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer f  
; OTHER INFORMATION: PCR or LDR  
US-09-927-737C-5

Query Match 67.0%; Score 13.4; DB 4; Length 29;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 3 CCTGTCTCCACGG 17  
|||||  
Db 14 CCTGTCTCCACGG 28

RESULT 16

US-09-927-737C-7  
; Sequence 7, Application US/09927737C  
; Patent No. 6576453  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFE  
; FILE REFERENCE: 19603/459  
; CURRENT APPLICATION NUMBER: US/09/927,737C  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/022,535  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-19  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer :

1 09:38:26 2004

us-10-090-326-7.max.rni

ATTENTION: PCR or LDR

asure

10)

ATTENTION: N at position 10 is either A, C, G, or T

67.0%; Score 13.4; DB 4; Length 29;  
ilarity 93.3%; Pred. No. 8.6e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTGCTCCACGG 17  
|||||  
TTGTGCTCCACGG 28

/c  
pplication US/08860165A  
34557

ATION:

WARDS, Stirling John

X, John Cooper

BB, Elizabeth Ann

AZER, Ian

ENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

IC: 17227/130

ICATION NUMBER: US/08/860,165A

NG DATE: 1997-09-22

ICATION NUMBER: PCT/AU95/00868

NG DATE: 1995-12-20

ICATION NUMBER: AU PN0157

NG DATE: 1994-12-20

Q ID NOS: 15

entIn Ver. 2.0

rtificial Sequence

ATTENTION: Description of Artificial Sequence: Primer

66.0%; Score 13.2; DB 3; Length 30;  
ilarity 83.3%; Pred. No. 1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTTGCTCTCCACGG 18  
|||||  
TCCTCTCTCTCCCGGG 3

/c  
pplication US/09358645  
03128

ATION:

BB, Elizabeth Ann

WARDS, Stirling John

ENTION: IMPROVED METHOD FOR PROTEIN EXPRESSION

IC: 017227/0145

ICATION NUMBER: US/09/358,645

NG DATE: 1999-07-23

ICATION NUMBER: US 08/860,165

NG DATE: 1997-09-22

ICATION NUMBER: PCT/AU95/00868

NG DATE: 1995-12-20

ICATION NUMBER: AU PN 0157/94

NG DATE: 1994-12-20

Q ID NOS: 12

tentIn Ver. 2.0

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide used for PCR amplification  
US-09-358-645-8

Query Match 66.0%; Score 13.2; DB 4; Length 30;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGG 18  
|||||  
Db 20 ATCCTCTCTCTCCCGGG 3

RESULT 19

US-09-359-382-8/c  
; Sequence 8, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 017227/0148

; CURRENT APPLICATION NUMBER: US/09/359,382

; EARLIER FILING DATE: 1999-07-23

; EARLIER APPLICATION NUMBER: US 08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Oligonucleotide used for PCR amplification

US-09-359-382-8

Query Match 66.0%; Score 13.2; DB 4; Length 30;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGG 18  
|||||  
Db 20 ATCCTCTCTCTCCCGGG 3

RESULT 20

US-08-239-889A-2

; Sequence 2, Application US/08239889A

; Patent No. 5677277

; GENERAL INFORMATION:

; APPLICANT: Yatsu, Frank M., Alam, Nargis A., and Alam, Syed S

; TITLE OF INVENTION: A No. 5677277el Brain Endothelial Cell Pr

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Benjamin A. Adler

; STREET: 8011 Candle Lane

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

09:38:26 2004

us-10-090-326-7.max.rni

SYSTEM: Macintosh  
Microsoft Word for Macintosh  
LOCATION DATA:  
ON NUMBER: US/08/239,889A  
TE: May 9, 1994  
ACTION: 514  
ENT INFORMATION:  
ler, Dr. Benjamin A.  
ION NUMBER: 35,423  
/DOCKET NUMBER: D5707  
CATION INFORMATION:  
: 713-777-2321  
713-777-6908  
OR SEQ ID NO: 2:  
ARACTERISTICS:  
32  
cleic acid  
ESS: double  
linear  
PE:  
ON: other nucleic acid  
L: No  
No  
URCE:  
L ISOLATE:  
NTAL STAGE:  
PE:  
:  
:  
66.0%; Score 13.2; DB 1; Length 32;  
ilarity 83.3%; Pred. No. 1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CCTTGTCTCTCCACGGG 18  
|||||  
CCTTCTCTCTCCACGGG 32  
plication PC/TUS9505659  
MATION:  
Yatsu, Frank M.; Alam, Nargis A.; and  
Alam, Syed S.  
VENTION: A Novel Brain Endothelial Cell  
VENTION: Protein And Methods For Its Use  
SEQUENCES: 5  
NCE ADDRESS:  
: James F. Weiler, Attorney-at-Law  
One Riverway, Suite 1560  
uston  
exas  
USA  
56  
ADABLE FORM:  
PE: DS, HD 1.44 Mb/1.44 Mo  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
WordPerfect 6.0  
LOCATION DATA:  
ON NUMBER: PCT/US95/05659  
TE: 08.05.95 (8 May 1995)  
ACTION:  
ENT INFORMATION:  
iler, James F.  
ION NUMBER: 16,040  
/DOCKET NUMBER: D-5707 PCT  
CATION INFORMATION:  
: 713-626-9646  
713-963-5833

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: other nucleic acid  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
PCT-US95-05659-2  
Query Match 66.0%; Score 13.2; DB 5; Length 32;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
Qy 1 ATCCTTGTCTCTCCACGGG 18  
|||||  
Db 15 ATCCTTGTCTCTCCACGGG 32  
RESULT 22  
US-09-422-978-1000  
; Sequence 1000, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Coher, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a b  
; FILE REFERENCE: GENSET.020CEP1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1000  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-18777-130 : polymorphic base C or T  
US-09-422-978-1000  
Query Match 66.0%; Score 13.2; DB 4; Length 47;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
Qy 2 TCCTTGTCTCTCCACGGGT 19  
|||||  
Db 2 TCCTTGTCTCTCGAAGGT 19  
RESULT 23  
US-09-621-976-13666/c  
; Sequence 13666, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.

1 09:38:26 2004

us-10-090-326-7.max.rni

Siordano, J.Y.  
ENTION: ESTs and Encoded Human Proteins.  
TE: GENSET.054PR2  
ICATION NUMBER: US/09/621,976  
NG DATE: 2000-07-21  
2 ID NOS: 19335  
tent.pm  
56

omo sapiens  
3666

66.0%; Score 13.2; DB 4; Length 55;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CCTTGCTCTCCACGGGT 19  
|||||  
CCTCCTCTCCACGGGT 1

91 Application US/08859998  
94076

RMATION:  
Chenchik, Alex  
Jokhadze, George  
Bibilashvilli, Robert  
NVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NVENTION: EXPRESSION  
SEQUENCES: 1375  
ENCE ADDRESS:  
E: Fish & Richardson, P.C.  
2200 Sand Hill Road, Suite 100  
enlo Park  
CA

US  
025  
EADABLE FORM:  
YPE: Diskette  
: IBM Compatible  
3 SYSTEM: Windows95  
: FastSeq for Windows Version 2.0  
PLICATION DATA:  
ION NUMBER: US/08/859,998  
ATE: 21-MAY-1997  
TATION: 435  
ICATION DATA:  
ION NUMBER:

AGENT INFORMATION:  
ield, Bret E.  
ION NUMBER: 37,620  
8/DOCKET NUMBER: 09096/002001  
ICATION INFORMATION:  
3: 415-322-5070  
415-854-0875  
FOR SEQ ID NO: 991:  
HARACTERISTICS:  
28 base pairs  
ucleic acid  
NESS: single  
: linear  
YPE: DNA

FORMATION: oligonucleotide primer  
91

64.0%; Score 12.8; DB 2; Length 28;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCCTTGCTCTCCACGG 17  
|||||  
Db 9 TCCTTGACCTCCACGG 24  
|||||

RESULT 25

US-09-225-928-991  
; Sequence 991, Application US/09225928  
; Patent No. 6352829  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Jokhadze, George  
; Bibilashvilli, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 991:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 991:  
US-09-225-928-991

Query Match 64.0%; Score 12.8; DB 4; Length 28;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACGG 17  
|||||  
Db 9 TCCTTGACCTCCACGG 24  
|||||

RESULT 26

US-09-225-201B-991  
; Sequence 991, Application US/09225201B  
; Patent No. 6489455  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Jokhadze, George  
; Bibilashvilli, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

## EXPRESSION

OF SEQUENCES: 1375  
ORDENANCE ADDRESS:  
DRESSEE: Fish & Richardson, P.C.  
REBT: 2200 Sand Hill Road, Suite 100  
TV: Menlo Park  
ATE: CA  
UNTRY: US  
P: 94025  
R READABLE FORM:  
DIUM TYPE: Diskette  
MUTER: IBM Compatible  
ERATING SYSTEM: Windows95  
FTWARE: FastSeq for Windows Version 2.0  
APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,201B  
LING DATE: 05-Jan-1999  
ASSIFICATION: <Unknown>  
APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
LING DATE: 21-MAY-1997  
Y/AGENT INFORMATION:  
ME: Field, Bret E.  
GISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
MUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
FOR SEQ ID NO: 991:  
E CHARACTERISTICS:  
NGTH: 28 base pairs  
PE: nucleic acid  
RANDEDNESS: single  
POLOGY: linear  
E TYPE: DNA  
:  
HER INFORMATION: oligonucleotide primer  
E DESCRIPTION: SEQ ID NO: 991:  
91

ilarity 64.0%; Score 12.8; DB 4; Length 28;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 3; Gaps 0;

'CTTGCTCTCCACCG 17  
|||||  
'CTTGACCTCCACCG 24

pplication US/08440103

0152  
MATION:  
Weiner, Amy J.  
Houghton, Michael  
VENTION: Immunoreactive Polypeptide Compositions  
SEQUENCES: 45  
NCE ADDRESS:  
: Chiron Corporation  
4560 Horton Street  
eryville  
A  
USA  
08  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
PLICATION DATA:  
ON NUMBER: US/08/440,103  
ATE: 12-MAY-1995

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,368  
FILING DATE:  
APPLICATION NUMBER: US 07/759,575  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0205.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2708  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-440-103-12  
Query Match 64.0%; Score 12.8; DB 1; Length 45;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
QY 1 ATCCCTGTCTCTCCACG 16  
|||||  
Db 28 ATCCCTGTCTCTCCACG 43  
RESULT 28  
US-08-440-542-12  
Sequence 12, Application US/08440542  
Patent No. 5670153  
GENERAL INFORMATION:  
APPLICANT: Weiner, Amy J.  
APPLICANT: Houghton, Michael  
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,542  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/231,368  
FILING DATE:  
APPLICATION NUMBER: US 07/759,575  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: 0205.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2708  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

1 09:38:26 2004

us-10-090-326-7.max.rni

```
: linear
2 YPE: DNA (genomic)

        64.0%; Score 12.8; DB 1; Length 45;
milarity 87.5%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCCTTGTCCTCCACG 16
|||||
TCCCTGTCTCTCCAG 43

2 Application US/08231368
56312
RMATION:
Weiner, Amy J.
Houghton, Michael
NVENTION: Immunoreactive Polypeptide Compositions
SEQUENCES: 45
ENCE ADDRESS:
E: Chiron Corporation
4560 Horton Street
meryville
CA
USA
608
EADABLE FORM:
YPE: Floppy disk
G SYSTEM: IBM PC compatible
: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
ION NUMBER: US/08/231,368
ATE:
CATION: 435
ION DATA:
ION NUMBER: US 07/759,575
ATE: 13-SEP-1991
GENT INFORMATION:
Cclung, Barbara G.
TION NUMBER: 33,113
E/DOCKET NUMBER: 0205.001
ICATION INFORMATION:
E: (510) 601-2708
(510) 655-3542
FOR SEQ ID NO: 12:
HARACTERISTICS:
45 base pairs
nucleic acid
NESS: single
YPE: DNA (genomic)
2

        64.0%; Score 12.8; DB 1; Length 45;
milarity 87.5%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCCTTGTCCTCCACG 16
|||||
ATCCCTGTCTCTCCAG 43

2 Application US/08440210
'66845
RMATION:
Weiner, Amy J.
Houghton, Michael

TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,210
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mcclung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-440-210-12

Query Match 64.0%; Score 12.8; DB 1; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 ATCCTTGTCCTCCACG 16
|||||
Db 28 ATCCCTGTCTCTCCAG 43

RESULT 31
US-09-046-604-12
; Sequence 12, Application US/09046604
; Patent No. 6303292
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,604
; FILING DATE:
; CLASSIFICATION:
```

09:38:26 2004

us-10-090-326-7.max.rni

CATION DATA:  
ON NUMBER: US/08/231,368  
TE: 13-SEP-1991  
ON NUMBER: US 07/759,575  
TE: 13-SEP-1991  
ENT INFORMATION:  
Clung, Barbara G.  
ION NUMBER: 33,113  
/DOCKET NUMBER: 0205.001  
CATION INFORMATION:  
: (510) 601-2708  
: (510) 655-3542  
OR SEQ ID NO: 12:  
ARACTERISTICS:  
45 base pairs  
cleic acid  
ESS: single  
linear  
PE: DNA (genomic)

64.0%; Score 12.8; DB 4; Length 45;  
ilarity 87.5%; Pred. No. 1.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CCTTGTCCTCCAGG 16  
'CCTTGTCCTCCAGG 43

232/c  
Application US/09313294A  
'6212

ATION:  
to, Laura Y.  
alguadi, Raghunath V.  
herman, Bradley K.  
ENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
TE: PL-0017 US  
CATION NUMBER: US/09/313,294A  
IG DATE: 1999-05-14  
ID NOS: 7600  
RL Program

a may

sc feature  
ATION: Incyte ID No. 6476212 700348015H1  
sure  
, 40, 47, 54-55  
ATION: a, t, c, g, or other  
,232

64.0%; Score 12.8; DB 4; Length 57;  
ilarity 82.4%; Pred. No. 1.8e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CCTTGTCCTCCAGG 17  
'CAATGTCCTCCAGG 16

.96/c  
Application US/08758306  
17743  
INATION:  
Stinchcomb, Dan T.  
McSwiggen, James A.  
VENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306  
FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1196:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The letter "N" stands for the stem II  
OTHER INFORMATION: region of a HH ribozyme.  
US-08-758-306-1196

Query Match 63.0%; Score 12.6; DB 1; Length 27;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0;

Oy 1 ATCCTTGTCCTCCAGGGTT 20  
Db 25 ATCCTTTTCATCAGGTT 6

RESULT 34  
US-08-356-405-12/c  
Sequence 12, Application US/08356405  
Patent No. 5807691  
GENERAL INFORMATION:  
APPLICANT: Amlaiky, No. 5807691rdine  
APPLICANT: Boschert, Ursula  
APPLICANT: Hen, Rene  
APPLICANT: Flasseat, Jean-Luc  
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor  
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for  
TITLE OF INVENTION: Polypeptides and Uses Thereof  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA

126-0107  
READABLE FORM:  
TYPE: Floppy disk  
: IBM PC compatible  
3 SYSTEM: PC-DOS/MS-DOS  
: PatentIn Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/356,405  
ATE:  
CATION: 435  
ICATION DATA:  
ION NUMBER: WO PCT/FR93/00650  
ATE: 29-JUN-1992  
ICATION DATA:  
ION NUMBER: FR 92/08081  
ATE: 01-JUL-1992  
GENT INFORMATION:  
mith, Julie K  
TION NUMBER: 38,619  
E/DOCKET NUMBER: EX92004-US  
ICATION INFORMATION:  
E: (610)454-3839  
FOR SEQ ID NO: 12:  
HARACTERISTICS:  
41 base pairs  
ucleic acid  
NESS: single  
: linear  
YPE: other nucleic acid  
: NO  
2

63.0%; Score 12.6; DB 1; Length 41;  
milarity 78.9%; Pred. No. 2.2e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCTTGCTCTCCACGGGTT 20  
|||||  
CCTTCACCTCCACAGCTT 11

plication US/08162597  
53225  
RMATION:  
CLARY, Douglas O.  
WESKAMP, Gisela  
AUSTIN, LeeAnn R.  
REICHARDT, Louis F.  
VENTION: ANTIBODIES THAT MIMIC ACTIONS OF  
SEQUENCES: 6  
ENCE ADDRESS:  
E: Townsend and Townsend Kourie and Crew  
Steuart Street Tower, One Market Plaza  
an Francisco  
California  
US  
105-1493  
READABLE FORM:  
TYPE: Floppy disk  
: IBM PC compatible  
3 SYSTEM: PC-DOS/MS-DOS  
: PatentIn Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/162,597  
ATE: 03-DEC-1993  
CATION: 424  
GENT INFORMATION:  
eber, Ellen L.  
TION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 2307G-541  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-162-597-6

Query Match 63.0%; Score 12.6; DB 1; Length 45;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 2 TCCTGCTCTCCACGGGTT 20  
|||||  
Db 24 TCCTGCTCTCCACGGGT 42

RESULT 36  
US-09-770-949-6  
; Sequence 6, Application US/09770949  
; Patent No. 6656465  
; GENERAL INFORMATION:  
; APPLICANT: CLARY, Douglas O.  
; WESKAMP, Gisela  
; AUSTIN, LeeAnn R.  
; REICHARDT, Louis F.  
; TITLE OF INVENTION: ANTIBODIES THAT MIMIC ACTIONS OF  
; NEUTROTROPHINS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/770,949  
; FILING DATE: 26-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/162,597  
; FILING DATE: 03-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 2307G-541  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-770-949-6

Query Match 63.0%; Score 12.6; DB 4; Length 45;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;



09:38:26 2004

us-10-090-326-7.max.rni

```
CTTGCTCCACGGGTT 20
|||||
CTTCTTCCACGGGTT 42
|||||

1
plication US/08883795A
5607
NATION:
Delcuve, Genevieve
Awang, Gregor
VENTION: Recombinant DNA Molecules and Expression
VENTION: Vectors for Tissue Plasminogen Activator
SEQUENCES: 39
NCE ADDRESS:
: BERESKIN & PARR
40 King Street West
ronto
ntario
Canada
3Y2
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
LICATON DATA:
ON NUMBER: US/08/883,795A
TE: 27-JUN-1997
ATION: 435
ENT INFORMATION:
avelle, Micheline
ION NUMBER: 40,261
/DOCKET NUMBER: 7841-062
CATION INFORMATION:
: (416) 364-7311
(416) 361-1398
OR SEQ ID NO: 21:
ABACTERISTICS:
52 base pairs
cleic acid
ESS: single
linear
PE: cDNA
URCE:
Homo sapiens
OURCE:
POS alpha
1
ilarity 63.0%; Score 12.6; DB 2; Length 52;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTTGCTCCACGGGTT 20
|||||
CTTGGCTCCAGAGGT 50
|||||

C
plication US/09769863
5451
ATION:
bott Laboratories
tuckerji, Pradip
uang, Yung-Sheng
as, Tapas
hurmond, Jennifer
ereira, Suzette L.
NITION: DESATURASE GENES AND USES THEREOF

FILE REFERENCE: 6763-US-01
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Reverse Primer RO838
US-09-769-863-4

Query Match 62.0%; Score 12.4; DB 4; Length 36;
Best Local Similarity 55.6%; Pred. No. 2.7e+03;
Matches 10; Conservative 6; Mismatches 2; Indels 0;

Qy 3 CCTGTCTCTCCACGGGTT 20
|:|:|:|:|:|:|:|:|:|
Db 28 CYTTCYACACAGYT 11

RESULT 39
US-09-079-812E-8/C
Sequence 8, Application US/09079812E
Patent No. 6340575
GENERAL INFORMATION:
APPLICANT: Bollag, Gideon
APPLICANT: Crompton, Anne
APPLICANT: No. 6340575th, Anne
APPLICANT: Sharma, Sanju
APPLICANT: Roscoe, William
TITLE OF INVENTION: Methods and Compositions for Treating Abnormal
TITLE OF INVENTION: Growth Related to Unwanted Guanine Nucleotide
FILE REFERENCE: 1028-US
CURRENT APPLICATION NUMBER: US/09/079,812E
CURRENT FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/049,879
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 21
TYPE: DNA
ORGANISM: Oligonucleotide
US-09-079-812E-8

Query Match 61.0%; Score 12.2; DB 4; Length 21;
Best Local Similarity 82.4%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 ATCCTGTCTCTCCACGG 17
|||||
Db 21 ATCCTGTCTCTCCGCG 5
|||||

RESULT 40
US-08-477-877B-3/c
Sequence 3, Application US/08477877B
Patent No. 5730979
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhi
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
```

368  
 SADBABLE FORM:  
 YPE: 3.5 inch diskette  
 : IBM PS/2  
 3 SYSTEM: MS-DOS  
 : WordPerfect 5.1  
 PLICATION DATA:  
 ION NUMBER: US/08/477,877B  
 ATE: 07-JUN-1995  
 CATION: 424  
 ION DATA:  
 ION NUMBER: 08/407,009  
 ATE: 29-MAR-1995  
 ION NUMBER: 08/119,032  
 ATE: 09-SEP-1993  
 ION NUMBER: 08/027,008  
 ATE: 05-MAR-1993  
 GENT INFORMATION:  
 lstein, Elliot M.  
 ION NUMBER: 24,025  
 E/DOCKET NUMBER: 61750-146  
 ION INFORMATION:  
 E: 201-994-1700  
 201-994-1744  
 FOR SEQ ID NO: 3:  
 CHARACTERISTICS:  
 31 bases  
 nucleic acid  
 NESS: single  
 : linear  
 YPE: oligonucleotide  
 : PCR primer  
 3

milarity 61.0%; Score 12.2; DB 1; Length 31;  
 82.4%; Pred. No. 3.3e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCCACGGTT 20  
 |||||  
 TGGACCTCCCGGTT 1

3/c  
 plication US/08472281A  
 17311

RMATION:  
 Bazin, Herv  
 Latine, Dominique  
 NVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation  
 SEQUENCES: 96  
 ENCE ADDRESS:  
 E: Carella, Byrne, Bain, Gilfillan,  
 E: Cecchi, Stewart & Olstein  
 6 Becker Farm Road  
 Oseland  
 New Jersey  
 U.S.A.  
 068  
 RADABLE FORM:  
 YPE: 3.5 inch diskette  
 : IBM PS/2  
 G SYSTEM: MS-DOS  
 : WordPerfect 5.1  
 PLICATION DATA:  
 ION NUMBER: US/08/472,281A  
 ATE: 07-JUN-1995  
 CATION: 424  
 ION DATA:  
 ION NUMBER: 08/407,009  
 ATE: 29-MAR-1995

APPLICATION NUMBER: 08/119,032  
 FILING DATE: 09-SEP-1993  
 APPLICATION NUMBER: 08/027,008  
 FILING DATE: 05-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olstein, Elliot M.  
 REGISTRATION NUMBER: 24,025  
 REFERENCE/DOCKET NUMBER: 61750-142  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: oligonucleotide  
 FEATURE:  
 NAME/KEY: PCR primer  
 US-08-472-281A-3

Query Match 61.0%; Score 12.2; DB 1; Length 31;  
 Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 4 CTGTCTCTCCACGGTT 20  
 |||||  
 Db 17 CTGGACCTCCCGGTT 1

## RESULT 42

US-08-477-989B-3/c  
 Sequence 3, Application US/08477989B  
 Patent No. 5951983  
 GENERAL INFORMATION:  
 APPLICANT: Bazin, Herv  
 APPLICANT: Latine, Dominique  
 APPLICANT: Kaplan, Ruth  
 APPLICANT: Kieber-Emmons, Thomas  
 APPLICANT: Postema, Christina E.  
 APPLICANT: White-Scharf, Mary  
 TITLE OF INVENTION: LO-CD2a Antibody and Uses  
 TITLE OF INVENTION: Thereof for Inhibiting  
 TITLE OF INVENTION: T-Cell Activation and  
 TITLE OF INVENTION: Proliferation  
 NUMBER OF SEQUENCES: 96  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
 ADDRESSEE: Cecchi, Stewart & Olstein  
 STREET: 6 Becker Farm Road  
 CITY: Roseland  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch diskette  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,989B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/407,009  
 FILING DATE: 29-MAR-1995  
 APPLICATION NUMBER: 08/119,032  
 FILING DATE: 09-SEP-1993  
 APPLICATION NUMBER: 08/027,008  
 FILING DATE: 05-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olstein, Elliot M.

ION NUMBER: 24,025  
/DOCKET NUMBER: 61750-147  
CATION INFORMATION:  
: 201-994-1700  
OR SEQ ID NO: 3:  
ARACTERISTICS:  
31 bases  
cleic acid  
ESS: single  
linear  
PE: oligonucleotide

## PCR primer

61.0%; Score 12.2; DB 2; Length 31;  
ilarity 82.4%; Pred. No. 3.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TGTCCTCCACGGTT 20  
GGACCTCCCGGTT 1

/c  
application US/08347792  
3925

ATION:  
Halazonetis, Thanos D.  
VENTION: p53 Proteins With Altered  
VENTION: Tetramerization Domains  
SEQUENCES: 37  
NCE ADDRESS:  
: Howson and Howson  
Spring House Corporate Cntr., PO Box 457  
ring House  
ennsylvania  
USA  
77

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/347,792  
ATE:  
ATION: 530  
ENT INFORMATION:  
ak, Mary E.  
ION NUMBER: 31,215  
/DOCKET NUMBER: WST58USA  
CATION INFORMATION:  
: 215-540-9206  
215-540-5818  
OR SEQ ID NO: 23:  
ARACTERISTICS:  
32 base pairs  
cleic acid  
ESS: single  
PE: DNA (genomic)  
}

61.0%; Score 12.2; DB 1; Length 32;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTTGCTCCACGG 17  
ACCTTGCTCCAGG 7

RESULT 44  
US-08-431-357-23/c  
; Sequence 23, Application US/08431357  
; Patent No. 5721340  
; GENERAL INFORMATION:  
; APPLICANT: Halazonetis, Thanos D.  
; TITLE OF INVENTION: p53 Proteins With Altered  
; TITLE OF INVENTION: Tetramerization Domains  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,357  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/347,792  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST58USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-431-357-23  
Query Match 61.0%; Score 12.2; DB 1; Length 32;  
Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
QY 1 ATCCTTGCTCCACGG 17  
Db 23 AACCTTGCTCCAGG 7  
RESULT 45  
PCT-US95-15353-23/c  
; Sequence 23, Application PC/TUS9515353  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy  
; APPLICANT: and Biology  
; APPLICANT: Halazonetis, Thanos D.  
; TITLE OF INVENTION: p53 Proteins With Altered  
; TITLE OF INVENTION: Tetramerization Domains  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:

09:38:26 2004

us-10-090-326-7.max.rni

PE: Floppy disk  
IBM PC Compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.30  
PLICATION DATA:  
ION NUMBER: PCT/US95/15353  
ATE:  
ATION:  
ICATION DATA:  
ION NUMBER: US 08/347,792  
ATE: 28-NOV-1994  
ICATION DATA:  
ION NUMBER: US 08/431,357  
ATE: 28-APR-1995  
ICATION DATA:  
ION NUMBER: US 08/456,623  
ATE: 01-JUN-1995  
ENT INFORMATION:  
ak, Mary E.  
ION NUMBER: 31,215  
DOCKET NUMBER: WST58CPCT  
ICATION INFORMATION:  
3: 215-540-9206  
FOR SEQ ID NO: 23:  
CHARACTERISTICS:  
32 base pairs  
nucleic acid  
NESS: single  
: linear  
YPE: DNA (genomic)  
23  
61.0%; Score 12.2; DB 5; Length 32;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
TCCTTGCTCTCCACGG 17  
|||||  
ACCTTGCTCTCCAAGG 7

d: February 29, 2004, 11:22:16  
623 secs

09:38:26 2004

us-10-090-326-7.max.rnpb

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 09:43:45 ; Search time 122.857 Seconds  
(without alignments)  
587.262 Million cell updates/sec

US-10-090-326-7

1 atcctgtcctccacgggtt 20

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2353733 seqs, 1803733377 residues

hits satisfying chosen parameters: 1448676

ength: 0

ength: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
75.0	25	14	US-10-098-263B-58079	Sequence 58079, A
74.0	20	9	US-09-911-1768-12	Sequence 12, Appl
74.0	20	9	US-09-911-1768-15	Sequence 15, Appl
74.0	20	14	US-10-180-762-12	Sequence 12, Appl
74.0	20	14	US-10-180-762-15	Sequence 15, Appl
74.0	20	14	US-10-241-258-12	Sequence 12, Appl
74.0	20	14	US-10-241-258-15	Sequence 15, Appl
74.0	20	14	US-10-194-370-53	Sequence 53, Appl
74.0	20	14	US-10-360-186-12	Sequence 12, Appl
74.0	20	14	US-10-360-186-15	Sequence 15, Appl
74.0	20	14	US-10-392-531-12	Sequence 12, Appl
74.0	20	14	US-10-392-531-15	Sequence 15, Appl
74.0	20	14	US-10-392-706-12	Sequence 12, Appl
74.0	20	14	US-10-392-706-15	Sequence 15, Appl
74.0	20	15	US-10-198-695-12	Sequence 12, Appl

14.8	74.0	20	15	US-10-198-695-15	Sequenc
14.8	74.0	25	14	US-10-098-263B-119019	Sequenc
14.4	72.0	38	9	US-09-950-902-8	Sequenc
14.2	71.0	20	9	US-09-814-777A-70	Sequenc
14.2	71.0	25	14	US-10-098-263B-76558	Sequenc
13.8	69.0	25	14	US-10-098-263B-54313	Sequenc
13.8	69.0	60	10	US-09-908-975-8542	Sequenc
13.6	68.0	24	9	US-09-110-716-19	Sequenc
13.4	67.0	25	14	US-10-098-263B-58080	Sequenc
13.4	67.0	29	10	US-09-927-737-5	Sequenc
13.4	67.0	29	10	US-09-927-737-7	Sequenc
13.2	66.0	50	15	US-10-131-827-2451	Sequenc
13.2	66.0	20	15	US-10-148-835-103	Sequenc
13.2	66.0	25	14	US-10-098-263B-119020	Sequenc
13.2	66.0	47	15	US-10-349-143-1000	Sequenc
13.2	66.0	60	10	US-09-908-975-7759	Sequenc
13.2	66.0	60	10	US-09-908-975-10055	Sequenc
13.2	66.0	60	10	US-09-908-975-16879	Sequenc
13	65.0	31	9	US-09-801-274-949	Sequenc
12.8	64.0	25	14	US-10-215-112-1640	Sequenc
12.8	64.0	25	14	US-10-098-263B-83941	Sequenc
12.8	64.0	25	14	US-10-098-263B-105401	Sequenc
12.8	64.0	50	15	US-10-131-827-830	Sequenc
12.8	64.0	53	14	US-10-305-555-20	Sequenc
12.6	63.0	25	14	US-10-098-263B-60174	Sequenc
12.6	63.0	25	14	US-10-098-263B-62313	Sequenc
12.6	63.0	25	14	US-10-098-263B-66128	Sequenc
12.6	63.0	25	14	US-10-098-263B-72882	Sequenc
12.6	63.0	25	14	US-10-098-263B-76557	Sequenc
12.6	63.0	25	14	US-10-098-263B-104826	Sequenc
12.6	63.0	25	14	US-10-098-263B-106063	Sequenc
12.6	63.0	29	9	US-09-729-674-218	Sequenc
12.6	63.0	31	14	US-10-308-891-17	Sequenc
12.6	63.0	41	14	US-10-260-351-8	Sequenc
12.6	63.0	41	14	US-10-260-352-8	Sequenc
12.6	63.0	43	15	US-09-837-306-4	Sequenc
12.6	63.0	43	15	US-10-045-674-4	Sequenc
12.6	63.0	53	15	US-10-320-191-9	Sequenc
12.6	63.0	57	15	US-10-403-337-11	Sequenc
12.6	63.0	57	15	US-10-351-890-11	Sequenc
12.6	63.0	59	10	US-09-966-459A-32	Sequenc
12.6	63.0	59	15	US-10-403-337-12	Sequenc
12.6	63.0	59	15	US-10-351-890-12	Sequenc
12.6	63.0	60	10	US-09-908-975-5888	Sequenc
12.6	63.0	60	10	US-09-908-975-13403	Sequenc
12.6	63.0	60	10	US-09-908-975-18272	Sequenc
12.6	63.0	60	10	US-09-908-975-18341	Sequenc
12.4	62.0	21	14	US-10-144-000-1	Sequenc
12.4	62.0	25	8	US-08-647-444-7	Sequenc
12.4	62.0	25	14	US-10-215-112-2425	Sequenc
12.4	62.0	25	14	US-10-215-112-3248	Sequenc
12.4	62.0	25	14	US-10-098-263B-55180	Sequenc
12.4	62.0	25	14	US-10-098-263B-82919	Sequenc
12.4	62.0	25	14	US-10-098-263B-86027	Sequenc
12.4	62.0	25	14	US-10-098-263B-116042	Sequenc
12.4	62.0	25	14	US-10-098-263B-129653	Sequenc
12.4	62.0	36	10	US-09-849-199A-4	Sequenc
12.4	62.0	36	10	US-09-769-863-4	Sequenc
12.4	62.0	36	14	US-10-120-637A-4	Sequenc
12.4	62.0	36	14	US-10-054-534B-4	Sequenc
12.4	62.0	36	14	US-10-431-952-4	Sequenc
12.4	62.0	60	10	US-09-908-975-22805	Sequenc
12.2	61.0	17	14	US-10-061-201-1082	Sequenc
12.2	61.0	20	14	US-10-325-273-8	Sequenc
12.2	61.0	21	15	US-10-054-435-8	Sequenc
12.2	61.0	25	14	US-10-098-263B-54314	Sequenc
12.2	61.0	25	14	US-10-098-263B-93758	Sequenc
12.2	61.0	25	14	US-10-098-263B-107614	Sequenc
12.2	61.0	25	14	US-10-098-263B-122908	Sequenc
12.2	61.0	25	14	US-10-061-201-3144	Sequenc
12.2	61.0	25	14	US-10-061-201-3145	Sequenc
12.2	61.0	25	14	US-10-061-201-3146	Sequenc
12.2	61.0	25	14	US-10-061-201-3147	Sequenc

61.0	25	14	US-10-061-201-3148	Sequence 3148, Ap	c 162	12	60.0	25	14	US-10-215-112-9009	Sequen
61.0	25	14	US-10-061-201-3149	Sequence 3149, Ap	c 163	12	60.0	25	14	US-10-098-263B-13792	Sequen
61.0	25	14	US-10-061-201-3150	Sequence 3150, Ap	c 164	12	60.0	25	14	US-10-098-263B-78413	Sequen
61.0	25	14	US-10-061-201-3151	Sequence 3151, Ap	c 165	12	60.0	25	14	US-10-098-263B-89149	Sequen
61.0	25	14	US-10-061-201-3152	Sequence 3152, Ap	c 166	12	60.0	30	8	US-08-591-486B-94	Sequenc
61.0	36	9	US-09-917-265-81	Sequence 81, Appl	c 167	12	60.0	30	9	US-09-333-527-41	Sequenc
61.0	37	9	US-09-402-100-5	Sequence 5, Appl	c 168	12	60.0	30	14	US-10-127-427-41	Sequen
61.0	45	10	US-09-946-374-168	Sequence 168, App	c 169	12	60.0	38	14	US-10-348-504-15	Sequen
61.0	45	14	US-10-006-856A-168	Sequence 168, App	c 170	12	60.0	38	14	US-10-348-504-19	Sequen
61.0	45	14	US-10-006-818A-168	Sequence 168, App	c 171	12	60.0	53	15	US-10-306-969-57	Sequen
61.0	45	14	US-10-015-393A-168	Sequence 168, App	c 172	12	60.0	57	9	US-09-893-615-12	Sequenc
61.0	45	14	US-10-015-869A-168	Sequence 168, App	c 173	12	60.0	57	9	US-09-893-615-60	Sequenc
61.0	45	14	US-10-012-121A-168	Sequence 168, App	c 174	12	60.0	57	15	US-10-601-171-12	Sequen
61.0	45	14	US-10-006-116A-168	Sequence 168, App	c 175	12	60.0	57	15	US-10-601-171-60	Sequen
61.0	45	14	US-10-006-117A-168	Sequence 168, App	c 176	12	60.0	60	10	US-09-908-975-6714	Sequen
61.0	45	14	US-10-017-527A-168	Sequence 168, App	c 177	12	60.0	60	10	US-09-908-975-7749	Sequen
61.0	45	14	US-10-013-913A-168	Sequence 168, App	c 178	12	60.0	60	10	US-09-908-975-22959	Sequen
61.0	45	14	US-10-007-194A-168	Sequence 168, App	c 179	11.8	59.0	20	12	US-10-398-308-29	Sequen
61.0	45	14	US-10-013-430A-168	Sequence 168, App	c 180	11.8	59.0	20	14	US-10-286-628-20	Sequen
61.0	45	14	US-10-011-671A-168	Sequence 168, App	c 181	11.8	59.0	21	14	US-10-324-618-56	Sequen
61.0	45	14	US-10-012-755A-168	Sequence 168, App	c 182	11.8	59.0	21	14	US-10-032-585-4053	Sequen
61.0	45	14	US-10-015-386A-168	Sequence 168, App	c 183	11.8	59.0	22	14	US-10-357-043-27	Sequen
61.0	45	14	US-10-011-692A-168	Sequence 168, App	c 184	11.8	59.0	25	14	US-10-098-263B-16441	Sequen
61.0	45	14	US-10-006-768A-168	Sequence 168, App	c 185	11.8	59.0	25	14	US-10-098-263B-16442	Sequen
61.0	45	14	US-10-017-610A-168	Sequence 168, App	c 186	11.8	59.0	25	14	US-10-098-263B-27134	Sequen
61.0	45	14	US-10-006-063A-168	Sequence 168, App	c 187	11.8	59.0	25	14	US-10-098-263B-28243	Sequen
61.0	45	14	US-10-020-063A-168	Sequence 168, App	c 188	11.8	59.0	25	14	US-10-098-263B-35176	Sequen
61.0	45	14	US-10-015-391A-168	Sequence 168, App	c 189	11.8	59.0	25	14	US-10-098-263B-38412	Sequen
61.0	45	14	US-10-017-407A-168	Sequence 168, App	c 190	11.8	59.0	25	14	US-10-098-263B-51601	Sequen
61.0	45	14	US-10-011-833A-168	Sequence 168, App	c 191	11.8	59.0	25	14	US-10-098-263B-67719	Sequen
61.0	45	14	US-10-006-041A-168	Sequence 168, App	c 192	11.8	59.0	25	14	US-10-098-263B-78478	Sequen
61.0	45	14	US-10-015-822A-168	Sequence 168, App	c 193	11.8	59.0	25	14	US-10-098-263B-83080	Sequen
61.0	45	14	US-10-015-387A-168	Sequence 168, App	c 194	11.8	59.0	25	14	US-10-098-263B-122203	Sequen
61.0	45	14	US-10-006-130A-168	Sequence 168, App	c 195	11.8	59.0	25	14	US-10-098-263B-128081	Sequen
61.0	45	14	US-10-006-172A-168	Sequence 168, App	c 196	11.8	59.0	27	10	US-09-205-520-5	Sequen
61.0	45	14	US-10-017-253A-168	Sequence 168, App	c 197	11.8	59.0	30	14	US-10-223-646-32	Sequen
61.0	45	14	US-10-015-392A-168	Sequence 168, App	c 198	11.8	59.0	41	15	US-10-167-634-52	Sequen
61.0	45	14	US-10-017-306A-168	Sequence 168, App	c 199	11.8	59.0	45	9	US-09-925-664-73	Sequenc
61.0	45	14	US-10-017-867A-168	Sequence 168, App	c 200	11.8	59.0	47	15	US-10-170-097-898	Sequen
61.0	45	14	US-10-012-064A-168	Sequence 168, App	c 201	11.8	59.0	47	15	US-10-349-143-2678	Sequen
61.0	45	14	US-10-013-909A-168	Sequence 168, App	c 202	11.8	59.0	48	10	US-09-848-754A-8797	Sequen
61.0	45	14	US-10-015-671A-168	Sequence 168, App	c 203	11.8	59.0	48	10	US-09-848-754A-9068	Sequen
61.0	45	14	US-10-015-610A-168	Sequence 168, App	c 204	11.8	59.0	50	15	US-10-131-827-3346	Sequen
61.0	45	14	US-10-012-137A-168	Sequence 168, App	c 205	11.8	59.0	54	15	US-10-188-056-8	Sequen
61.0	45	14	US-10-012-752A-168	Sequence 168, App	c 206	11.8	59.0	60	10	US-09-908-975-15164	Sequen
61.0	45	14	US-10-012-754A-168	Sequence 168, App	c 207	11.8	59.0	60	10	US-09-908-975-19581	Sequen
61.0	45	14	US-10-013-910A-168	Sequence 168, App	c 208	11.8	59.0	60	10	US-09-908-975-22836	Sequen
61.0	45	14	US-10-013-911A-168	Sequence 168, App	c 209	11.8	59.0	60	10	US-09-908-975-32193	Sequen
61.0	45	14	US-10-013-912A-168	Sequence 168, App	c 210	11.6	58.0	18	9	US-09-969-373-2482	Sequenc
61.0	45	14	US-10-015-653A-168	Sequence 168, App	c 211	11.6	58.0	18	9	US-09-969-373-2484	Sequenc
61.0	45	14	US-10-012-101B-168	Sequence 168, App	c 212	11.6	58.0	18	14	US-10-285-976-81	Sequen
61.0	45	14	US-10-015-480A-168	Sequence 168, App	c 213	11.6	58.0	20	12	US-10-380-137A-18	Sequen
61.0	45	14	US-10-015-715A-168	Sequence 168, App	c 214	11.6	58.0	21	13	US-10-011-064-3	Sequen
61.0	45	14	US-10-012-237A-168	Sequence 168, App	c 215	11.6	58.0	21	14	US-10-314-405-16	Sequen
61.0	45	14	US-10-013-906A-168	Sequence 168, App	c 216	11.6	58.0	23	10	US-09-911-904-41	Sequen
61.0	45	14	US-10-015-388A-168	Sequence 168, App	c 217	11.6	58.0	23	15	US-10-318-970-23	Sequen
61.0	45	14	US-10-012-753A-168	Sequence 168, App	c 218	11.6	58.0	25	9	US-09-919-298-8	Sequenc
61.0	45	14	US-10-015-385A-168	Sequence 168, App	c 219	11.6	58.0	25	9	US-09-918-702-6	Sequenc
61.0	45	14	US-10-007-236A-168	Sequence 168, App	c 220	11.6	58.0	25	14	US-10-098-263B-1064	Sequen
61.0	45	14	US-10-015-389A-168	Sequence 168, App	c 221	11.6	58.0	25	14	US-10-098-263B-1510	Sequen
61.0	45	15	US-10-013-915A-168	Sequence 168, App	c 222	11.6	58.0	25	14	US-10-098-263B-9655	Sequen
61.0	45	15	US-10-015-394A-168	Sequence 168, App	c 223	11.6	58.0	25	14	US-10-098-263B-23970	Sequen
61.0	45	15	US-10-015-390A-168	Sequence 168, App	c 224	11.6	58.0	25	14	US-10-098-263B-38046	Sequen
61.0	45	15	US-10-006-746A-168	Sequence 168, App	c 225	11.6	58.0	25	14	US-10-098-263B-64247	Sequen
61.0	45	15	US-10-011-795A-168	Sequence 168, App	c 226	11.6	58.0	25	14	US-10-098-263B-64761	Sequen
61.0	45	15	US-10-012-231A-168	Sequence 168, App	c 227	11.6	58.0	25	14	US-10-098-263B-67986	Sequen
61.0	51	13	US-10-158-895-44	Sequence 44, Appl	c 228	11.6	58.0	25	14	US-10-098-263B-72431	Sequen
61.0	51	14	US-10-384-743-44	Sequence 44, Appl	c 229	11.6	58.0	25	14	US-10-098-263B-109831	Sequen
61.0	54	15	US-10-339-268A-23	Sequence 23, Appl	c 230	11.6	58.0	25	14	US-10-098-263B-111822	Sequen
61.0	60	10	US-09-908-975-8739	Sequence 8739, Ap	c 231	11.6	58.0	25	14	US-10-098-263B-118813	Sequen
61.0	60	10	US-09-908-975-10051	Sequence 10051, A	c 232	11.6	58.0	25	14	US-10-098-263B-119297	Sequen
60.0	17	15	US-10-297-068-1010	Sequence 1010, Ap	c 233	11.6	58.0	25	14	US-10-098-263B-124304	Sequen
					c 234	11.6	58.0	25	14	US-10-098-263B-126886	Sequen

58.0	27	9	US-09-834-624-6	Sequence 6, Appli	c 308	11.4	57.0	25	10	US-09-754-853A-935	Sequence
58.0	27	14	US-10-423-007-6	Sequence 6, Appli	c 309	11.4	57.0	25	10	US-09-940-185-4287	Sequence
58.0	28	9	US-09-827-937A-11	Sequence 11, Appl	c 310	11.4	57.0	25	14	US-10-215-112-6452	Sequence
58.0	30	9	US-09-402-317-5	Sequence 5, Appli	311	11.4	57.0	25	14	US-10-098-263B-10399	Sequence
58.0	31	9	US-09-801-274-666	Sequence 666, App	312	11.4	57.0	25	14	US-10-098-263B-17085	Sequence
58.0	31	9	US-09-801-274-666	Sequence 1605, App	c 313	11.4	57.0	25	14	US-10-098-263B-18808	Sequence
58.0	37	9	US-09-791-171-25	Sequence 25, Appl	314	11.4	57.0	25	14	US-10-098-263B-30041	Sequence
58.0	37	10	US-09-804-980-25	Sequence 25, Appl	315	11.4	57.0	25	14	US-10-098-263B-34047	Sequence
58.0	39	14	US-10-128-714-4022	Sequence 4022, App	316	11.4	57.0	25	14	US-10-098-263B-43222	Sequence
58.0	41	14	US-10-005-956-643	Sequence 643, App	317	11.4	57.0	25	14	US-10-098-263B-65486	Sequence
58.0	42	9	US-09-887-784-11	Sequence 11, Appl	318	11.4	57.0	25	14	US-10-098-263B-86642	Sequence
58.0	42	9	US-09-887-784-12	Sequence 12, Appl	c 319	11.4	57.0	25	14	US-10-098-263B-86642	Sequence
58.0	42	14	US-10-257-909A-35	Sequence 35, Appl	c 320	11.4	57.0	25	14	US-10-098-263B-112943	Sequence
58.0	42	14	US-10-257-909A-36	Sequence 36, Appl	321	11.4	57.0	25	14	US-10-061-201-3140	Sequence
58.0	42	15	US-10-233-958-27	Sequence 27, Appl	322	11.4	57.0	25	14	US-10-061-201-3141	Sequence
58.0	42	15	US-10-233-958-31	Sequence 31, Appl	323	11.4	57.0	25	14	US-10-061-201-3142	Sequence
58.0	43	10	US-09-991-209-80	Sequence 80, Appl	324	11.4	57.0	25	14	US-10-061-201-3143	Sequence
58.0	47	15	US-10-349-143-3710	Sequence 3710, App	c 325	11.4	57.0	25	14	US-10-251-385-116	Sequence
58.0	48	14	US-10-283-028-15	Sequence 15, Appl	c 326	11.4	57.0	30	15	US-10-027-632-53223	Sequence
58.0	50	15	US-10-131-827-5437	Sequence 5437, App	c 327	11.4	57.0	30	15	US-10-027-632-53227	Sequence
58.0	50	15	US-10-131-827-5992	Sequence 5992, App	328	11.4	57.0	31	9	US-09-895-072-49	Sequence
58.0	54	15	US-10-245-227B-10	Sequence 10, Appl	329	11.4	57.0	31	9	US-09-896-552-49	Sequence
58.0	57	9	US-09-740-211-5	Sequence 5, Appli	330	11.4	57.0	31	14	US-10-306-686-49	Sequence
58.0	57	13	US-10-007-968-5	Sequence 5, Appli	331	11.4	57.0	33	14	US-10-133-858-2	Sequence
58.0	57	14	US-10-293-400-5	Sequence 5, Appli	332	11.4	57.0	36	10	US-09-981-002-1	Sequence
58.0	60	10	US-09-908-975-5580	Sequence 5580, App	333	11.4	57.0	36	10	US-09-981-002-14	Sequence
58.0	60	10	US-09-908-975-5785	Sequence 5785, App	334	11.4	57.0	36	10	US-09-981-002-16	Sequence
58.0	60	10	US-09-908-975-7374	Sequence 7374, App	c 335	11.4	57.0	36	15	US-10-394-511-14	Sequence
58.0	60	10	US-09-908-975-11431	Sequence 11431, A	336	11.4	57.0	38	15	US-10-453-483-108	Sequence
58.0	60	10	US-09-908-975-11868	Sequence 11868, A	c 337	11.4	57.0	41	12	US-10-453-827-254	Sequence
58.0	60	10	US-09-908-975-13082	Sequence 13082, A	338	11.4	57.0	41	14	US-10-224-683-23	Sequence
58.0	60	10	US-09-908-975-13822	Sequence 13822, A	c 339	11.4	57.0	46	15	US-10-453-483-107	Sequence
58.0	60	10	US-09-908-975-14378	Sequence 14378, A	c 340	11.4	57.0	47	15	US-10-170-097-900	Sequence
58.0	60	10	US-09-908-975-16551	Sequence 16551, A	c 341	11.4	57.0	47	15	US-10-349-143-3692	Sequence
58.0	60	10	US-09-908-975-17383	Sequence 17383, A	c 342	11.4	57.0	48	10	US-09-848-754A-8286	Sequence
58.0	60	10	US-09-908-975-17398	Sequence 17398, A	c 343	11.4	57.0	48	14	US-10-230-006-2577	Sequence
58.0	60	10	US-09-908-975-19207	Sequence 19207, A	c 344	11.4	57.0	50	15	US-10-131-827-1222	Sequence
58.0	60	14	US-10-005-675-25	Sequence 25, Appl	345	11.4	57.0	50	15	US-10-131-827-2273	Sequence
57.0	16	10	US-09-918-026A-11	Sequence 11, Appl	346	11.4	57.0	60	9	US-09-559-671A-8	Sequence
57.0	17	10	US-09-740-332-570	Sequence 570, App	347	11.4	57.0	60	10	US-09-954-692-8	Sequence
57.0	17	10	US-09-817-879-3985	Sequence 3985, App	c 348	11.4	57.0	60	10	US-09-908-975-5710	Sequence
57.0	17	10	US-09-817-879-3985	Sequence 570, App	c 349	11.4	57.0	60	10	US-09-908-975-9852	Sequence
57.0	17	14	US-10-238-700-3287	Sequence 3287, App	c 350	11.4	57.0	60	10	US-09-908-975-12154	Sequence
57.0	17	14	US-10-061-201-1078	Sequence 1078, App	c 351	11.4	57.0	60	10	US-09-908-975-31510	Sequence
57.0	17	14	US-10-061-201-1079	Sequence 1079, App	c 352	11.2	56.0	17	9	US-09-866-108-8556	Sequence
57.0	17	14	US-10-061-201-1080	Sequence 1080, App	c 353	11.2	56.0	17	9	US-09-866-108-8557	Sequence
57.0	17	14	US-10-061-201-1081	Sequence 1081, App	354	11.2	56.0	17	14	US-09-848-754A-1540	Sequence
57.0	17	14	US-10-061-201-1081	Sequence 1081, App	355	11.2	56.0	17	14	US-10-061-201-1083	Sequence
57.0	18	10	US-09-864-636A-305	Sequence 305, App	c 356	11.2	56.0	18	15	US-10-349-143-5304	Sequence
57.0	18	10	US-09-864-636A-310	Sequence 310, App	c 357	11.2	56.0	19	14	US-10-010-920-67	Sequence
57.0	18	10	US-09-864-636A-453	Sequence 453, App	c 358	11.2	56.0	19	14	US-10-008-721-67	Sequence
57.0	18	10	US-09-758-282-191	Sequence 191, App	359	11.2	56.0	19	14	US-10-251-117-726	Sequence
57.0	18	10	US-09-758-282-196	Sequence 196, App	c 360	11.2	56.0	19	14	US-10-251-117-1033	Sequence
57.0	18	11	US-09-864-426A-305	Sequence 305, App	361	11.2	56.0	20	14	US-10-348-485-67	Sequence
57.0	18	11	US-09-864-426A-310	Sequence 310, App	c 362	11.2	56.0	20	14	US-10-133-779-94	Sequence
57.0	18	11	US-09-864-426A-453	Sequence 453, App	363	11.2	56.0	21	9	US-09-765-081-233	Sequence
57.0	18	14	US-10-265-689-35	Sequence 35, Appl	364	11.2	56.0	21	10	US-09-978-600-14	Sequence
57.0	18	14	US-10-084-839-305	Sequence 305, App	365	11.2	56.0	21	10	US-09-382-860-227	Sequence
57.0	18	14	US-10-084-839-310	Sequence 310, App	366	11.2	56.0	22	15	US-10-319-315-96	Sequence
57.0	18	14	US-10-084-839-453	Sequence 453, App	367	11.2	56.0	22	15	US-10-092-665-95	Sequence
57.0	19	14	US-10-028-332-8	Sequence 332, App	368	11.2	56.0	24	10	US-09-940-185-680	Sequence
57.0	19	14	US-10-349-320-18	Sequence 18, Appl	369	11.2	56.0	24	15	US-10-351-275-19	Sequence
57.0	20	9	US-09-800-629A-60	Sequence 60, Appl	c 370	11.2	56.0	25	9	US-09-866-108-13448	Sequence
57.0	20	12	US-10-380-127A-19	Sequence 19, Appl	c 371	11.2	56.0	25	9	US-09-866-108-13449	Sequence
57.0	20	15	US-10-154-708-24	Sequence 24, Appl	c 372	11.2	56.0	25	9	US-09-866-108-13450	Sequence
57.0	20	15	US-10-154-708-97	Sequence 97, Appl	c 373	11.2	56.0	25	9	US-09-866-108-13451	Sequence
57.0	21	9	US-09-216-393-255	Sequence 255, App	c 374	11.2	56.0	25	9	US-09-866-108-13452	Sequence
57.0	21	14	US-10-321-856-255	Sequence 255, App	c 375	11.2	56.0	25	9	US-09-866-108-13453	Sequence
57.0	22	15	US-10-115-479-196	Sequence 196, App	c 376	11.2	56.0	25	9	US-09-866-108-13454	Sequence
57.0	23	14	US-10-093-365-23	Sequence 23, Appl	c 377	11.2	56.0	25	9	US-09-866-108-13455	Sequence
57.0	24	10	US-09-940-185-309	Sequence 309, App	c 378	11.2	56.0	25	9	US-09-866-108-13456	Sequence
57.0	24	10	US-09-853-105-17	Sequence 17, Appl	c 379	11.2	56.0	25	9	US-09-866-108-13457	Sequence
57.0	25	10	US-09-754-853A-695	Sequence 85, App	c 380	11.2	56.0	25	9	US-09-946-678-14	Sequence

56.0	25	9	US-09-946-678-21	Sequence 21, Appl	C 454	11.2	56.0	57	15	US-10-380-873B-16	Sequen
56.0	25	10	US-09-940-185-4646	Sequence 4646, Ap	C 455	11.2	56.0	58	15	US-10-408-456-14	Sequen
56.0	25	14	US-10-215-112-1531	Sequence 1531, Ap	C 456	11.2	56.0	59	14	US-10-232-544-84	Sequen
56.0	25	14	US-10-215-112-2834	Sequence 2834, Ap	C 457	11.2	56.0	60	9	US-09-739-068-16	Sequen
56.0	25	14	US-10-215-112-4453	Sequence 4453, Ap	C 458	11.2	56.0	60	10	US-09-908-975-5820	Sequen
56.0	25	14	US-10-215-112-4577	Sequence 4577, Ap	C 459	11.2	56.0	60	10	US-09-908-975-8268	Sequen
56.0	25	14	US-10-215-112-11892	Sequence 11892, A	C 460	11.2	56.0	60	10	US-09-908-975-8676	Sequen
56.0	25	14	US-10-215-112-13909	Sequence 13909, A	C 461	11.2	56.0	60	10	US-09-908-975-8913	Sequen
56.0	25	14	US-10-098-263B-632	Sequence 632, App	C 462	11.2	56.0	60	10	US-09-908-975-11436	Sequen
56.0	25	14	US-10-098-263B-2202	Sequence 2202, Ap	C 463	11.2	56.0	60	10	US-09-908-975-11496	Sequen
56.0	25	14	US-10-098-263B-2247	Sequence 2247, Ap	C 464	11.2	56.0	60	10	US-09-908-975-12048	Sequen
56.0	25	14	US-10-098-263B-9074	Sequence 9074, Ap	C 465	11.2	56.0	60	10	US-09-908-975-12149	Sequen
56.0	25	14	US-10-098-263B-30300	Sequence 30300, A	C 466	11.2	56.0	60	10	US-09-908-975-12541	Sequen
56.0	25	14	US-10-098-263B-32382	Sequence 32382, A	C 467	11.2	56.0	60	10	US-09-908-975-13713	Sequen
56.0	25	14	US-10-098-263B-32561	Sequence 32561, A	C 468	11.2	56.0	60	10	US-09-908-975-16166	Sequen
56.0	25	14	US-10-098-263B-36120	Sequence 36120, A	C 469	11.2	56.0	60	10	US-09-908-975-16941	Sequen
56.0	25	14	US-10-098-263B-44881	Sequence 44881, A	C 470	11.2	56.0	60	10	US-09-908-975-19221	Sequen
56.0	25	14	US-10-098-263B-60390	Sequence 60390, A	C 471	11.2	56.0	60	10	US-09-908-975-19877	Sequen
56.0	25	14	US-10-098-263B-72671	Sequence 72671, A	C 472	11.2	56.0	60	10	US-09-908-975-23378	Sequen
56.0	25	14	US-10-098-263B-75687	Sequence 75687, A	C 473	11	55.0	18	10	US-09-944-049-43	Sequen
56.0	25	14	US-10-098-263B-83942	Sequence 83942, A	C 474	11	55.0	18	15	US-10-388-263-317	Sequen
56.0	25	14	US-10-098-263B-84773	Sequence 84773, A	C 475	11	55.0	20	9	US-09-791-408-62	Sequen
56.0	25	14	US-10-098-263B-84774	Sequence 84774, A	C 476	11	55.0	20	10	US-09-850-948-15	Sequen
56.0	25	14	US-10-098-263B-95670	Sequence 95670, A	C 477	11	55.0	20	10	US-09-954-556-71	Sequen
56.0	25	14	US-10-098-263B-96767	Sequence 96767, A	C 478	11	55.0	20	10	US-09-954-679-64	Sequen
56.0	25	14	US-10-098-263B-103242	Sequence 103242, A	C 479	11	55.0	20	10	US-09-985-440-25	Sequen
56.0	25	14	US-10-098-263B-103372	Sequence 103372, A	C 480	11	55.0	20	14	US-10-273-575-15	Sequen
56.0	25	14	US-10-098-263B-105402	Sequence 105402, A	C 481	11	55.0	20	14	US-10-128-714-4014	Sequen
56.0	25	14	US-10-098-263B-106205	Sequence 106205, A	C 482	11	55.0	20	14	US-10-020-721-5	Sequen
56.0	25	14	US-10-098-263B-106901	Sequence 106901, A	C 483	11	55.0	20	15	US-10-289-762-5351	Sequen
56.0	25	14	US-10-098-263B-119858	Sequence 119858, A	C 484	11	55.0	21	15	US-10-085-198-461	Sequen
56.0	25	14	US-10-061-201-3153	Sequence 3153, Ap	C 485	11	55.0	22	9	US-09-956-636A-4	Sequen
56.0	26	15	US-10-023-634-104	Sequence 104, App	C 486	11	55.0	22	14	US-10-185-867-19	Sequen
56.0	28	15	US-10-321-039-332	Sequence 332, App	C 487	11	55.0	23	14	US-10-320-647-17	Sequen
56.0	29	15	US-10-443-976-18	Sequence 18, Appl	C 488	11	55.0	24	10	US-09-940-185-3492	Sequen
56.0	30	10	US-09-794-517-23	Sequence 23, Appl	C 489	11	55.0	24	15	US-10-004-378A-149	Sequen
56.0	30	10	US-09-794-529-23	Sequence 23, Appl	C 490	11	55.0	25	12	US-09-837-306-178	Sequen
56.0	30	10	US-09-794-832-23	Sequence 23, Appl	C 491	11	55.0	25	14	US-10-215-112-1525	Sequen
56.0	30	14	US-10-170-713A-23	Sequence 23, Appl	C 492	11	55.0	25	14	US-10-215-112-2456	Sequen
56.0	30	14	US-10-171-734-23	Sequence 23, Appl	C 493	11	55.0	25	14	US-10-215-112-2474	Sequen
56.0	30	15	US-10-411-954-245	Sequence 245, App	C 494	11	55.0	25	14	US-10-215-112-2600	Sequen
56.0	31	9	US-09-801-274-348	Sequence 348, App	C 495	11	55.0	25	14	US-10-098-263B-1502	Sequen
56.0	32	9	US-09-814-786-40	Sequence 40, Appl	C 496	11	55.0	25	14	US-10-098-263B-2700	Sequen
56.0	32	14	US-10-097-554A-1	Sequence 1, Appl	C 497	11	55.0	25	14	US-10-098-263B-8594	Sequen
56.0	32	15	US-10-154-884B-10984	Sequence 10984, A	C 498	11	55.0	25	14	US-10-098-263B-27887	Sequen
56.0	39	14	US-10-315-515-162	Sequence 162, App	C 499	11	55.0	25	14	US-10-098-263B-38235	Sequen
56.0	41	14	US-10-005-956-923	Sequence 923, App	C 500	11	55.0	25	14	US-10-098-263B-39793	Sequen
56.0	41	14	US-10-005-956-949	Sequence 949, App	C 501	11	55.0	25	14	US-10-098-263B-39813	Sequen
56.0	44	14	US-10-422-934-32	Sequence 32, Appl	C 502	11	55.0	25	14	US-10-098-263B-40257	Sequen
56.0	46	10	US-09-377-885A-16	Sequence 16, Appl	C 503	11	55.0	25	14	US-10-098-263B-51731	Sequen
56.0	46	10	US-09-377-885A-17	Sequence 17, Appl	C 504	11	55.0	25	14	US-10-098-263B-51732	Sequen
56.0	47	15	US-10-170-097-921	Sequence 921, App	C 505	11	55.0	25	14	US-10-098-263B-60173	Sequen
56.0	47	15	US-10-349-143-43	Sequence 43, Appl	C 506	11	55.0	25	14	US-10-098-263B-62314	Sequen
56.0	47	15	US-10-349-143-2093	Sequence 2093, Ap	C 507	11	55.0	25	14	US-10-098-263B-63350	Sequen
56.0	47	15	US-10-349-143-2526	Sequence 2526, Ap	C 508	11	55.0	25	14	US-10-098-263B-66127	Sequen
56.0	49	15	US-10-380-873B-44	Sequence 44, Appl	C 509	11	55.0	25	14	US-10-098-263B-72881	Sequen
56.0	50	15	US-10-131-827-1626	Sequence 1626, Ap	C 510	11	55.0	25	14	US-10-098-263B-77417	Sequen
56.0	50	15	US-10-131-827-5003	Sequence 5003, Ap	C 511	11	55.0	25	14	US-10-098-263B-83962	Sequen
56.0	50	15	US-10-131-827-7338	Sequence 7338, Ap	C 512	11	55.0	25	14	US-10-098-263B-84564	Sequen
56.0	50	15	US-10-131-827-7994	Sequence 7994, Ap	C 513	11	55.0	25	14	US-10-098-263B-89291	Sequen
56.0	53	9	US-09-788-297-10	Sequence 10, Appl	C 514	11	55.0	25	14	US-10-098-263B-93652	Sequen
56.0	53	9	US-09-788-297-11	Sequence 11, Appl	C 515	11	55.0	25	14	US-10-098-263B-94030	Sequen
56.0	53	9	US-09-911-088-4	Sequence 4, Appl	C 516	11	55.0	25	14	US-10-098-263B-104058	Sequen
56.0	53	15	US-10-320-191-4	Sequence 4, Appl	C 517	11	55.0	25	14	US-10-098-263B-104825	Sequen
56.0	54	10	US-09-300-345A-145	Sequence 145, App	C 518	11	55.0	25	14	US-10-098-263B-106064	Sequen
56.0	54	14	US-10-083-620A-25	Sequence 25, Appl	C 519	11	55.0	25	14	US-10-098-263B-109967	Sequen
56.0	54	14	US-10-034-015-25	Sequence 15, Appl	C 520	11	55.0	25	14	US-10-098-263B-116369	Sequen
56.0	54	14	US-10-305-765-179	Sequence 179, App	C 521	11	55.0	25	15	US-10-098-263B-126896	Sequen
56.0	54	14	US-10-305-633-179	Sequence 179, App	C 522	11	55.0	25	15	US-10-045-674-350	Sequen
56.0	54	15	US-10-339-268A-34	Sequence 34, Appl	C 523	11	55.0	26	11	US-10-045-674-396	Sequen
56.0	56	10	US-09-870-932-3	Sequence 3, Appl	C 524	11	55.0	26	11	US-09-080-140-24	Sequen
56.0	56	14	US-10-232-544-133	Sequence 133, App	C 525	11	55.0	27	9	US-09-911-969-20	Sequen
56.0	56	14			C 526	11	55.0	27	10	US-09-895-940B-5	Sequen



55.0	28	14	US-10-214-419-86	Sequence 86, Appl	600	11	55.0	45	12	US-09-837-306-310	Sequenc
55.0	28	15	US-10-407-416-56	Sequence 56, Appl	601	11	55.0	45	12	US-09-837-306-311	Sequenc
55.0	30	8	US-08-796-570A-14	Sequence 14, Appl	602	11	55.0	45	12	US-09-837-306-312	Sequenc
55.0	30	9	US-09-896-720-7	Sequence 7, Appl	603	11	55.0	45	12	US-10-164-749A-160	Sequenc
55.0	30	10	US-09-895-940B-23	Sequence 23, Appl	604	11	55.0	45	13	US-10-001-054-70	Sequenc
55.0	30	13	US-10-067-477-14	Sequence 14, Appl	605	11	55.0	45	14	US-10-017-081A-160	Sequenc
55.0	31	10	US-09-912-263-220	Sequence 220, App	606	11	55.0	45	14	US-10-167-749-160	Sequenc
55.0	31	10	US-09-999-220B-27	Sequence 27, Appl	607	11	55.0	45	14	US-10-013-921A-160	Sequenc
55.0	31	10	US-09-999-220B-86	Sequence 86, Appl	608	11	55.0	45	14	US-10-013-921A-160	Sequenc
55.0	31	10	US-09-999-220B-98	Sequence 98, Appl	609	11	55.0	45	14	US-10-016-177A-160	Sequenc
55.0	31	16	US-10-236-012-3	Sequence 3, Appl	610	11	55.0	45	14	US-10-166-709A-160	Sequenc
55.0	32	12	US-10-449-978-33	Sequence 33, Appl	611	11	55.0	45	14	US-10-143-031A-160	Sequenc
55.0	32	15	US-10-452-038-29	Sequence 29, Appl	612	11	55.0	45	14	US-10-143-030A-160	Sequenc
55.0	33	14	US-10-134-643-16	Sequence 16, Appl	613	11	55.0	45	14	US-10-002-967A-160	Sequenc
55.0	34	9	US-09-924-417-35	Sequence 35, Appl	614	11	55.0	45	14	US-10-017-083A-160	Sequenc
55.0	35	14	US-10-165-060-10	Sequence 10, Appl	615	11	55.0	45	14	US-10-145-128A-160	Sequenc
55.0	35	14	US-10-165-968-10	Sequence 10, Appl	616	11	55.0	45	14	US-10-017-191A-160	Sequenc
55.0	35	14	US-10-318-905-23	Sequence 23, Appl	617	11	55.0	45	14	US-10-143-028A-160	Sequenc
55.0	36	9	US-09-004-068-7	Sequence 7, Appl	618	11	55.0	45	14	US-10-143-029A-160	Sequenc
55.0	38	15	US-10-351-275-36	Sequence 36, Appl	619	11	55.0	45	14	US-10-145-089A-160	Sequenc
55.0	40	10	US-09-900-112-21	Sequence 21, Appl	620	11	55.0	45	14	US-10-165-067A-160	Sequenc
55.0	41	12	US-10-453-827-221	Sequence 221, App	621	11	55.0	45	14	US-10-145-017A-160	Sequenc
55.0	41	14	US-10-128-714-4015	Sequence 415, Ap	622	11	55.0	45	14	US-10-164-728A-160	Sequenc
55.0	41	14	US-10-224-683-62	Sequence 62, Appl	623	11	55.0	45	14	US-10-013-926A-160	Sequenc
55.0	44	12	US-09-837-306-317	Sequence 317, App	624	11	55.0	45	14	US-10-165-247A-160	Sequenc
55.0	44	12	US-09-837-306-318	Sequence 318, App	625	11	55.0	45	14	US-10-145-124A-160	Sequenc
55.0	44	12	US-09-837-306-319	Sequence 319, App	626	11	55.0	45	14	US-10-160-502A-160	Sequenc
55.0	44	12	US-09-837-306-320	Sequence 320, App	627	11	55.0	45	14	US-10-145-087A-160	Sequenc
55.0	44	12	US-09-837-306-327	Sequence 327, App	628	11	55.0	45	14	US-10-017-086A-160	Sequenc
55.0	44	12	US-09-837-306-328	Sequence 328, App	629	11	55.0	45	14	US-10-164-829A-160	Sequenc
55.0	44	12	US-09-837-306-329	Sequence 329, App	630	11	55.0	45	14	US-10-164-829A-160	Sequenc
55.0	44	12	US-09-837-306-330	Sequence 330, App	631	11	55.0	45	14	US-10-013-922A-160	Sequenc
55.0	44	15	US-10-240-460-4	Sequence 4, Appl	632	11	55.0	45	14	US-10-020-445A-160	Sequenc
55.0	44	15	US-10-045-674-400	Sequence 400, App	633	11	55.0	45	15	US-10-013-924A-160	Sequenc
55.0	44	15	US-10-045-674-401	Sequence 401, App	634	11	55.0	45	15	US-10-017-084A-160	Sequenc
55.0	44	15	US-10-045-674-402	Sequence 402, App	635	11	55.0	45	15	US-10-017-085A-160	Sequenc
55.0	44	15	US-10-045-674-403	Sequence 403, App	636	11	55.0	45	15	US-10-013-916A-160	Sequenc
55.0	44	15	US-10-045-674-410	Sequence 410, App	637	11	55.0	45	15	US-10-143-026B-160	Sequenc
55.0	44	15	US-10-045-674-411	Sequence 411, App	638	11	55.0	45	15	US-10-013-918A-160	Sequenc
55.0	44	15	US-10-045-674-412	Sequence 412, App	639	11	55.0	45	15	US-10-013-928A-160	Sequenc
55.0	44	15	US-10-045-674-413	Sequence 413, App	640	11	55.0	45	15	US-10-162-522A-160	Sequenc
55.0	45	9	US-09-978-295A-160	Sequence 160, App	641	11	55.0	45	15	US-10-013-923A-160	Sequenc
55.0	45	9	US-09-978-697-160	Sequence 160, App	642	11	55.0	45	15	US-10-013-925A-160	Sequenc
55.0	45	9	US-09-978-192A-160	Sequence 160, App	643	11	55.0	45	15	US-10-013-927A-160	Sequenc
55.0	45	9	US-09-999-832A-160	Sequence 160, App	644	11	55.0	45	15	US-10-145-093A-160	Sequenc
55.0	45	10	US-09-978-189-160	Sequence 160, App	645	11	55.0	45	15	US-10-013-919A-160	Sequenc
55.0	45	10	US-09-978-608A-160	Sequence 160, App	646	11	55.0	45	15	US-10-013-920A-160	Sequenc
55.0	45	10	US-09-978-585A-160	Sequence 160, App	647	11	55.0	47	15	US-10-349-143-2917	Sequenc
55.0	45	10	US-09-978-191A-160	Sequence 160, App	648	11	55.0	48	10	US-09-877-478-5506	Sequenc
55.0	45	10	US-09-978-403A-160	Sequence 160, App	649	11	55.0	48	10	US-09-877-478-5506	Sequenc
55.0	45	10	US-09-978-564A-160	Sequence 160, App	650	11	55.0	50	15	US-10-131-827-255	Sequenc
55.0	45	10	US-09-999-833A-160	Sequence 160, App	651	11	55.0	50	15	US-10-131-827-2675	Sequenc
55.0	45	10	US-09-981-915A-160	Sequence 160, App	652	11	55.0	50	15	US-10-131-827-3936	Sequenc
55.0	45	10	US-09-978-824-160	Sequence 160, App	653	11	55.0	50	15	US-10-131-827-4766	Sequenc
55.0	45	10	US-09-918-585A-160	Sequence 160, App	654	11	55.0	50	15	US-10-131-827-4855	Sequenc
55.0	45	10	US-09-978-423A-160	Sequence 160, App	655	11	55.0	50	15	US-10-131-827-7375	Sequenc
55.0	45	10	US-09-978-193A-160	Sequence 160, App	656	11	55.0	51	15	US-10-418-182-228	Sequenc
55.0	45	10	US-09-999-830A-160	Sequence 160, App	657	11	55.0	54	12	US-10-429-849-9	Sequenc
55.0	45	10	US-09-978-757A-160	Sequence 160, App	658	11	55.0	57	14	US-10-159-339-85	Sequenc
55.0	45	10	US-09-978-187B-160	Sequence 160, App	659	11	55.0	57	14	US-10-308-891-13	Sequenc
55.0	45	10	US-09-978-643A-160	Sequence 160, App	660	11	55.0	58	9	US-09-748-451-12	Sequenc
55.0	45	10	US-09-978-375A-160	Sequence 160, App	661	11	55.0	58	14	US-10-275-071-15	Sequenc
55.0	45	10	US-09-978-298A-160	Sequence 160, App	662	11	55.0	59	9	US-09-878-178-1609	Sequenc
55.0	45	10	US-09-978-188A-160	Sequence 160, App	663	11	55.0	59	13	US-10-046-935-1609	Sequenc
55.0	45	10	US-09-978-681A-160	Sequence 160, App	664	11	55.0	59	14	US-10-146-502-1609	Sequenc
55.0	45	10	US-09-978-194A-160	Sequence 160, App	665	11	55.0	60	10	US-09-908-975-5051	Sequenc
55.0	45	10	US-09-998-829A-160	Sequence 160, App	666	11	55.0	60	10	US-09-908-975-5283	Sequenc
55.0	45	10	US-09-978-299A-160	Sequence 160, App	667	11	55.0	60	10	US-09-908-975-6983	Sequenc
55.0	45	10	US-09-978-544A-160	Sequence 160, App	668	11	55.0	60	10	US-09-908-975-7923	Sequenc
55.0	45	10	US-09-978-665A-160	Sequence 160, App	669	11	55.0	60	10	US-09-908-975-8686	Sequenc
55.0	45	10	US-09-978-802A-160	Sequence 160, App	670	11	55.0	60	10	US-09-908-975-9038	Sequenc
55.0	45	12	US-09-837-306-308	Sequence 308, App	671	11	55.0	60	10	US-09-908-975-9205	Sequenc
55.0	45	12	US-09-837-306-309	Sequence 309, App	672	11	55.0	60	10	US-09-908-975-10428	Sequenc

55.0	60	10	US-09-308-975-11059	Sequence 11059, A	746	10.8	54.0	25	14	US-10-098-263B-69510	Sequen
55.0	60	10	US-09-308-975-11777	Sequence 11777, A	c 747	10.8	54.0	25	14	US-10-098-263B-69059	Sequen
55.0	60	10	US-09-308-975-13290	Sequence 13290, A	748	10.8	54.0	25	14	US-10-098-263B-71766	Sequen
55.0	60	10	US-09-308-975-13641	Sequence 13641, A	749	10.8	54.0	25	14	US-10-098-263B-76776	Sequen
55.0	60	10	US-09-308-975-13840	Sequence 13840, A	c 750	10.8	54.0	25	14	US-10-098-263B-82920	Sequen
55.0	60	10	US-09-308-975-13889	Sequence 13889, A	c 751	10.8	54.0	25	14	US-10-098-263B-83330	Sequen
55.0	60	10	US-09-308-975-14126	Sequence 14126, A	752	10.8	54.0	25	14	US-10-098-263B-86028	Sequen
55.0	60	10	US-09-308-975-14438	Sequence 14438, A	753	10.8	54.0	25	14	US-10-098-263B-87293	Sequen
55.0	60	10	US-09-308-975-16431	Sequence 16431, A	754	10.8	54.0	25	14	US-10-098-263B-87909	Sequen
55.0	60	10	US-09-308-975-18862	Sequence 18862, A	c 755	10.8	54.0	25	14	US-10-098-263B-88017	Sequen
55.0	60	10	US-09-308-975-19003	Sequence 19003, A	c 756	10.8	54.0	25	14	US-10-098-263B-88790	Sequen
55.0	60	10	US-09-308-975-19363	Sequence 19363, A	c 757	10.8	54.0	25	14	US-10-098-263B-90716	Sequen
55.0	60	10	US-09-308-975-19898	Sequence 19898, A	758	10.8	54.0	25	14	US-10-098-263B-92406	Sequen
55.0	60	10	US-09-308-975-21030	Sequence 21030, A	759	10.8	54.0	25	14	US-10-098-263B-93902	Sequen
55.0	60	10	US-09-308-975-22174	Sequence 22174, A	760	10.8	54.0	25	14	US-10-098-263B-94301	Sequen
55.0	60	10	US-09-308-975-22672	Sequence 22672, A	761	10.8	54.0	25	14	US-10-098-263B-94519	Sequen
55.0	60	10	US-09-308-975-31303	Sequence 31303, A	762	10.8	54.0	25	14	US-10-098-263B-94919	Sequen
55.0	60	10	US-09-308-975-31497	Sequence 31497, A	c 763	10.8	54.0	25	14	US-10-098-263B-96090	Sequen
55.0	60	10	US-09-308-975-31560	Sequence 31560, A	c 764	10.8	54.0	25	14	US-10-098-263B-96172	Sequen
55.0	60	10	US-09-308-975-31704	Sequence 31704, A	c 765	10.8	54.0	25	14	US-10-098-263B-97032	Sequen
54.0	14	10	US-09-510-378-235	Sequence 235, App	c 766	10.8	54.0	25	14	US-10-098-263B-98560	Sequen
54.0	17	10	US-09-780-533A-2096	Sequence 2096, Ap	c 767	10.8	54.0	25	14	US-10-098-263B-100037	Sequen
54.0	17	10	US-09-780-533A-2368	Sequence 2368, Ap	c 768	10.8	54.0	25	14	US-10-098-263B-105458	Sequen
54.0	17	10	US-09-780-533A-2369	Sequence 2369, Ap	c 769	10.8	54.0	25	14	US-10-098-263B-111988	Sequen
54.0	17	10	US-09-510-378-243	Sequence 243, App	c 770	10.8	54.0	25	14	US-10-098-263B-113306	Sequen
54.0	17	14	US-10-163-552-491	Sequence 491, App	c 771	10.8	54.0	25	14	US-10-098-263B-114549	Sequen
54.0	17	14	US-10-163-552-492	Sequence 492, App	c 772	10.8	54.0	25	14	US-10-098-263B-116041	Sequen
54.0	18	9	US-09-969-373-1909	Sequence 1909, App	c 773	10.8	54.0	25	14	US-10-098-263B-120077	Sequen
54.0	18	9	US-09-969-373-3784	Sequence 3784, Ap	774	10.8	54.0	25	14	US-10-098-263B-120199	Sequen
54.0	18	14	US-10-141-620-29	Sequence 29, Appl	775	10.8	54.0	25	14	US-10-098-263B-129654	Sequen
54.0	18	15	US-10-388-263-267	Sequence 267, App	776	10.8	54.0	25	14	US-10-098-263B-129995	Sequen
54.0	20	10	US-09-972-469-49	Sequence 49, Appl	c 777	10.8	54.0	26	12	US-09-754-853A-946	Sequen
54.0	20	10	US-09-877-843-75	Sequence 75, Appl	c 778	10.8	54.0	26	12	US-10-349-557A-8	Sequen
54.0	20	14	US-10-213-452A-21	Sequence 21, Appl	c 779	10.8	54.0	26	12	US-10-349-557A-9	Sequen
54.0	20	14	US-10-143-266-8	Sequence 8, Appli	c 780	10.8	54.0	26	12	US-10-349-557A-22	Sequen
54.0	20	14	US-10-025-145A-71	Sequence 71, Appl	c 781	10.8	54.0	26	12	US-10-349-557A-23	Sequen
54.0	20	15	US-10-190-366-34	Sequence 68, Appl	c 782	10.8	54.0	26	14	US-10-267-411B-8	Sequen
54.0	20	15	US-10-190-366-231	Sequence 34, Appl	783	10.8	54.0	26	14	US-10-267-411B-9	Sequen
54.0	21	14	US-10-090-011-24	Sequence 231, App	c 784	10.8	54.0	26	14	US-10-267-411B-22	Sequen
54.0	23	10	US-09-510-378-233	Sequence 24, Appl	785	10.8	54.0	26	14	US-10-267-411B-23	Sequen
54.0	23	10	US-09-510-378-234	Sequence 233, App	786	10.8	54.0	26	14	US-10-118-854-33	Sequen
54.0	23	14	US-10-215-457-6	Sequence 234, App	787	10.8	54.0	27	9	US-09-735-787-6	Sequen
54.0	24	10	US-09-940-185-1692	Sequence 6, Appli	c 788	10.8	54.0	27	9	US-09-529-063-95	Sequen
54.0	25	9	US-09-238-351-14	Sequence 14, Appl	c 789	10.8	54.0	27	14	US-10-141-620-28	Sequen
54.0	25	9	US-09-238-351-42	Sequence 42, Appl	790	10.8	54.0	27	14	US-10-138-870-6	Sequen
54.0	25	9	US-09-917-265-86	Sequence 86, Appl	c 791	10.8	54.0	27	14	US-10-414-378-95	Sequen
54.0	25	9	US-09-917-265-88	Sequence 88, Appl	c 792	10.8	54.0	28	9	US-09-775-925-15	Sequen
54.0	25	9	US-09-971-118-5	Sequence 5, Appli	c 793	10.8	54.0	28	9	US-09-785-548-11	Sequen
54.0	25	9	US-09-962-537-39	Sequence 39, Appl	c 794	10.8	54.0	28	10	US-09-951-121A-4	Sequen
54.0	25	9	US-09-962-537-40	Sequence 40, Appl	795	10.8	54.0	28	10	US-09-951-121A-5	Sequen
54.0	25	14	US-10-215-112-2299	Sequence 2299, Ap	c 796	10.8	54.0	28	14	US-10-295-905-5	Sequen
54.0	25	14	US-10-215-112-2618	Sequence 2618, Ap	c 797	10.8	54.0	28	14	US-10-255-032-6	Sequen
54.0	25	14	US-10-215-112-3374	Sequence 3374, Ap	798	10.8	54.0	28	14	US-10-255-032-7	Sequen
54.0	25	14	US-10-215-112-10353	Sequence 10353, A	c 799	10.8	54.0	28	14	US-10-295-682-4	Sequen
54.0	25	14	US-10-215-112-12688	Sequence 12688, A	800	10.8	54.0	28	14	US-10-295-682-5	Sequen
54.0	25	14	US-10-144-000-2	Sequence 2, Appli	c 801	10.8	54.0	28	14	US-10-281-673-40	Sequen
54.0	25	14	US-10-098-263B-9802	Sequence 9802, Ap	c 802	10.8	54.0	28	15	US-10-167-634-9	Sequen
54.0	25	14	US-10-098-263B-10023	Sequence 10023, A	c 803	10.8	54.0	28	15	US-10-167-634-11	Sequen
54.0	25	14	US-10-098-263B-10438	Sequence 10438, A	804	10.8	54.0	28	15	US-10-321-039-207	Sequen
54.0	25	14	US-10-098-263B-23492	Sequence 23492, A	c 805	10.8	54.0	29	9	US-09-957-974-8	Sequen
54.0	25	14	US-10-098-263B-27718	Sequence 27718, A	c 806	10.8	54.0	29	14	US-10-157-305A-204	Sequen
54.0	25	14	US-10-098-263B-35445	Sequence 35445, A	c 807	10.8	54.0	29	14	US-10-157-391-204	Sequen
54.0	25	14	US-10-098-263B-36617	Sequence 36617, A	c 808	10.8	54.0	29	14	US-10-157-096-204	Sequen
54.0	25	14	US-10-098-263B-37755	Sequence 37755, A	c 809	10.8	54.0	29	14	US-10-157-302-204	Sequen
54.0	25	14	US-10-098-263B-39255	Sequence 39255, A	c 810	10.8	54.0	29	14	US-10-157-215A-204	Sequen
54.0	25	14	US-10-098-263B-41032	Sequence 41032, A	c 811	10.8	54.0	29	14	US-10-157-299-204	Sequen
54.0	25	14	US-10-098-263B-55179	Sequence 55179, A	812	10.8	54.0	29	14	US-10-118-854-18	Sequen
54.0	25	14	US-10-098-263B-56083	Sequence 56083, A	813	10.8	54.0	29	14	US-10-118-854-32	Sequen
54.0	25	14	US-10-098-263B-57098	Sequence 57098, A	c 814	10.8	54.0	29	14	US-10-154-951B-204	Sequen
54.0	25	14	US-10-098-263B-57882	Sequence 57882, A	c 815	10.8	54.0	29	14	US-10-156-831-204	Sequen
54.0	25	14	US-10-098-263B-59743	Sequence 59743, A	c 816	10.8	54.0	29	14	US-10-157-147-204	Sequen
54.0	25	14	US-10-098-263B-63002	Sequence 63002, A	c 817	10.8	54.0	29	14	US-10-157-166-204	Sequen
54.0	25	14			c 818	10.8	54.0	29	14	US-10-156-902-204	Sequen

54.0	29	14	US-10-157-318-204	Sequence 204, App	892	10.8	54.0	50	15	US-10-131-827-5498	Sequenc
54.0	29	15	US-10-156-811-204	Sequence 204, App	893	10.8	54.0	50	15	US-10-131-827-5498	Sequenc
54.0	29	15	US-10-157-320A-204	Sequence 204, App	c 894	10.8	54.0	50	15	US-10-131-827-6869	Sequenc
54.0	29	15	US-10-157-418A-204	Sequence 204, App	c 895	10.8	54.0	54	14	US-10-141-620-20	Sequenc
54.0	29	15	US-10-157-317-204	Sequence 204, App	c 896	10.8	54.0	54	14	US-10-141-620-25	Sequenc
54.0	29	15	US-10-157-339-204	Sequence 204, App	c 897	10.8	54.0	54	15	US-10-141-508-7	Sequenc
54.0	31	9	US-09-801-274-1208	Sequence 1208, Ap	c 898	10.8	54.0	54	15	US-10-141-508-10	Sequenc
54.0	31	9	US-09-801-274-1373	Sequence 1373, Ap	899	10.8	54.0	55	14	US-10-295-905-8	Sequenc
54.0	31	10	US-09-510-378-167	Sequence 167, App	900	10.8	54.0	57	9	US-09-238-351-25	Sequenc
54.0	31	14	US-10-238-700-4571	Sequence 4571, Ap	901	10.8	54.0	57	9	US-09-238-351-43	Sequenc
54.0	31	14	US-10-157-305A-206	Sequence 206, App	902	10.8	54.0	59	14	US-10-029-386-14316	Sequenc
54.0	31	14	US-10-157-391-206	Sequence 206, App	903	10.8	54.0	60	9	US-09-923-876-1507	Sequenc
54.0	31	14	US-10-157-096-206	Sequence 206, App	c 904	10.8	54.0	60	9	US-09-739-707-10	Sequenc
54.0	31	14	US-10-157-302-206	Sequence 206, App	c 905	10.8	54.0	60	10	US-09-908-975-7401	Sequenc
54.0	31	14	US-10-157-215A-206	Sequence 206, App	906	10.8	54.0	60	10	US-09-908-975-9586	Sequenc
54.0	31	14	US-10-157-299-206	Sequence 206, App	907	10.8	54.0	60	10	US-09-908-975-10225	Sequenc
54.0	31	14	US-10-154-951B-206	Sequence 206, App	908	10.8	54.0	60	10	US-09-908-975-10301	Sequenc
54.0	31	14	US-10-156-831-206	Sequence 206, App	c 909	10.8	54.0	60	10	US-09-908-975-10947	Sequenc
54.0	31	14	US-10-157-147-206	Sequence 206, App	c 910	10.8	54.0	60	10	US-09-908-975-11219	Sequenc
54.0	31	14	US-10-156-166-206	Sequence 206, App	c 911	10.8	54.0	60	10	US-09-908-975-11559	Sequenc
54.0	31	14	US-10-156-902-206	Sequence 206, App	c 912	10.8	54.0	60	10	US-09-908-975-12001	Sequenc
54.0	31	14	US-10-157-318-206	Sequence 206, App	c 913	10.8	54.0	60	10	US-09-908-975-12501	Sequenc
54.0	31	15	US-10-156-811-206	Sequence 206, App	914	10.8	54.0	60	10	US-09-908-975-13766	Sequenc
54.0	31	15	US-10-157-320A-206	Sequence 206, App	915	10.8	54.0	60	10	US-09-908-975-15931	Sequenc
54.0	31	15	US-10-157-418A-206	Sequence 206, App	916	10.8	54.0	60	10	US-09-908-975-15966	Sequenc
54.0	31	15	US-10-157-317-206	Sequence 206, App	c 917	10.8	54.0	60	10	US-09-908-975-16472	Sequenc
54.0	31	15	US-10-157-339-206	Sequence 206, App	c 918	10.8	54.0	60	10	US-09-908-975-16772	Sequenc
54.0	32	9	US-09-962-537-55	Sequence 55, Appl	c 919	10.8	54.0	60	10	US-09-908-975-16885	Sequenc
54.0	32	14	US-10-029-386-14453	Sequence 14453, A	c 920	10.8	54.0	60	10	US-09-908-975-17410	Sequenc
54.0	32	14	US-10-141-620-27	Sequence 27, Appl	921	10.8	54.0	60	10	US-09-908-975-17504	Sequenc
54.0	33	15	US-10-141-620-11	Sequence 11, Appl	922	10.8	54.0	60	10	US-09-908-975-18086	Sequenc
54.0	33	15	US-10-141-508-11	Sequence 11, Appl	c 923	10.8	54.0	60	10	US-09-908-975-21950	Sequenc
54.0	36	9	US-09-968-851-20	Sequence 20, Appl	c 924	10.8	54.0	60	10	US-09-908-975-22291	Sequenc
54.0	36	9	US-09-968-851-23	Sequence 23, Appl	c 925	10.8	54.0	60	10	US-09-908-975-31499	Sequenc
54.0	36	14	US-10-141-620-24	Sequence 24, Appl	926	10.8	54.0	60	11	US-09-923-876-1507	Sequenc
54.0	36	15	US-09-988-626-156	Sequence 9, Appli	c 927	10.8	54.0	60	14	US-10-060-036-3623	Sequenc
54.0	38	10	US-09-988-687-156	Sequence 156, App	c 928	10.8	54.0	60	14	US-10-263-970-3	Sequenc
54.0	38	10	US-09-988-686-156	Sequence 156, App	c 929	10.8	54.0	60	14	US-10-106-698-3567	Sequenc
54.0	39	12	US-10-453-827-303	Sequence 303, App	930	10.6	53.0	17	10	US-09-930-423-748	Sequenc
54.0	39	12	US-10-453-827-304	Sequence 304, App	c 931	10.6	53.0	17	10	US-09-740-332-329	Sequenc
54.0	40	14	US-10-224-683-61	Sequence 61, Appl	932	10.6	53.0	17	10	US-09-740-332-4226	Sequenc
54.0	40	16	US-10-303-199A-22	Sequence 22, Appl	933	10.6	53.0	17	10	US-09-745-237A-748	Sequenc
54.0	40	16	US-10-303-199A-49	Sequence 49, Appl	c 934	10.6	53.0	17	10	US-09-817-879-329	Sequenc
54.0	40	16	US-10-303-199A-50	Sequence 50, Appl	935	10.6	53.0	17	10	US-09-817-879-4226	Sequenc
54.0	42	14	US-10-141-620-30	Sequence 30, Appl	c 936	10.6	53.0	17	14	US-10-230-006-2204	Sequenc
54.0	42	15	US-10-141-620-12	Sequence 12, Appl	c 937	10.6	53.0	17	14	US-10-230-006-2205	Sequenc
54.0	45	14	US-10-141-620-22	Sequence 22, Appl	938	10.6	53.0	18	15	US-10-108-260A-5381	Sequenc
54.0	45	15	US-10-141-620-8	Sequence 8, Appli	c 939	10.6	53.0	19	14	US-10-226-992-63	Sequenc
54.0	47	14	US-10-071-179-41	Sequence 41, Appl	940	10.6	53.0	19	14	US-10-226-992-146	Sequenc
54.0	47	14	US-10-071-179-62	Sequence 62, Appl	941	10.6	53.0	20	9	US-09-734-846-41	Sequenc
54.0	47	14	US-10-211-160-23	Sequence 23, Appl	942	10.6	53.0	20	9	US-09-754-167-59	Sequenc
54.0	47	14	US-10-126-704-41	Sequence 41, Appl	943	10.6	53.0	20	9	US-09-990-385-9	Sequenc
54.0	47	14	US-10-126-704-62	Sequence 62, Appl	944	10.6	53.0	20	10	US-09-932-300-68	Sequenc
54.0	47	14	US-10-051-681A-23	Sequence 23, Appl	945	10.6	53.0	20	10	US-09-920-677-30	Sequenc
54.0	47	15	US-10-349-143-690	Sequence 690, App	946	10.6	53.0	20	12	US-10-213-796-31	Sequenc
54.0	47	15	US-10-349-143-919	Sequence 919, App	c 947	10.6	53.0	20	12	US-10-213-796-120	Sequenc
54.0	47	15	US-10-349-143-3644	Sequence 3644, Ap	948	10.6	53.0	20	13	US-10-060-301-59	Sequenc
54.0	48	9	US-09-864-785-2998	Sequence 2998, Ap	949	10.6	53.0	20	14	US-10-302-262-41	Sequenc
54.0	48	10	US-09-848-754A-8650	Sequence 8650, Ap	c 950	10.6	53.0	20	15	US-10-349-505-2	Sequenc
54.0	48	10	US-09-776-474-2772	Sequence 2772, Ap	951	10.6	53.0	20	15	US-10-289-762-2507	Sequenc
54.0	48	10	US-09-930-423-4341	Sequence 4341, Ap	952	10.6	53.0	20	16	US-10-210-838-35	Sequenc
54.0	48	10	US-09-827-395A-2550	Sequence 2550, Ap	c 953	10.6	53.0	20	16	US-10-210-838-140	Sequenc
54.0	48	10	US-09-827-395A-2589	Sequence 2589, Ap	954	10.6	53.0	22	9	US-09-874-162A-16	Sequenc
54.0	48	10	US-09-745-237A-4341	Sequence 4341, Ap	955	10.6	53.0	23	14	US-10-077-624-19	Sequenc
54.0	48	14	US-10-141-620-26	Sequence 26, Appl	c 956	10.6	53.0	24	9	US-09-215-652-38	Sequenc
54.0	48	14	US-10-157-580A-133	Sequence 133, App	c 957	10.6	53.0	24	9	US-09-810-933-44	Sequenc
54.0	48	14	US-10-230-006-2283	Sequence 2283, Ap	c 958	10.6	53.0	24	14	US-10-010-802-364	Sequenc
54.0	49	9	US-09-238-351-8	Sequence 8, Appli	c 959	10.6	53.0	24	14	US-10-251-210-44	Sequenc
54.0	50	10	US-09-993-346-511	Sequence 511, App	c 960	10.6	53.0	25	10	US-09-754-853A-745	Sequenc
54.0	50	15	US-10-131-827-4465	Sequence 4465, Ap	961	10.6	53.0	25	10	US-09-393-696-8	Sequenc
54.0	50	15	US-10-131-827-4565	Sequence 4565, Ap	962	10.6	53.0	25	10	US-09-393-696-10	Sequenc
54.0	50	15	US-10-131-827-5023	Sequence 5023, Ap	963	10.6	53.0	25	10	US-09-393-696-12	Sequenc
54.0	50	15			964	10.6	53.0	25	13	US-10-077-874-8	Sequenc

53.0 25 13 US-10-077-874-10 Sequence 10, Appl  
 53.0 25 13 US-10-077-874-12 Sequence 12, Appl  
 53.0 25 14 US-10-215-112-3109 Sequence 3109, Ap  
 53.0 25 14 US-10-215-112-9154 Sequence 9154, Ap  
 53.0 25 14 US-10-215-112-11404 Sequence 11404, A  
 53.0 25 14 US-10-215-112-11816 Sequence 11816, A  
 53.0 25 14 US-10-215-112-13218 Sequence 13218, A  
 53.0 25 14 US-10-215-112-13659 Sequence 13659, A  
 53.0 25 14 US-10-098-263B-1435 Sequence 1435, Ap  
 53.0 25 14 US-10-098-263B-1436 Sequence 1436, Ap  
 53.0 25 14 US-10-098-263B-14929 Sequence 14929, A  
 53.0 25 14 US-10-098-263B-15274 Sequence 15274, A  
 53.0 25 14 US-10-098-263B-15565 Sequence 15565, A  
 53.0 25 14 US-10-098-263B-16201 Sequence 16201, A  
 53.0 25 14 US-10-098-263B-16202 Sequence 16202, A  
 53.0 25 14 US-10-098-263B-17677 Sequence 17677, A  
 53.0 25 14 US-10-098-263B-18391 Sequence 18391, A  
 53.0 25 14 US-10-098-263B-26256 Sequence 26256, A  
 53.0 25 14 US-10-098-263B-27837 Sequence 27837, A  
 53.0 25 14 US-10-098-263B-29164 Sequence 29164, A  
 53.0 25 14 US-10-098-263B-31041 Sequence 31041, A  
 53.0 25 14 US-10-098-263B-33460 Sequence 33460, A  
 53.0 25 14 US-10-098-263B-39788 Sequence 39788, A  
 53.0 25 14 US-10-098-263B-40047 Sequence 40047, A  
 53.0 25 14 US-10-098-263B-40048 Sequence 40048, A  
 53.0 25 14 US-10-098-263B-40503 Sequence 40503, A  
 53.0 25 14 US-10-098-263B-41131 Sequence 41131, A  
 53.0 25 14 US-10-098-263B-41198 Sequence 41198, A  
 53.0 25 14 US-10-098-263B-41829 Sequence 41829, A  
 53.0 25 14 US-10-098-263B-46029 Sequence 46029, A  
 53.0 25 14 US-10-098-263B-47227 Sequence 47227, A  
 53.0 25 14 US-10-098-263B-47971 Sequence 47971, A  
 53.0 25 14 US-10-098-263B-51625 Sequence 51625, A  
 53.0 25 14 US-10-098-263B-53282 Sequence 53282, A  
 53.0 25 14 US-10-098-263B-63010 Sequence 63010, A  
 53.0 25 14 US-10-098-263B-69912 Sequence 69912, A

## ALIGNMENTS

58079  
 '9, Application US/10098263B  
 Co. US20030104410A1  
 INVENTOR: Michael  
 Hittman, Michael  
 TITLE: Human Microarray  
 DATE: 2001-03-16  
 FILING DATE: 2003-01-08  
 PUBLICATION NUMBER: US/10/098,263B  
 NG DATE: 2003-01-08  
 ATION NUMBER: 66/276,759  
 DATE: 2001-03-16  
 Q ID NOS: 131056  
 croarray Probe Sequence Listing Generator V 1.1  
 79

homo sapien  
 58079  
 milarity 75.0%; Score 15; DB 14; Length 25;  
 milarity 100.0%; Pred. No. 1.3e+03;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATCCTGTCCTCCAC 15  
 |||||  
 ATCCTGTCCTCCAC 17

12  
 Application US/0991176B

Patent No. US20020156243A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 TITLE OF INVENTION: ANTIBODIES THAT BIND AN  
 TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
 FILE REFERENCE: 97-30D1  
 CURRENT APPLICATION NUMBER: US/09/911.176B  
 CURRENT FILING DATE: 2001-07-23  
 PRIOR APPLICATION NUMBER: 09/118,408  
 PRIOR FILING DATE: 1998-07-17  
 PRIOR APPLICATION NUMBER: 60/053,154  
 PRIOR FILING DATE: 1997-07-18  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 12  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Oligonucleotide ZC13651  
 US-09-911-176B-12  
 Query Match 74.0%; Score 14.8; DB 9; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 QY 3 CCTTGTCCTCCACGGTTT 20  
 Db 1 CTTTGTCCTCCACGGTTT 18  
 RESULT 3  
 US-09-911-176B-15/c  
 Sequence 15, Application US/09911176B  
 Patent No. US20020156243A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 TITLE OF INVENTION: ANTIBODIES THAT BIND AN  
 TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG  
 FILE REFERENCE: 97-30D1  
 CURRENT APPLICATION NUMBER: US/09/911.176B  
 CURRENT FILING DATE: 2001-07-23  
 PRIOR APPLICATION NUMBER: 09/118,408  
 PRIOR FILING DATE: 1998-07-17  
 PRIOR APPLICATION NUMBER: 60/053,154  
 PRIOR FILING DATE: 1997-07-18  
 NUMBER OF SEQ ID NOS: 52  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 15  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Oligonucleotide ZC13650  
 US-09-911-176B-15  
 Query Match 74.0%; Score 14.8; DB 9; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 QY 3 CCTTGTCCTCCACGGTTT 20  
 Db 20 CTTTGTCCTCCACGGTTT 3

RESULT 4  
 US-10-180-762-12  
 Sequence 12, Application US/10180762  
 Publication No. US20030022838A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Lasser, Gerald W.  
 APPLICANT: Bishop, Paul D.

## NTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION

E: 99-12C3  
CATION NUMBER: US/10/180,762  
G DATE: 2002-06-25  
TION NUMBER: 09/253,604  
DATE: 1999-02-19  
TION NUMBER: 09/444,794  
DATE: 1999-11-22  
TION NUMBER: 09/506,855  
DATE: 2000-02-17  
ID NOS: 55  
tSEQ for Windows Version 3.0

## tificial Sequence

ATION: Oligonucleotide ZC13651

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20  
|||||  
TTGTCTCTCCACGGTT 18

## /c

pplication US/10180762  
US20030022838A1

## ATION:

eppard, Paul O.  
isher, Gerald W.

## NTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION

E: 99-12C3  
CATION NUMBER: US/10/180,762  
G DATE: 2002-06-25  
TION NUMBER: 09/253,604  
DATE: 1999-02-19  
TION NUMBER: 09/444,794  
DATE: 1999-11-22  
TION NUMBER: 09/506,855  
DATE: 2000-02-17  
ID NOS: 55  
tSEQ for Windows Version 3.0

## tificial Sequence

ATION: Oligonucleotide ZC13650

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20  
|||||  
TTGTCTCTCCACGGTT 3

pplication US/10241258  
US20030078206A1  
ATION:  
eppard, Paul O.  
asser, Gerald W.

; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; FILE REFERENCE: 99-12

; CURRENT APPLICATION NUMBER: US/10/241,258  
; CURRENT FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13651  
US-10-241-258-12

Query Match 74.0%; Score 14.8; DB 14; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

OY 3 CTTGTCTCTCCACGGTT 20  
|||||  
DB 1 CTTGTCTCTCCACGGTT 18

## RESULT 7

US-10-241-258-15/c  
; Sequence 15, Application US/10241258  
; Publication No. US20030078206A1  
; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.

; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; FILE REFERENCE: 99-12

; CURRENT APPLICATION NUMBER: US/10/241,258  
; CURRENT FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 20

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Oligonucleotide ZC13650  
US-10-241-258-15

Query Match 74.0%; Score 14.8; DB 14; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

OY 3 CTTGTCTCTCCACGGTT 20  
|||||  
DB 20 CTTGTCTCTCCACGGTT 3

## RESULT 8

US-10-194-370-53  
; Sequence 53, Application US/10194370  
; Publication No. US20030096270A1  
; GENERAL INFORMATION:

; APPLICANT: Paul Andrew Whittaker et al  
; TITLE OF INVENTION: Disease-Associated Gene

; FILE REFERENCE: Case 4-32067A/HO 41  
; CURRENT APPLICATION NUMBER: US/10/194,370  
; CURRENT FILING DATE: 2002-07-12

; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53

; LENGTH: 20  
; TYPE: DNA

; ORGANISM: Homo sapiens

```
3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-360-186-15

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

TCCTGTCTCTCCACGGG 18
|||||
TCCTGTCTCTCCACTGG 20

2
Application US/10360186
O. US20030144208A1
VATION:
heppard, Paul O.
Lasser, Gerald W.
Bishop, Paul D.
ENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
CE: 99-12C3
ICATION NUMBER: US/10/360,186
NG DATE: 2003-02-07
ACTION NUMBER: US/09/619,740
DATE: 2000-07-19
ACTION NUMBER: 09/253,604
DATE: 1999-02-19
ACTION NUMBER: 09/444,794
DATE: 1999-11-22
ACTION NUMBER: 09/506,855
DATE: 2000-02-17
Q ID NOS: 55
stSEQ for Windows Version 3.0

rtificial Sequence
VATION: Oligonucleotide ZC13651
2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13651
US-10-392-531-12

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

CTTGTCCTCCACGGGTT 20
|||||
TTTGTCCTCCACGGTTT 18

5/c
Application US/10360186
O. US20030144208A1
VATION:
heppard, Paul O.
Lasser, Gerald W.
Bishop, Paul D.
ENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
CE: 99-12C3
ICATION NUMBER: US/10/360,186
NG DATE: 2003-02-07
ACTION NUMBER: US/09/619,740
DATE: 2000-07-19
ACTION NUMBER: 09/253,604
DATE: 1999-02-19
ACTION NUMBER: 09/444,794
DATE: 1999-11-22
ACTION NUMBER: 09/506,855
DATE: 2000-02-17
Q ID NOS: 55
stSEQ for Windows Version 3.0

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-360-186-15

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY      3 CCTGTCTCTCCACGGGTT 20
Db      1 CTTGTCTCTCCACGGTTT 18

RESULT 11
US-10-392-531-12
; Sequence 12, Application US/10392531
; Publication No. US20030176658A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/10/392,531
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US/09/506,852
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13651
US-10-392-531-12

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY      3 CCTGTCTCTCCACGGGTT 20
Db      1 CTTGTCTCTCCACGGTTT 18

RESULT 12
US-10-392-531-15/c
; Sequence 15, Application US/10392531
; Publication No. US20030176658A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/10/392,531
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US/09/506,852
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-392-531-15
```

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTGTCTCCACGGTT 20  
TTGTCTCCACGGTTT 3  
pplication US/10392706  
US20030176659A1  
eppard, Paul O.  
NITION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
E: 97-30  
CATION NUMBER: US/10/392,706  
G DATE: 2003-03-20  
TION NUMBER: US/09/506,852  
DATE: 2000-02-17  
TION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154  
DATE: EARLIER FILING DATE: 1997-07-18  
ID NOS: 44  
tSEQ for Windows Version 3.0

## tificial Sequence

ATION: Oligonucleotide ZC13651

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTGTCTCCACGGTT 20  
TTGTCTCCACGGTTT 18

/c

pplication US/10392706  
US20030176659A1  
ATION:  
eppard, Paul O.  
NITION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
E: 97-30  
CATION NUMBER: US/10/392,706  
G DATE: 2003-03-20  
TION NUMBER: US/09/506,852  
DATE: 2000-02-17  
TION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154  
DATE: EARLIER FILING DATE: 1997-07-18  
ID NOS: 44  
tSEQ for Windows Version 3.0

## tificial Sequence

ATION: Oligonucleotide ZC13650

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTGTCTCCACGGTT 20  
TTGTCTCCACGGTTT 3

RESULT 15

US-10-198-695-12  
; Sequence 12, Application US/10198695  
; Publication No. US20040014650A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; TITLE OF INVENTION: IMMUNE FUNCTION  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/10/198,695  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13651  
US-10-198-695-12

Query Match 74.0%; Score 14.8; DB 15; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CCTGTCTCTCCACGGTTT 20  
| | | | | | | | | | | | | | | | | |  
Db 1 CTTTGTCTCTCCACGGTTT 18

RESULT 16

US-10-198-695-15/c  
; Sequence 15, Application US/10198695  
; Publication No. US20040014650A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; TITLE OF INVENTION: IMMUNE FUNCTION  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/10/198,695  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13650  
US-10-198-695-15

Query Match 74.0%; Score 14.8; DB 15; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CCTGTCTCTCCACGGTTT 20  
| | | | | | | | | | | | | | | | | |  
Db 20 CTTTGTCTCTCCACGGTTT 3

RESULT 17

US-10-098-263B-119019  
; Sequence 119019, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray

FE: 3118.1  
CATION NUMBER: US/10/098,263B  
G DATE: 2003-01-08  
ATION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
roarray Probe Sequence Listing Generator V 1.1  
119

omo sapien  
19019

74.0%; Score 14.8; DB 14; Length 25;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCTCCACGGGT 19  
|||||  
CTTGTCTCCACGGGT 24

/c  
pplication US/09950902  
20020127615A1  
ATION:  
ne Trustees of Columbia University in the City of  
ENTION: TRAF-3 DELETION ISOFORMS AND USES THEREOF  
TE: 58732-A-PCT  
ICATION NUMBER: US/09/950,902  
NG DATE: 2001-09-10  
ATION NUMBER: PCT/US00/06503  
DATE: 2000-03-10  
ATION NUMBER: 09/268,544  
DATE: 1999-03-11  
ID NOS: 14  
tentIn ver. 2.1

## rtificial Sequence

MATION: Description of Artificial Sequence:forward primer  
MATION: ZnRING

ilarity 72.0%; Score 14.4; DB 9; Length 38;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTTGCTCTCCACGG 17  
|||||  
ACTTGCTCTCCACGG 17

## 70/c

Application US/09814777A  
20020142415A1  
MATION:  
OPMAN, Peter Anthony  
MUSCAT, George Eugene Orlando  
ENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM  
CE: 21415-0003  
ICATION NUMBER: US/09/814,777A  
NG DATE: 2001-03-23  
ATION NUMBER: AU P06457  
DATE: 2000-03-24  
Q ID NOS: 128  
tentIn version 3.0

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Sox18 B primer  
US-09-814-777A-70

Query Match 71.0%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTGCTCTCCACGGGTT 20  
|||||  
Db 19 TCCTGTGCTCTCCACGGCTT 1

## RESULT 20

US-10-098-263B-76558/c  
Sequence 76558, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 76558  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-76558

Query Match 71.0%; Score 14.2; DB 14; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTGCTCTCCACGGGTT 20  
|||||  
Db 25 TCCTGTGCTCTCCACGGCTT 7

## RESULT 21

US-10-098-263B-54313  
Sequence 54313, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 54313  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-54313

Query Match 69.0%; Score 13.8; DB 14; Length 25;  
Best Local Similarity 88.2%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTGTGCTCTCCACGGGTT 20  
|||||  
Db 1 CTGTGCTCTCCACGGTGT 17



342  
Application US/09908975  
US20030165843A1  
ATION:  
OSHAN, Avi  
VASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat  
AIGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
E: 36688-0005  
G DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0

omo sapiens  
342  
69.0%; Score 13.8; DB 10; Length 60;  
ilarity 88.2%; Pred. No. 4.5e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTTGCTCTCCACGG 17  
|||||  
CCTTGCTCTCTGG 36

/c  
Application US/09110716A  
0020034739A1  
ATION:  
hrer, Robert I.  
hao, Chengquan  
asgow, Benjamin J.  
TION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS  
E: 22000-20596.00  
ATION NUMBER: US/09/110,716A  
G DATE: 1998-07-07  
ID NOS: 41  
entIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: primer

68.0%; Score 13.6; DB 9; Length 24;  
ilarity 80.0%; Pred. No. 6e+03; 4; Indels 0; Gaps 0;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCTTGCTCTCCACGGTT 20  
|||||  
ACCATGCTCTCCAGAGTT 2

38080  
Application US/10098263B  
US20030104410A1  
ATION:  
ittman, Michael

; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 58080  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-58080

Query Match 67.0%; Score 13.4; DB 14; Length 25;  
Best Local Similarity 93.3%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 ATCCTTGCTCTCCAC 15  
|||||  
Db 3 ATCCTTGCTCCACC 17

RESULT 25  
US-09-927-737-5  
; Sequence 5, Application US/09927737  
; Publication No. US20030082545A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFI  
; FILE REFERENCE: 19603/457  
; CURRENT APPLICATION NUMBER: US/09/927,737  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
; OTHER INFORMATION: PCR or LDR  
US-09-927-737-5

Query Match 67.0%; Score 13.4; DB 10; Length 29;  
Best Local Similarity 93.3%; Pred. No. 7.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 3 CCTTGCTCTCCACGG 17  
|||||  
Db 14 CCTTGCTCTCCACGG 28

RESULT 26  
US-09-927-737-7  
; Sequence 7, Application US/09927737  
; Publication No. US20030082545A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFI  
; FILE REFERENCE: 19603/457  
; CURRENT APPLICATION NUMBER: US/09/927,737  
; CURRENT FILING DATE: 2001-08-10

ATION NUMBER: 08/891,292  
DATE: 1997-07-10  
Q ID NOS: 96  
tentIn Ver. 2.1

## rtificial Sequence

MATION: Description of Artificial Sequence: Primer for  
MATION: PCR or LDR  
nsure

MATION: N at position 10 is either A, C, G, or T

67.0%; Score 13.4; DB 10; Length 29;  
milarity 93.3%; Pred. No. 7.3e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CTGTGCTCCACGG 17  
|||||  
CTGTGCTCCACGG 28

451  
Application US/10131827  
G. US20040009479A1

MATION:

chlgemuth, Jay

Fry, Kirk

Woodward, Robert

Ly, Ngoc

ENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
ENTION: CHRONIC INFLAMMATORY DISEASES

CE: 506612000120

ICATION NUMBER: US/10/131,827

NG DATE: 2002-09-06

ATION NUMBER: US 10/006,290

DATE: 2001-10-22

ATION NUMBER: US 60/296,764

DATE: 2001-06-08

Q ID NOS: 9090

tentIn version 3.1

1

omo sapiens

451

67.0%; Score 13.4; DB 15; Length 50;  
milarity 93.3%; Pred. No. 7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGTCCTCCACGGGT 19  
|||||  
TGTCCTCCACGGGT 25

.03/c

Application US/10148835

o. US20030207380A1

MATION:

AITO et al.

ENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

ICE: 2185-0648P

ICATION NUMBER: US/10/148,835

NG DATE: 2002-10-11

Q ID NOS: 213

tentIn Ver. 2.0

1

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Designed  
OTHER INFORMATION: oligonucleotide primer for PCR  
US-10-148-835-103

Query Match 66.0%; Score 13.2; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGGT 19  
|||||  
DB 20 TCCGTCTCTCCACGGAT 3

## RESULT 29

US-10-098-263B-119020

Sequence 119020, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 119020

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-119020

Query Match 66.0%; Score 13.2; DB 14; Length 25;  
Best Local Similarity 83.3%; Pred. No. 9.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGGT 19  
|||||  
DB 7 TCCTTGACTCCACGGGT 24

## RESULT 30

US-10-349-143-1000

Sequence 1000, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a

FILE REFERENCE: GENSET 020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,

PRIOR FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,

PRIOR FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 1000

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

;

ATION: 99-18777-130 : polymorphic base C or T  
00

66.0%; Score 13.2; DB 15; Length 47;  
ilarity 83.3%; Pred. No. 8.6e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTTGCTCTCCACGGGT 19  
|||||  
CTTCTCTCGAGGGT 19

59/c

Application US/09908975

. US20030165843A1

ATION:

OSHAN, Avi

ASSERMAN, Alon

MINTZ, Eli

MINTZ, Liat

AIGLER, Simchon

NTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

NTION: THAT POPULATE A TRANSCRIPTOME

E: 36688-0005

CATION NUMBER: US/09/908,975

G DATE: 2001-07-20

TION NUMBER: US 60/287,724

DATE: 2001-05-02

TION NUMBER: US 60/221,607

DATE: 2000-07-28

ID NOS: 32337

entIn version 3.0

mo sapiens

59

66.0%; Score 13.2; DB 10; Length 60;  
ilarity 83.3%; Pred. No. 8.6e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTTGCTCTCCACGGGT 19  
|||||  
CTTGCTCTCACTGGT 3

055/c

Application US/09908975

. US20030165843A1

ATION:

OSHAN, Avi

ASSERMAN, Alon

MINTZ, Eli

MINTZ, Liat

AIGLER, Simchon

NTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

NTION: THAT POPULATE A TRANSCRIPTOME

E: 36688-0005

CATION NUMBER: US/09/908,975

G DATE: 2001-07-20

TION NUMBER: US 60/287,724

DATE: 2001-05-02

TION NUMBER: US 60/221,607

DATE: 2000-07-28

ID NOS: 32337

entIn version 3.0

5

ORGANISM: Homo sapiens  
US-09-908-975-10055

Query Match 66.0%; Score 13.2; DB 10; Length 60;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 3 CCTTGCTCTCCACGGGT 20  
|||||  
Db 23 CCTTGCTCTCAAGGGT 6

RESULT 33

US-09-908-975-16879/c

; Sequence 16879, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: MINTZ, Liat

; APPLICANT: FAIGLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRP

; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908,975

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287,724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221,607

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16879

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-908-975-16875

Query Match 66.0%; Score 13.2; DB 10; Length 60;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCCTTGCTCTCCACGGGT 19  
|||||  
Db 33 TCCTTGCTCTCATGGGT 16

RESULT 34

US-09-801-274-949/c

; Sequence 949, Application US/09801274

; Patent No. US20020032319A1

; GENERAL INFORMATION:

; APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.

; APPLICANT: Lander, Eric S.

; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

; FILE REFERENCE: 2825.2009-001

; CURRENT APPLICATION NUMBER: US/09/801,274

; CURRENT FILING DATE: 2001-03-07

; PRIOR APPLICATION NUMBER: US 60/187,510

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 60/206,129

; PRIOR FILING DATE: 2000-05-22

; NUMBER OF SEQ ID NOS: 1802

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 949

; LENGTH: 31

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-801-274-949

Query Match

65.0%; Score 13; DB 9; Length 31;

1 09:38:26 2004

us-10-090-326-7.max.rnpb

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 1; Mismatches 1;

CTTGCTCCACGG 17  
||||| : |||||  
CTTGTCWCACGG 10

640/c  
, Application US/10215112  
O. US20030082596A1  
MATION: Mittmann

ENTION: Method of Genetic Analysis of Probes:  
ENTION: Test3  
CE: 3119

ICATION NUMBER: US/10/215,112  
NG DATE: 2002-08-08  
Q ID NOS: 14936  
stSEQ for Windows Version 4.0  
0

rtificial Sequence

MATION: Synthetic Oligonucleotide  
640

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGTCCTCCACGGTT 20  
||||| : |||||  
TGTCCTCCACGGTTT 7

83941/c  
1, Application US/10098263B  
O. US2003010410A1  
MATION:

ittman, Michael  
ENTION: Human Microarray  
CE: 3118.1  
ICATION NUMBER: US/10/098,263B  
NG DATE: 2003-01-08  
ATION NUMBER: 60/276,759  
DATE: 2001-03-16  
Q ID NOS: 131066

croarray Probe Sequence Listing Generator V 1.1  
41

omo sapien  
83941

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTTGCTCCACGG 17  
||||| : |||||  
TCTCGTCTCCACGG 9

105401/c  
01, Application US/10098263B  
O. US2003010410A1  
MATION:  
ittman, Michael

; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 105401  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-105401

Query Match 64.0%; Score 12.8; DB 14; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 ATCCTTGCTCCACG 16  
||||| : |||||  
Db 21 AACCTTGCTCTACG 6

RESULT 38

US-10-131-827-830  
; Sequence 830, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk, Robert  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 830  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-830

Query Match 64.0%; Score 12.8; DB 15; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGCTCTCCACGG 18  
||||| : |||||  
Db 22 CCTTGCTCTCTGGG 37

RESULT 39

US-10-305-555-20  
; Sequence 20, Application US/10305555  
; Publication No. US20030157525A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPR  
; FILE REFERENCE: D0196 NP  
; CURRENT APPLICATION NUMBER: US/10/305,555  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: U.S. 60/333,337  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: U.S. 60/355,619  
; PRIOR FILING DATE: 2002-02-06

L 09:38:26 2004

us-10-090-326-7.max.rnpb

} ID NOS: 42  
-ent in version 3.1

amo sapiens  
}

ilarity 64.0%; Score 12.8; DB 14; Length 53;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTGTCCTCCACGG 17  
|||||  
CTGTGTCCTCCACGG 39

0174/c  
; Application US/10098263B  
; US20030104410A1  
; Applicant: Human Microarray  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 66128  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-66128

Query Match 63.0%; Score 12.6; DB 14; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.8e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 2 TCCTGTCTCTCCACGGGTT 20  
|||||  
Db 2 TCCTGTCTCTCCACGGGTT 20  
|||||

RESULT 43

US-10-098-263B-72882/c  
; Sequence 72882, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 72882  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-72882

Query Match 63.0%; Score 12.6; DB 14; Length 25;  
Best Local Similarity 78.9%; Pred. No. 1.8e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 2 TCCTGTCTCTCCACGGGTT 20  
|||||  
Db 20 TCCTGTCTCTCTCCACGGGTT 2  
|||||

RESULT 44

US-10-098-263B-76557/c  
; Sequence 76557, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066

ilarity 63.0%; Score 12.6; DB 14; Length 25;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTGTGTCCTCCACGGT 19  
|||||  
GTTTGTCTCCACGGTGT 24

1 09:38:26 2004

us-10-090-326-7.max.rnpb

croarray Probe Sequence Listing Generator V 1.1  
57

omo sapien  
76557

63.0%; Score 12.6; DB 14; Length 25;  
milarity 78.9%; Pred.No. 1.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CCTTGTCCTCCACGGGTT 20  
|||||  
CCGTGTCCTCGTCGGCTT 7

104826/c  
26, Application US/10098263B  
o. US20030104410A1  
MATION:  
ittman, Michael  
ENTION: Human Microarray  
CE: 3118.1  
ICATION NUMBER: US/10/098,263B  
NG DATE: 2003-01-08  
ACTION NUMBER: 60/276,759  
DATE: 2001-03-16  
Q ID NOS: 131066  
croarray Probe Sequence Listing Generator V 1.1  
826

omo sapien  
104826

53.0%; Score 12.6; DB 14; Length 25;  
milarity 78.9%; Pred.No. 1.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CCTTGTCCTCCACGGGTT 20  
|||||  
CCGTGTCCTCCACGAGAT 7

d: February 29, 2004, 13:42:44  
857 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1501.3 Seconds  
(without alignments)  
397.818 Million cell updates/sec

US-10-090-326-7

20

1 atccttgctccacgggtt 20

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gsst:\*

29: gb\_gsst2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
71.0	54	14	CA797539		CA797539 Cac BL_46
69.0	59	14	CF298713		CF298713 7LEAF--02
68.0	55	14	T70039		T70039 vcl17b01.s1
66.0	35	10	AW140195		AW140195 SWAMCAC44

57.0	49	9	AU243854	151	11	55.0	54	9	AA190045
57.0	51	28	AZ495072	c 152	11	55.0	56	9	AU258629
57.0	52	28	BH897343	153	11	55.0	56	14	H69956
57.0	54	14	CA397523	154	11	55.0	57	28	AI905179
56.0	35	28	AZ421500	c 155	11	55.0	58	9	AZ45424
56.0	37	28	BZ763407	c 156	11	55.0	58	9	AI656273
56.0	39	28	BZ665246	157	11	55.0	58	12	BM534325
56.0	40	9	AI813961	c 158	11	55.0	59	9	AI246100
56.0	40	28	BH128122	c 159	11	55.0	60	14	CD288877
56.0	43	9	AA181395	c 160	11	55.0	60	14	H55293
56.0	45	9	AI555917	c 161	10.8	54.0	19	28	AZ783569
56.0	45	12	BI754711	c 162	10.8	54.0	25	14	L32062
56.0	45	28	BH855442	c 163	10.8	54.0	26	28	BZ660808
56.0	47	28	BH856951	c 164	10.8	54.0	27	28	AZ831513
56.0	50	9	AU105489	c 165	10.8	54.0	31	28	AZ816189
56.0	50	9	AU105492	c 166	10.8	54.0	31	29	AG256531
56.0	50	9	AU107202	c 167	10.8	54.0	32	29	CG708456
56.0	50	9	AU107203	c 168	10.8	54.0	34	28	AZ485756
56.0	50	9	AU107206	c 169	10.8	54.0	37	9	AA927558
56.0	50	9	AU107207	c 170	10.8	54.0	38	28	AZ821943
56.0	50	9	AU107210	c 171	10.8	54.0	39	28	AZ852950
56.0	50	9	AU107213	c 172	10.8	54.0	40	9	AA018337
56.0	50	9	AU107214	c 173	10.8	54.0	40	9	AI073810
56.0	50	9	AU107216	c 174	10.8	54.0	41	29	BX150554
56.0	50	28	CC024195	c 175	10.8	54.0	42	28	BH905673
56.0	51	28	AZ761115	c 176	10.8	54.0	42	28	BH905673
56.0	52	9	AA929532	c 177	10.8	54.0	43	9	AA193759
56.0	55	13	AI224478	c 178	10.8	54.0	43	28	BZ288372
56.0	55	13	BQ289498	c 179	10.8	54.0	44	28	BH910443
56.0	56	14	CF857035	c 180	10.8	54.0	46	9	AI282441
56.0	58	29	BX891429	c 181	10.8	54.0	46	9	AI282441
56.0	59	12	BH669126	c 182	10.8	54.0	46	9	AI631068
56.0	59	14	T61794	c 183	10.8	54.0	46	14	W30168
56.0	59	28	BH848880	c 184	10.8	54.0	46	29	CC886211
56.0	60	28	BQ3761	c 185	10.8	54.0	47	28	AZ860255
56.0	60	28	BZ290591	c 186	10.8	54.0	48	29	BX661317
55.0	27	28	AZ307201	c 187	10.8	54.0	49	9	AA804906
55.0	28	9	AA905471	c 188	10.8	54.0	49	28	AZ964788
55.0	28	9	AZ633359	c 189	10.8	54.0	50	9	AU102994
55.0	35	28	AZ657249	c 190	10.8	54.0	50	9	AU107902
55.0	36	12	BQ041351	c 191	10.8	54.0	50	28	AZ807846
55.0	36	29	TA362C11P	c 192	10.8	54.0	51	28	BH640903
55.0	37	28	AZ832358	c 193	10.8	54.0	52	10	BF645565
55.0	38	28	BH851440	c 194	10.8	54.0	52	10	BE315620
55.0	38	29	BX896340	c 195	10.8	54.0	52	28	BH225527
55.0	41	28	AZ663826	c 196	10.8	54.0	52	29	BX219012
55.0	41	28	BH625409	c 197	10.8	54.0	53	28	AQ025275
55.0	41	29	BX162572	c 198	10.8	54.0	53	28	AZ356283
55.0	43	9	AI477210	c 199	10.8	54.0	55	9	AA872208
55.0	43	14	W86565	c 200	10.8	54.0	55	28	CC325110
55.0	43	29	DME545852	c 201	10.8	54.0	56	10	BF026677
55.0	44	28	AZ801644	c 202	10.8	54.0	56	28	AZ865094
55.0	46	29	AL952906	c 203	10.8	54.0	58	9	AA663265
55.0	47	12	BI685348	c 204	10.8	54.0	58	9	AI327266
55.0	49	9	AA854556	c 205	10.8	54.0	58	14	CF863585
55.0	49	9	AI744869	c 206	10.8	54.0	59	12	BI760827
55.0	49	28	AZ805592	c 207	10.8	54.0	59	29	CG672163
55.0	49	28	BZ381817	c 208	10.8	54.0	60	28	AZ603495
55.0	49	29	AI771128	c 209	10.8	54.0	60	29	DR42K185
55.0	50	9	AI771128	c 210	10.6	53.0	25	9	AI017105
55.0	50	9	AI04312	c 211	10.6	53.0	33	9	AU006896
55.0	50	9	AI04314	c 212	10.6	53.0	33	10	BF184963
55.0	50	9	AI04316	c 213	10.6	53.0	33	28	CC182131
55.0	50	12	BGS26086	c 214	10.6	53.0	37	28	AZ660325
55.0	50	28	AZ922086	c 215	10.6	53.0	37	29	BX293466
55.0	50	28	BZ357218	c 216	10.6	53.0	39	9	AU256556
55.0	50	29	BX654687	c 217	10.6	53.0	39	28	AZ499899
55.0	51	13	BQ627447	c 218	10.6	53.0	42	12	BI668257
55.0	51	29	BX627447	c 219	10.6	53.0	42	28	BH864588
55.0	52	9	AI098966	c 220	10.6	53.0	42	28	BZ584441
55.0	52	9	AI343111	c 221	10.6	53.0	43	9	AA931447
55.0	52	28	AZ647203	c 222	10.6	53.0	43	12	BG244016
55.0	53	29	BX002086	c 223	10.6	53.0	44	28	BH854174



53.0	46	9	AI191806	AI191806 qd47e10.x	297	10.6	53.0	50	9	AUI07816	AUI07816
53.0	46	14	D67712	D67712 CELK07GHZF	298	10.6	53.0	50	9	AUI07817	AUI07817
53.0	48	28	BH637902	BH637902 1008019D0	299	10.6	53.0	50	9	AUI07819	AUI07819
53.0	48	29	CG732540	CG732540 1119149C0	300	10.6	53.0	50	9	AUI07820	AUI07820
53.0	48	29	AG216175	AG216175 Drosophil	301	10.6	53.0	50	9	AUI07821	AUI07821
53.0	49	9	AI095125	AI095125 qa19c03.x	302	10.6	53.0	50	9	AUI07822	AUI07822
53.0	49	9	AV856631	AV856631 AV856631	303	10.6	53.0	50	9	AUI07823	AUI07823
53.0	49	12	BM021294	BM021294 ie75c11.y	304	10.6	53.0	50	9	AUI07825	AUI07825
53.0	49	29	CG721821	CG721821 1119069B0	305	10.6	53.0	50	9	AUI07826	AUI07826
53.0	50	9	AI042693	AI042693 uc76e08.x	306	10.6	53.0	50	9	AUI07827	AUI07827
53.0	50	9	AUI02256	AUI02256 AUI02256	307	10.6	53.0	50	28	AZ875367	AZ875367
53.0	50	9	AUI04315	AUI04315 AUI04315	308	10.6	53.0	50	28	BH890468	BH890468
53.0	50	9	AUI07747	AUI07747 AUI07747	309	10.6	53.0	51	28	AZ621614	AZ621614
53.0	50	9	AUI07748	AUI07748 AUI07748	310	10.6	53.0	52	9	AA638823	AA638823
53.0	50	9	AUI07749	AUI07749 AUI07749	311	10.6	53.0	52	9	AI504673	AI504673
53.0	50	9	AUI07750	AUI07750 AUI07750	312	10.6	53.0	52	28	BH790794	BH790794
53.0	50	9	AUI07751	AUI07751 AUI07751	313	10.6	53.0	52	28	CC248941	CC248941
53.0	50	9	AUI07753	AUI07753 AUI07753	314	10.6	53.0	54	9	AI930813	AI930813
53.0	50	9	AUI07754	AUI07754 AUI07754	315	10.6	53.0	54	9	AI786998	AI786998
53.0	50	9	AUI07755	AUI07755 AUI07755	316	10.6	53.0	54	12	BG526210	BG526210
53.0	50	9	AUI07756	AUI07756 AUI07756	317	10.6	53.0	54	28	AZ815205	AZ815205
53.0	50	9	AUI07757	AUI07757 AUI07757	318	10.6	53.0	54	28	BZ358880	BZ358880
53.0	50	9	AUI07759	AUI07759 AUI07759	319	10.6	53.0	55	9	AA434258	AA434258
53.0	50	9	AUI07760	AUI07760 AUI07760	320	10.6	53.0	55	28	BH415675	BH415675
53.0	50	9	AUI07761	AUI07761 AUI07761	321	10.6	53.0	55	28	BZ581514	BZ581514
53.0	50	9	AUI07764	AUI07764 AUI07764	322	10.6	53.0	56	9	AL847510	AL847510
53.0	50	9	AUI07765	AUI07765 AUI07765	323	10.6	53.0	56	28	AZ492220	AZ492220
53.0	50	9	AUI07766	AUI07766 AUI07766	324	10.6	53.0	56	28	B44818	B44818
53.0	50	9	AUI07767	AUI07767 AUI07767	325	10.6	53.0	56	28	CC022423	CC022423
53.0	50	9	AUI07768	AUI07768 AUI07768	326	10.6	53.0	56	28	CNS02BNW	CNS02BNW
53.0	50	9	AUI07769	AUI07769 AUI07769	327	10.6	53.0	57	28	AZ660093	AZ660093
53.0	50	9	AUI07774	AUI07774 AUI07774	328	10.6	53.0	57	28	BH223365	BH223365
53.0	50	9	AUI07775	AUI07775 AUI07775	329	10.6	53.0	57	28	BH635027	BH635027
53.0	50	9	AUI07776	AUI07776 AUI07776	330	10.6	53.0	58	13	BQ626004	BQ626004
53.0	50	9	AUI07777	AUI07777 AUI07777	331	10.6	53.0	58	14	W74798	W74798
53.0	50	9	AUI07778	AUI07778 AUI07778	332	10.6	53.0	58	28	BZ766894	BZ766894
53.0	50	9	AUI07779	AUI07779 AUI07779	333	10.6	53.0	58	29	AL757800	AL757800
53.0	50	9	AUI07780	AUI07780 AUI07780	334	10.6	53.0	59	10	AW248773	AW248773
53.0	50	9	AUI07781	AUI07781 AUI07781	335	10.6	53.0	59	28	AZ351787	AZ351787
53.0	50	9	AUI07782	AUI07782 AUI07782	336	10.6	53.0	60	13	BQ473102	BQ473102
53.0	50	9	AUI07783	AUI07783 AUI07783	337	10.6	53.0	60	14	CA851565	CA851565
53.0	50	9	AUI07784	AUI07784 AUI07784	338	10.6	53.0	60	14	CD525559	CD525559
53.0	50	9	AUI07785	AUI07785 AUI07785	339	10.6	52.0	22	12	BG926061	BG926061
53.0	50	9	AUI07786	AUI07786 AUI07786	340	10.4	52.0	22	28	AZ762378	AZ762378
53.0	50	9	AUI07787	AUI07787 AUI07787	341	10.4	52.0	26	28	AZ825865	AZ825865
53.0	50	9	AUI07788	AUI07788 AUI07788	342	10.4	52.0	30	28	AZ783604	AZ783604
53.0	50	9	AUI07789	AUI07789 AUI07789	343	10.4	52.0	33	10	BE739126	BE739126
53.0	50	9	AUI07790	AUI07790 AUI07790	344	10.4	52.0	37	14	H69029	H69029
53.0	50	9	AUI07791	AUI07791 AUI07791	345	10.4	52.0	37	29	CG707299	CG707299
53.0	50	9	AUI07792	AUI07792 AUI07792	346	10.4	52.0	38	29	AL767019	AL767019
53.0	50	9	AUI07793	AUI07793 AUI07793	347	10.4	52.0	39	29	CL002872	CL002872
53.0	50	9	AUI07794	AUI07794 AUI07794	348	10.4	52.0	40	9	AA811470	AA811470
53.0	50	9	AUI07795	AUI07795 AUI07795	349	10.4	52.0	40	9	AL933274	AL933274
53.0	50	9	AUI07796	AUI07796 AUI07796	350	10.4	52.0	40	28	BZ767501	BZ767501
53.0	50	9	AUI07797	AUI07797 AUI07797	351	10.4	52.0	41	28	BH849731	BH849731
53.0	50	9	AUI07798	AUI07798 AUI07798	352	10.4	52.0	42	28	BZ583894	BZ583894
53.0	50	9	AUI07799	AUI07799 AUI07799	353	10.4	52.0	42	29	CG715948	CG715948
53.0	50	9	AUI07800	AUI07800 AUI07800	354	10.4	52.0	43	12	BG745981	BG745981
53.0	50	9	AUI07801	AUI07801 AUI07801	355	10.4	52.0	43	14	CF292564	CF292564
53.0	50	9	AUI07802	AUI07802 AUI07802	356	10.4	52.0	44	14	H64101	H64101
53.0	50	9	AUI07803	AUI07803 AUI07803	357	10.4	52.0	45	28	AZ817198	AZ817198
53.0	50	9	AUI07804	AUI07804 AUI07804	358	10.4	52.0	45	28	AZ820873	AZ820873
53.0	50	9	AUI07805	AUI07805 AUI07805	359	10.4	52.0	45	28	BH802881	BH802881
53.0	50	9	AUI07806	AUI07806 AUI07806	360	10.4	52.0	45	29	CC888123	CC888123
53.0	50	9	AUI07807	AUI07807 AUI07807	361	10.4	52.0	45	29	CG711564	CG711564
53.0	50	9	AUI07808	AUI07808 AUI07808	362	10.4	52.0	46	9	AA869036	AA869036
53.0	50	9	AUI07809	AUI07809 AUI07809	363	10.4	52.0	46	9	AA877316	AA877316
53.0	50	9	AUI07810	AUI07810 AUI07810	364	10.4	52.0	46	9	AA244435	AA244435
53.0	50	9	AUI07811	AUI07811 AUI07811	365	10.4	52.0	46	28	AZ585571	AZ585571
53.0	50	9	AUI07812	AUI07812 AUI07812	366	10.4	52.0	46	29	TA316B04Q	TA316B04Q
53.0	50	9	AUI07813	AUI07813 AUI07813	367	10.4	52.0	47	28	BH804707	BH804707
53.0	50	9	AUI07814	AUI07814 AUI07814	368	10.4	52.0	47	28	BH866277	BH866277
53.0	50	9	AUI07815	AUI07815 AUI07815	369	10.4	52.0	48	28	BH803091	BH803091

52.0	48	29	CG715950	CG715950 1119043H1	C 443	10.2	51.0	45	28	BH619838	BH619838
52.0	49	9	AA999946	AA999946 ov06a03.s	C 444	10.2	51.0	45	28	BZ766643	BZ766643
52.0	49	28	CC040332	CC040332 3591_1_13	C 445	10.2	51.0	46	9	AA890005	AA890005
52.0	50	9	AU102878	AU102878 AU102878	C 446	10.2	51.0	47	28	CC199541	CC199541
52.0	50	9	AU103828	AU103828 AU103828	C 447	10.2	51.0	47	29	BX130979	BX130979
52.0	50	9	AU105941	AU105941 AU105941	C 448	10.2	51.0	47	29	BX534569	BX534569
52.0	50	13	BX719963	BX719963 BX719963	C 449	10.2	51.0	47	29	TA137G10Q	TA137G10Q
52.0	51	10	BF720146	BF720146 mab49f05.	C 450	10.2	51.0	48	28	AZ443721	AZ443721
52.0	51	12	BF744702	BF744702 602722811	C 451	10.2	51.0	48	29	HSCHO6F06	HSCHO6F06
52.0	51	28	BZ289497	BZ289497 SALK_0228	C 452	10.2	51.0	49	9	AI205223	AI205223
52.0	51	28	BZ595480	BZ595480 SALK_0872	C 453	10.2	51.0	49	12	BM898100	BM898100
52.0	51	29	CC817207	CC817207 10C003A04	C 454	10.2	51.0	49	14	RS4986	RS4986
52.0	51	29	CNS04KRA	AA295183 Tetraodon	C 455	10.2	51.0	50	9	AU105583	AU105583
52.0	52	9	AA498959	AA498959 v183f10.f	C 456	10.2	51.0	50	9	AU107215	AU107215
52.0	52	10	BF642000	BF642000 NF028A02I	C 457	10.2	51.0	50	9	AU107217	AU107217
52.0	52	14	CD722425	CD722425 o109e12.Y	C 458	10.2	51.0	50	9	AU107219	AU107219
52.0	52	28	AZ445396	AZ445396 1M0241H10	C 459	10.2	51.0	50	9	AU107224	AU107224
52.0	52	28	B05626	B05626 CSRU-6895-u	C 460	10.2	51.0	50	9	AU107226	AU107226
52.0	52	28	BH90815	BH90815 3526_1_15	C 461	10.2	51.0	50	9	AU107227	AU107227
52.0	53	12	B1417223	B1417223 LJNEST16d	C 462	10.2	51.0	50	9	AU107228	AU107228
52.0	53	13	BX704759	BX704759 BX704759	C 463	10.2	51.0	50	9	AU107229	AU107229
52.0	53	28	AZ767784	AZ767784 1M0567L17	C 464	10.2	51.0	50	9	AU107922	AU107922
52.0	53	28	BZ661202	BZ661202 SALK_0246	C 465	10.2	51.0	50	9	AU107923	AU107923
52.0	54	12	B031926	B031926 E031926	C 466	10.2	51.0	50	14	CB221512	CB221512
52.0	54	28	AZ584844	AZ584844 1M0389H13	C 467	10.2	51.0	50	28	AZ397298	AZ397298
52.0	54	28	BH804831	BH804831 1008105B1	C 468	10.2	51.0	50	28	AZ473583	AZ473583
52.0	55	9	AA764972	AA764972 n277C09.s	C 469	10.2	51.0	50	29	BX650618	BX650618
52.0	55	9	AI971428	AI971428 w04h12.x	C 470	10.2	51.0	51	13	B0565192	B0565192
52.0	55	9	AA232965	AA232965 z169304.s	C 471	10.2	51.0	51	29	AL751559	AL751559
52.0	55	10	AW460390	AW460390 da33908.Y	C 472	10.2	51.0	51	29	AL756331	AL756331
52.0	55	28	CC054106	CC054106 SALK_0529	C 473	10.2	51.0	52	9	AI204024	AI204024
52.0	56	29	CC594954	CC594954 CH240_336	C 474	10.2	51.0	52	9	AI310821	AI310821
52.0	56	29	CG717651	CG717651 1119049R0	C 475	10.2	51.0	52	12	BG694580	BG694580
52.0	57	14	CB211852	CB211852 OML02132	C 476	10.2	51.0	52	14	T74448	T74448
52.0	58	28	BH410854	BH410854 1007020D0	C 477	10.2	51.0	52	14	W90057	W90057
52.0	58	28	BZ666412	BZ666412 SGT5752-5	C 478	10.2	51.0	52	28	BH810858	BH810858
52.0	58	28	CC030721	CC030721 3591_1_11	C 479	10.2	51.0	52	28	BZ353423	BZ353423
52.0	58	29	AA215537	AA215537 Drosophil	C 480	10.2	51.0	53	9	AA674581	AA674581
52.0	59	9	AG207740	AG207740 mv78n05.f	C 481	10.2	51.0	53	14	T61489	T61489
52.0	59	14	CB365837	CB365837 ZF001-P00	C 482	10.2	51.0	53	28	BH909817	BH909817
52.0	59	29	CG869846	CG869846 XS0320 Sa	C 483	10.2	51.0	53	29	CNS0111Q	CNS0111Q
52.0	60	9	AU255553	AU255553 AU255553	C 484	10.2	51.0	54	28	BH846266	BH846266
52.0	60	29	AL937700	AL937700 Arabidops	C 485	10.2	51.0	54	29	CG466747	CG466747
51.0	22	28	AZ788617	AZ788617 2M0035F21	C 486	10.2	51.0	55	9	AA050107	AA050107
51.0	25	28	AZ508011	AZ508011 1M0349M21	C 487	10.2	51.0	55	9	AI299849	AI299849
51.0	25	28	AZ635195	AZ635195 1M0491J19	C 488	10.2	51.0	55	9	AA506552	AA506552
51.0	28	13	BX549420	BX549420 BX549420	C 489	10.2	51.0	55	14	H14140	H14140
51.0	29	28	AZ805819	AZ805819 2M0067K19	C 490	10.2	51.0	55	28	BH221315	BH221315
51.0	31	9	AA266787	AA266787 m298a07.f	C 491	10.2	51.0	55	28	BZ379766	BZ379766
51.0	31	28	AZ596685	AZ596685 1M0410A07	C 492	10.2	51.0	55	28	CC036784	CC036784
51.0	33	28	AZ429658	AZ429658 1M0213A18	C 493	10.2	51.0	55	29	CG466773	CG466773
51.0	34	9	AA871250	AA871250 VG33a02.f	C 494	10.2	51.0	55	29	LEAF073A12	LEAF073A12
51.0	34	10	BF693313	BF693313 602081119	C 495	10.2	51.0	56	12	BI555192	BI555192
51.0	35	28	AZ491926	AZ491926 1M0325G18	C 496	10.2	51.0	56	12	BM515079	BM515079
51.0	37	9	AA100873	AA100873 zc23407.s	C 497	10.2	51.0	56	28	BH221475	BH221475
51.0	37	9	AI966055	AI966055 sz26d04.Y	C 498	10.2	51.0	56	29	CC552392	CC552392
51.0	38	10	BF506863	BF506863 10005P-31	C 499	10.2	51.0	56	29	CG466748	CG466748
51.0	38	28	AZ663634	AZ663634 1M0543D21	C 500	10.2	51.0	57	9	AA889441	AA889441
51.0	38	29	BX534570	BX534570 Arabidops	C 501	10.2	51.0	57	9	AI318136	AI318136
51.0	40	9	AA767606	AA767606 ob47e05.s	C 502	10.2	51.0	57	12	BM131376	BM131376
51.0	40	9	AA860078	AA860078 ak45c03.s	C 503	10.2	51.0	57	29	CG466724	CG466724
51.0	40	9	AI697005	AI697005 wc76g07.x	C 504	10.2	51.0	58	9	AA968615	AA968615
51.0	40	9	AA417630	AA417630 zu99g11.s	C 505	10.2	51.0	58	9	AI619543	AI619543
51.0	40	10	AW247854	AW247854 2820389.3	C 506	10.2	51.0	58	10	BF577406	BF577406
51.0	41	28	BZ585244	BZ585244 3590_1_30	C 507	10.2	51.0	58	28	BH850962	BH850962
51.0	41	29	BX1411088	BX1411088 Danic Ter	C 508	10.2	51.0	58	28	BZ381640	BZ381640
51.0	42	28	AZ440878	AZ440878 1M0231C19	C 509	10.2	51.0	58	29	CG727548	CG727548
51.0	43	29	CG774833	CG774833 1123021A1	C 510	10.2	51.0	60	9	AI094259	AI094259
51.0	44	9	AV854185	AV854185 AV854185	C 511	10.2	51.0	60	10	BF632704	BF632704
51.0	44	13	BX620555	BX620555 BX620555	C 512	10.2	51.0	60	10	BF638486	BF638486
51.0	44	28	BZ597313	BZ597313 SALK_1019	C 513	10.2	51.0	60	10	BF168687	BF168687
51.0	45	9	AU265554	AU265554 AU265554	C 514	10.2	51.0	60	12	BI494203	BI494203
51.0	45	9	AU265554	AU265554 AU265554	C 515	10.2	51.0	60	28	AZ440924	AZ440924

51.0	60	28	AZ810580	AZ810580	2M0076M09	C 589	10	50.0	50	9	AU102250	AU102250
51.0	60	29	CG774431	CG774431	1123018H0	C 590	10	50.0	50	9	AU102251	AU102251
50.0	20	28	AZ646291	AZ646291	1M0512D07	C 591	10	50.0	50	9	AU102252	AU102252
50.0	21	9	AU254493	AU254493	AU254493	C 592	10	50.0	50	9	AU103027	AU103027
50.0	24	12	BM397860	BM397860	5009-0-38	C 593	10	50.0	50	9	AU103896	AU103896
50.0	24	28	AZ486303	AZ486303	1M0314A16	C 594	10	50.0	50	9	AU105349	AU105349
50.0	27	28	AZ836891	AZ836891	2M0131N22	C 595	10	50.0	50	9	AU105892	AU105892
50.0	28	9	AU1376409	AU1376409	tc29G03.x	C 596	10	50.0	50	9	AU106503	AU106503
50.0	28	28	AZ591223	AZ591223	1M0401N04	C 597	10	50.0	50	9	AU107741	AU107741
50.0	30	29	TA386A07Q	AL498258	T. brucei	C 598	10	50.0	50	9	AU107743	AU107743
50.0	31	9	AU1721551	AL721551	fc29b04.x	C 599	10	50.0	50	9	AU107744	AU107744
50.0	31	28	AZ437063	AZ437063	1M0225C07	C 600	10	50.0	50	9	AU107746	AU107746
50.0	31	28	AZ628881	AZ628881	1M0481A19	C 601	10	50.0	50	9	AU107752	AU107752
50.0	34	9	AA876855	AA876855	ny47B08.s	C 602	10	50.0	50	9	AU107771	AU107771
50.0	34	9	AI1813858	AI1813858	wk61a07.x	C 603	10	50.0	50	10	BB616279	BB616279
50.0	34	9	AU256758	AU256758	AU256758	C 604	10	50.0	50	12	BG169998	BG169998
50.0	34	14	W82790	W82790	mF06a09.r1	C 605	10	50.0	50	12	BI651733	BI651733
50.0	35	9	AU1010975	AU1010975	AU1010975	C 606	10	50.0	50	29	CC886961	CC886961
50.0	35	9	AU011065	AU011065	AU011065	C 607	10	50.0	51	9	AI442949	AI442949
50.0	35	28	AZ438946	AZ438946	1M0229L15	C 608	10	50.0	51	10	BE796221	BE796221
50.0	35	29	TA38G04P	AL453560	T. brucei	C 609	10	50.0	51	12	BG910450	BG910450
50.0	36	9	AV832396	AV832396	AV832396	C 610	10	50.0	51	13	BQ795927	BQ795927
50.0	36	12	BJ066815	BJ066815	BJ066815	C 611	10	50.0	51	28	AZ377021	AZ377021
50.0	37	9	AA862538	AA862538	ch44a01.s	C 612	10	50.0	51	28	B00630	B00630
50.0	37	9	AI182409	AI182409	uc23n07.r	C 613	10	50.0	51	28	BH225836	BH225836
50.0	37	10	BF211603	BF211603	601812103	C 614	10	50.0	51	29	AL768627	AL768627
50.0	38	29	AG221585	AG221585	Lotus cor	C 615	10	50.0	52	9	AA793166	AA793166
50.0	38	29	AG229213	AG229213	Lotus cor	C 616	10	50.0	52	9	AI591308	AI591308
50.0	39	12	B1223730	B1223730	602943295	C 617	10	50.0	52	12	BI828531	BI828531
50.0	39	28	AZ812635	AZ812635	2M0079M24	C 618	10	50.0	52	14	H25995	H25995
50.0	40	9	AI790682	AI790682	ul03d07.x	C 619	10	50.0	52	28	AZ645017	AZ645017
50.0	40	28	BH797868	BH797868	1008096A0	C 620	10	50.0	52	28	B04675	B04675
50.0	40	28	CC042936	CC042936	3591.1.15	C 621	10	50.0	52	29	CG724166	CG724166
50.0	40	29	CG773514	CG773514	1123010A1	C 622	10	50.0	53	9	AI272031	AI272031
50.0	41	14	R76301	R76301	V123b12.s1	C 623	10	50.0	53	9	AA271767	AA271767
50.0	41	29	TA38G04Q	AL454614	T. brucei	C 624	10	50.0	53	14	D18203	D18203
50.0	42	10	BF982579	BF982579	602305709	C 625	10	50.0	53	28	AZ601066	AZ601066
50.0	42	12	BG616575	BG616575	602614759	C 626	10	50.0	53	28	BZ592285	BZ592285
50.0	42	12	BI830168	BI830168	603072810	C 627	10	50.0	53	29	BX222167	BX222167
50.0	42	14	R92825	R92825	Yq17h11.r1	C 628	10	50.0	54	9	AI213234	AI213234
50.0	42	28	BH634932	BH634932	1008001F0	C 629	10	50.0	54	9	AL640222	AL640222
50.0	42	28	BH635416	BH635416	1008004F1	C 630	10	50.0	54	10	BF791883	BF791883
50.0	42	28	BH637601	BH637601	1008017F0	C 631	10	50.0	54	28	AZ940260	AZ940260
50.0	42	28	BH801154	BH801154	1008123E0	C 632	10	50.0	54	29	BX656314	BX656314
50.0	42	28	CC053818	CC053818	SALK. 0489	C 633	10	50.0	55	9	AA742858	AA742858
50.0	43	9	AA744543	AA744543	ny79c03.s	C 634	10	50.0	55	9	AA118536	AA118536
50.0	43	9	AI215059	AI215059	QG52c05.x	C 635	10	50.0	55	9	AU007462	AU007462
50.0	43	9	AA534781	AA534781	nf81e01.s	C 636	10	50.0	55	12	BG818482	BG818482
50.0	43	28	AZ797401	AZ797401	2M0053C07	C 637	10	50.0	55	14	CA785045	CA785045
50.0	45	10	BF578678	BF578678	602093151	C 638	10	50.0	55	28	AZ404505	AZ404505
50.0	45	28	AZ423992	AZ423992	1M0203A16	C 639	10	50.0	55	28	BH790396	BH790396
50.0	45	28	AZ453414	AZ453414	1M0254112	C 640	10	50.0	55	29	CG779217	CG779217
50.0	46	9	AI581136	AI581136	tl93h03.x	C 641	10	50.0	56	9	AA286566	AA286566
50.0	46	9	AI669689	AI669689	wc12d11.x	C 642	10	50.0	56	10	AA444409	AA444409
50.0	46	12	BI562485	BI562485	603256393	C 643	10	50.0	56	28	AZ849734	AZ849734
50.0	46	14	CH884957	CH884957	Mal17079.H	C 644	10	50.0	57	9	AL856271	AL856271
50.0	46	28	BH847712	BH847712	SALK. 0559	C 645	10	50.0	57	12	BI852649	BI852649
50.0	46	29	AG223095	AG223095	Lotus cor	C 646	10	50.0	58	9	AI290333	AI290333
50.0	46	29	AG232171	AG232171	Lotus cor	C 647	10	50.0	58	14	CB274888	CB274888
50.0	47	10	BF969163	BF969163	602269853	C 648	10	50.0	58	29	CG869888	CG869888
50.0	47	28	AZ307665	AZ307665	1M0009324	C 649	10	50.0	58	29	BX892307	BX892307
50.0	47	28	AZ615286	AZ615286	1M0444106	C 650	10	50.0	59	12	BI559801	BI559801
50.0	47	28	AZ634774	AZ634774	1M0490F16	C 651	10	50.0	59	14	CB277362	CB277362
50.0	47	28	AZ816650	AZ816650	2M0085D03	C 652	10	50.0	59	14	CB914731	CB914731
50.0	47	29	AL760998	AL760998	Arabidops	C 653	10	50.0	59	29	CG733006	CG733006
50.0	47	29	TA132E04P	AL465544	T. brucei	C 654	10	50.0	59	29	BX122142	BX122142
50.0	48	14	AZ805973	AZ805973	2M0067M10	C 655	10	50.0	60	10	BE960567	BE960567
50.0	48	18	H22280	H22280	Y136b03.r1	C 656	10	50.0	60	12	BM133144	BM133144
50.0	49	28	BZ763363	BZ763363	SALK. 1168	C 657	10	50.0	60	13	BQ241547	BQ241547
50.0	50	9	AU102246	AU102246	AU102246	C 658	10	50.0	60	14	W73125	W73125
50.0	50	9	AU102248	AU102248	AU102248	C 659	10	50.0	60	28	BZ587863	BZ587863
50.0	50	9	AU102249	AU102249	AU102249	C 660	10	50.0	60	29	CNS06WH6	AI18432
50.0	50	9	AU102249	AU102249	AU102249	C 661	9.8	49.0	22	9	AI677768	AI677768

49.0	23	28	AZ768060	49.0	23	28	AZ768060	1M0567P13	C 735	9.8	49.0	47	29	CG799680	CG79968
49.0	26	28	AZ320242	49.0	26	28	AZ320242	1M0040M12	C 736	9.8	49.0	47	29	CG802164	CG80216
49.0	26	28	AZ819797	49.0	26	28	AZ819797	2M0091E09	C 737	9.8	49.0	48	9	AA513303	AA513303
49.0	26	29	CG721091	49.0	26	29	CG721091	1119065D0	C 738	9.8	49.0	48	12	BI094799	BI09479
49.0	27	28	AZ868893	49.0	27	28	AZ868893	2M0180117	C 739	9.8	49.0	49	9	AA018289	AA018289
49.0	28	14	CF316792	49.0	28	14	CF316792	HD--06-D1	C 740	9.8	49.0	49	9	AA828893	AA828893
49.0	28	14	W19872	49.0	28	14	W19872	zb40f08.r1	C 741	9.8	49.0	49	12	BG342381	BG34238
49.0	29	12	BG897986	49.0	29	12	BG897986	HOA2-H-12	C 742	9.8	49.0	50	9	AU102295	AU102295
49.0	29	14	CF317167	49.0	29	14	CF317167	HD--06-M0	C 743	9.8	49.0	50	9	AU102382	AU102382
49.0	29	14	CF327123	49.0	29	14	CF327123	NACL--01-	C 744	9.8	49.0	50	9	AU102858	AU102858
49.0	30	14	CF311738	49.0	30	14	CF311738	ABF--07-C	C 745	9.8	49.0	50	9	AU102873	AU102873
49.0	30	14	CF313400	49.0	30	14	CF313400	HD--01-I0	C 746	9.8	49.0	50	9	AU103108	AU103108
49.0	30	14	CF314025	49.0	30	14	CF314025	HD--02-G0	C 747	9.8	49.0	50	9	AU103109	AU103109
49.0	30	14	CF314237	49.0	30	14	CF314237	HD--02-K2	C 748	9.8	49.0	50	9	AU103110	AU103110
49.0	30	14	CF314484	49.0	30	14	CF314484	HD--03-A1	C 749	9.8	49.0	50	9	AU103111	AU103111
49.0	30	14	CF316772	49.0	30	14	CF316772	HD--06-D0	C 750	9.8	49.0	50	9	AU103112	AU103112
49.0	30	14	CF317266	49.0	30	14	CF317266	HD--06-O1	C 751	9.8	49.0	50	9	AU103113	AU103113
49.0	30	14	CF317281	49.0	30	14	CF317281	HD--06-O1	C 752	9.8	49.0	50	9	AU103114	AU103114
49.0	30	14	CF337708	49.0	30	14	CF337708	JMT--07-J	C 753	9.8	49.0	50	9	AU103116	AU103116
49.0	30	28	AU511083	49.0	30	28	AU511083	1M0355022	C 754	9.8	49.0	50	9	AU103117	AU103117
49.0	30	28	BH810436	49.0	30	28	BH810436	SALK 0495	C 755	9.8	49.0	50	9	AU103118	AU103118
49.0	31	12	BM046977	49.0	31	12	BM046977	603627229	C 756	9.8	49.0	50	9	AU103119	AU103119
49.0	31	14	CF313407	49.0	31	14	CF313407	HD--01-I1	C 757	9.8	49.0	50	9	AU103120	AU103120
49.0	31	14	CF313764	49.0	31	14	CF313764	HD--02-A0	C 758	9.8	49.0	50	9	AU103122	AU103122
49.0	31	14	CF316529	49.0	31	14	CF316529	HD--05-N1	C 759	9.8	49.0	50	9	AU103123	AU103123
49.0	31	14	CF319713	49.0	31	14	CF319713	HD--10-F0	C 760	9.8	49.0	50	9	AU103124	AU103124
49.0	31	14	CF336854	49.0	31	14	CF336854	JMT--07-F	C 761	9.8	49.0	50	9	AU103125	AU103125
49.0	31	14	CF337032	49.0	31	14	CF337032	JMT--07-F	C 762	9.8	49.0	50	9	AU103126	AU103126
49.0	31	14	CF337142	49.0	31	14	CF337142	JMT--07-H	C 763	9.8	49.0	50	9	AU103127	AU103127
49.0	31	28	BZ292419	49.0	31	28	BZ292419	SALK 1242	C 764	9.8	49.0	50	9	AU103128	AU103128
49.0	31	29	CG722536	49.0	31	29	CG722536	1119072D1	C 765	9.8	49.0	50	9	AU103129	AU103129
49.0	32	14	CF313280	49.0	32	14	CF313280	HD--01-F1	C 766	9.8	49.0	50	9	AU103130	AU103130
49.0	32	14	CF313422	49.0	32	14	CF313422	HD--01-I1	C 767	9.8	49.0	50	9	AU103131	AU103131
49.0	32	14	CF313772	49.0	32	14	CF313772	HD--02-A1	C 768	9.8	49.0	50	9	AU103132	AU103132
49.0	32	14	CF316885	49.0	32	14	CF316885	HD--06-F2	C 769	9.8	49.0	50	9	AU103133	AU103133
49.0	32	28	AZ387193	49.0	32	28	AZ387193	1M0146N19	C 770	9.8	49.0	50	9	AU103134	AU103134
49.0	33	12	BJ057899	49.0	33	12	BJ057899	BJ057899	C 771	9.8	49.0	50	9	AU103135	AU103135
49.0	33	14	CF316372	49.0	33	14	CF316372	HD--05-K0	C 772	9.8	49.0	50	9	AU103138	AU103138
49.0	34	9	AI149355	49.0	34	9	AI149355	QC82B03.x	C 773	9.8	49.0	50	9	AU103139	AU103139
49.0	35	10	BF161333	49.0	35	10	BF161333	601770096	C 774	9.8	49.0	50	9	AU103140	AU103140
49.0	35	28	AZ490139	49.0	35	28	AZ490139	1M0322L21	C 775	9.8	49.0	50	9	AU103142	AU103142
49.0	37	28	AZ603813	49.0	37	28	AZ603813	1M0423B21	C 776	9.8	49.0	50	9	AU103143	AU103143
49.0	37	28	AZ807121	49.0	37	28	AZ807121	2M0069111	C 777	9.8	49.0	50	9	AU103149	AU103149
49.0	38	12	BH80282	49.0	38	12	BH80282	602331114	C 778	9.8	49.0	50	9	AU103150	AU103150
49.0	38	28	AZ758198	49.0	38	28	AZ758198	1M0550P03	C 779	9.8	49.0	50	9	AU103186	AU103186
49.0	38	28	BZ762336	49.0	38	28	BZ762336	SALK 0995	C 780	9.8	49.0	50	9	AU103191	AU103191
49.0	39	9	AI001077	49.0	39	9	AI001077	0866D04.s	C 781	9.8	49.0	50	9	AU104067	AU104067
49.0	39	14	CF295261	49.0	39	14	CF295261	30DGS--05	C 782	9.8	49.0	50	9	AU105482	AU105482
49.0	39	29	AL938262	49.0	39	29	AL938262	Arabidops	C 783	9.8	49.0	50	9	AU105634	AU105634
49.0	40	9	AU008056	49.0	40	9	AU008056	AU008056	C 784	9.8	49.0	50	9	AU105725	AU105725
49.0	41	12	BM393667	49.0	41	12	BM393667	50072-2-1	C 785	9.8	49.0	50	9	AU107204	AU107204
49.0	43	9	AA975798	49.0	43	9	AA975798	0q47606.s	C 786	9.8	49.0	50	9	AU107211	AU107211
49.0	43	9	AA116340	49.0	43	9	AA116340	wq70G12.r	C 787	9.8	49.0	50	9	AU107212	AU107212
49.0	43	9	AI588855	49.0	43	9	AI588855	tg28C10.x	C 788	9.8	49.0	50	9	AU107315	AU107315
49.0	43	9	AI786712	49.0	43	9	AI786712	uj56b03.x	C 789	9.8	49.0	50	9	AU107325	AU107325
49.0	43	9	AA423162	49.0	43	9	AA423162	ve36b01.r	C 790	9.8	49.0	50	9	AU108008	AU108008
49.0	43	14	W93529	49.0	43	14	W93529	mq72B04.r1	C 791	9.8	49.0	50	13	BU660153	BU660153
49.0	43	28	AZ339977	49.0	43	28	AZ339977	1M0071N12	C 792	9.8	49.0	50	14	D18208	D18208
49.0	43	28	AZ799757	49.0	43	28	AZ799757	2M0057F24	C 793	9.8	49.0	50	28	AZ602141	AZ602141
49.0	43	29	BX536103	49.0	43	29	BX536103	Arabidops	C 794	9.8	49.0	50	28	AZ813958	AZ813958
49.0	44	28	BZ355239	49.0	44	28	BZ355239	SALK 1265	C 795	9.8	49.0	50	28	AZ920008	AZ920008
49.0	45	28	AZ480534	49.0	45	28	AZ480534	1M0302E07	C 796	9.8	49.0	50	29	CC516353	CC516353
49.0	46	9	AI360975	49.0	46	9	AI360975	qy02F12.x	C 797	9.8	49.0	50	29	AL760941	AL760941
49.0	46	9	AI564698	49.0	46	9	AI564698	to18a08.x	C 798	9.8	49.0	51	9	AI861081	AI861081
49.0	46	9	AI937592	49.0	46	9	AI937592	wp81d11.x	C 799	9.8	49.0	51	12	BI832800	BI832800
49.0	46	12	BM394139	49.0	46	12	BM394139	50072-2-2	C 800	9.8	49.0	51	12	BM395094	BM395094
49.0	46	14	CF313180	49.0	46	14	CF313180	HD--01-D1	C 801	9.8	49.0	51	13	EQ081640	EQ081640
49.0	46	14	H57798	49.0	46	14	H57798	Yr22d12.r1	C 802	9.8	49.0	51	28	AZ330814	AZ330814
49.0	46	28	AZ809743	49.0	46	28	AZ809743	2M0073E23	C 803	9.8	49.0	51	28	AZ431412	AZ431412
49.0	46	28	BH418068	49.0	46	28	BH418068	3286-B1 M	C 804	9.8	49.0	51	28	AZ643908	AZ643908
49.0	46	28	BH628167	49.0	46	28	BH628167	1007080F1	C 805	9.8	49.0	51	28	AZ660720	AZ660720
49.0	46	28	BZ355101	49.0	46	28	BZ355101	SALK 1263	C 806	9.8	49.0	51	28	BH218963	BH218963
49.0	47	28	CC049920	49.0	47	28	CC049920	01S0518-0	C 807	9.8	49.0	51	28	BH789953	BH789953

49.0	51	28	BZ355247	BZ355247 SALK_1265	881	9.6	48.0	31	9	AA479970	AA479970
49.0	51	29	BZ36833	BZ36833 Danilo rer	C 882	9.6	48.0	31	10	BF671365	BF671365
49.0	51	29	BX897114	BX897114 Arabidops	C 883	9.6	48.0	31	28	AZ836178	AZ836178
49.0	52	9	AA652918	AA652918 ms68C10.s	C 884	9.6	48.0	32	12	BZ064949	BZ064949
49.0	52	9	AI098966	AI098966 tg99g03.r	C 885	9.6	48.0	32	28	BH858487	BH858487
49.0	52	9	AI582154	AI582154 tg63a03.x	C 886	9.6	48.0	32	29	DR15F9S	DR15F9S
49.0	52	10	BF647779	BF647779 NF011G03E	C 887	9.6	48.0	33	14	H92789	H92789
49.0	52	10	BZ320399	BZ320399 NF029G03R	C 888	9.6	48.0	33	28	BH812027	BH812027
49.0	52	28	AZ580226	AZ580226 IM0368G24	C 889	9.6	48.0	34	9	AA906808	AA906808
49.0	52	28	AZ590017	AZ590017 IM0399D24	C 890	9.6	48.0	34	9	AA933898	AA933898
49.0	52	28	AZ958009	AZ958009 2M0225A07	C 891	9.6	48.0	34	9	AI016849	AI016849
49.0	52	28	B05441	B05441 CSRL-62611-	C 892	9.6	48.0	34	9	AI012823	AI012823
49.0	53	9	AU257573	AU257573 AU257573	C 893	9.6	48.0	34	14	R50309	R50309
49.0	53	10	BZ372900	BZ372900 601224855	C 894	9.6	48.0	35	9	AV957679	AV957679
49.0	53	28	AZ782877	AZ782877 2M0024C11	C 895	9.6	48.0	36	12	BM145495	BM145495
49.0	54	9	AI174298	AI174298 am67D05.s	C 896	9.6	48.0	36	28	AZ655463	AZ655463
49.0	54	10	BF131931	BF131931 601820892	C 897	9.6	48.0	37	9	AA916948	AA916948
49.0	54	14	T80667	T80667 yd22b12.r1	C 898	9.6	48.0	37	9	AI444944	AI444944
49.0	54	28	B01723	B01723 CSRL-138B2-	C 899	9.6	48.0	37	9	AI629177	AI629177
49.0	54	28	BH810022	BH810022 SALK_0404	C 900	9.6	48.0	38	9	AU255151	AU255151
49.0	54	29	EX132447	EX132447 Danilo rer	C 901	9.6	48.0	38	28	BH810071	BH810071
49.0	55	9	AI098452	AI098452 uc05G04.r	C 902	9.6	48.0	38	28	BH858486	BH858486
49.0	55	9	AI159145	AI159145 vz83h01.r	C 903	9.6	48.0	38	28	BH858486	BH858486
49.0	55	9	AI188278	AI188278 qd11h05.x	C 904	9.6	48.0	39	29	TA129B06P	TA129B06P
49.0	55	29	CG672176	CG672176 RRL140.Ba	C 905	9.6	48.0	40	9	AA681836	AA681836
49.0	55	29	CG696182	CG696182 BARC.BFLG	C 906	9.6	48.0	40	9	AI151322	AI151322
49.0	55	29	CG894942	CG894942 0384734-0	C 907	9.6	48.0	40	9	AI609954	AI609954
49.0	56	9	AI246108	AI246108 qi28h01.x	C 908	9.6	48.0	41	28	DR46L115S	DR46L115S
49.0	56	9	AA185070	AA185070 mt93a01.r	C 909	9.6	48.0	41	28	BZ764101	BZ764101
49.0	56	12	BG315269	BG315269 PO1.0.290	C 910	9.6	48.0	42	29	CC055084	CC055084
49.0	56	12	BF964808	BF964808 ie56h10.Y	C 911	9.6	48.0	42	29	BX228728	BX228728
49.0	56	12	BF964808	BF964808 ie56h10.Y	C 912	9.6	48.0	43	9	AA896934	AA896934
49.0	56	18	CF319453	CF319453 HD--09-P0	C 913	9.6	48.0	43	9	AA987068	AA987068
49.0	56	28	AZ760050	AZ760050 IM0553L21	C 914	9.6	48.0	43	9	AI283683	AI283683
49.0	56	28	AZ778224	AZ778224 2M0013G18	C 915	9.6	48.0	43	9	AI766391	AI766391
49.0	56	28	BH846935	BH846935 SALK_0120	C 916	9.6	48.0	43	12	BG615463	BG615463
49.0	56	28	BZ355226	BZ355226 SALK_1265	C 917	9.6	48.0	43	28	AZ816639	AZ816639
49.0	57	28	B00299	B00299 CSRL-106e4-	C 918	9.6	48.0	44	9	BZ288962	BZ288962
49.0	57	29	CG733686	CG733686 1119158E0	C 919	9.6	48.0	44	9	AA687683	AA687683
49.0	58	9	AA755595	AA755595 ts20f05.r	C 920	9.6	48.0	45	14	CF277394	CF277394
49.0	58	9	AI433571	AI433571 ti47C05.x	C 921	9.6	48.0	46	9	AA010457	AA010457
49.0	58	9	AA506019	AA506019 ni02e05.s	C 922	9.6	48.0	46	9	AA994622	AA994622
49.0	58	14	N23403	N23403 YX83hl2.sl	C 923	9.6	48.0	46	9	AI690532	AI690532
49.0	58	29	TA280H04Q	TA280H04Q T. brucei	C 924	9.6	48.0	46	9	AI941389	AI941389
49.0	59	10	AW259870	AW259870 um79e08.Y	C 925	9.6	48.0	46	14	CF291149	CF291149
49.0	59	12	B036427	B036427 B036427	C 926	9.6	48.0	46	14	CF291149	CF291149
49.0	59	28	AZ812360	AZ812360 2M0079C02	C 927	9.6	48.0	47	14	R94759	R94759
49.0	59	28	BH227137	BH227137 1061337E0	C 928	9.6	48.0	47	28	AZ778132	AZ778132
49.0	59	28	CC037087	CC037087 3591.1.85	C 929	9.6	48.0	47	28	BH790193	BH790193
49.0	59	29	CG785294	CG785294 00S013-0	C 930	9.6	48.0	47	28	CC029912	CC029912
49.0	59	29	BX536102	BX536102 Arabidops	C 931	9.6	48.0	48	12	BJ075818	BJ075818
49.0	60	9	AU060311	AU060311 AU060311	C 932	9.6	48.0	48	28	BH840645	BH840645
49.0	60	14	CF554395	CF554395 SSHG9W191	C 933	9.6	48.0	48	28	BH911342	BH911342
49.0	60	28	AZ436822	AZ436822 IM0224C16	C 934	9.6	48.0	48	29	BX185367	BX185367
49.0	60	28	AZ693621	AZ693621 AST-1HDB1	C 935	9.6	48.0	49	9	AA687445	AA687445
49.0	60	28	AZ839359	AZ839359 2M0135M24	C 936	9.6	48.0	49	9	AA890440	AA890440
49.0	60	28	AZ963429	AZ963429 2M0232P05	C 937	9.6	48.0	49	14	CF312452	CF312452
49.0	60	28	BH814811	BH814811 SALK_0670	C 938	9.6	48.0	49	28	AZ472469	AZ472469
49.0	60	29	CG715527	CG715527 1119042B0	C 939	9.6	48.0	49	28	CC023128	CC023128
49.0	60	29	CG779790	CG779790 1123035G1	C 940	9.6	48.0	49	29	CC886568	CC886568
48.0	20	14	CF306620	CF306620 HDAL--04-	C 941	9.6	48.0	50	9	AU102302	AU102302
48.0	21	14	D20000	D20000 HUMGS00970	C 942	9.6	48.0	50	9	AU102363	AU102363
48.0	22	28	AZ762337	AZ762337 IM0557P13	C 943	9.6	48.0	50	9	AU102364	AU102364
48.0	22	28	AZ797469	AZ797469 2M0053P10	C 944	9.6	48.0	50	9	AU102365	AU102365
48.0	23	28	AZ323912	AZ323912 IM0045B12	C 945	9.6	48.0	50	9	AU102368	AU102368
48.0	25	9	AI739003	AI739003 wi34b01.x	C 946	9.6	48.0	50	9	AU102372	AU102372
48.0	25	13	BQ584791	BQ584791 E011673-0	C 947	9.6	48.0	50	9	AU102373	AU102373
48.0	25	28	BZ596723	BZ596723 SALK_0958	C 948	9.6	48.0	50	9	AU102496	AU102496
48.0	30	9	AB080292	AB080292 AB080292	C 949	9.6	48.0	50	9	AU102578	AU102578
48.0	30	14	CF324474	CF324474 HDN--06-K	C 950	9.6	48.0	50	9	AU102651	AU102651
48.0	30	28	AZ456295	AZ456295 IM0259J04	C 951	9.6	48.0	50	9	AU102652	AU102652
48.0	30	28	AZ477920	AZ477920 IM0297H05	C 952	9.6	48.0	50	9	AU102653	AU102653
48.0	31	9	AI565928	AI565928 ts95G06.x	C 953	9.6	48.0	50	9		
48.0	31	9	AI697078	AI697078 wc85g12.x							

## ALIGNMENTS

te, E.N. and Jones, C.A.  
The discovery and microarray analysis of cacao (*Theobroma cacao*) varieties  
ita 216 (2), 255-264 (2002)  
37596

69.0%; Score 13.8; DB 14; Length 59;  
 ilarity 88.2%; Pred. No. 1e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCCTCCACGGG 18  
 |||||  
 CCTCTCCTCCACGGG 42

39 55 bp mRNA linear EST 23-FEB-1995  
 b01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone  
 IE:80905 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR  
 NUCLEOPROTEINS C1/C2 (HUMAN); mRNA sequence.

39 GI:681187  
 sapiens (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 bases 1 to 55)  
 ier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 soc, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
 ins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
 is, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 feng, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 askis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,  
 Marra, M.  
 ration and analysis of 280,000 human expressed sequence tags  
 me Res. 6 (9), 807-828 (1996)  
 4478  
 549  
 act: Wilson RK  
 ington University School of Medicine  
 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 314 286 1800  
 314 286 1810  
 l: est@watson.wustl.edu  
 quality sequence starts: 1  
 quality sequence stops: 1  
 ce: IMAGE Consortium, LLNL  
 clone is available royalty-free through LLNL; contact the  
 E Consortium (info@image.llnl.gov) for further information.  
 e considered overall poor quality  
 primer: -21ml3  
 quality sequence stop: 1.  
 Location/Qualifiers  
 1. .55  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:484522"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:80905"  
 /sex="male"  
 /dev\_stage="72 years"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /clone\_lib="Stratagene lung (#937210)"  
 /note="Organ: lung; Vector: pBluescript SK-; Site: 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dr. normal lung. Average insert size: 1.0 kb;  
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG  
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

68.0%; Score 13.6; DB 14; Length 55;  
 ilarity 80.0%; Pred. No. 1.2e+05;  
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTTGTCCTCCACGGGTT 20  
 |||||

Db 36 ATCCTGTGCTTCCCATGTT 17

RESULT 4  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AW140195 35 bp mRNA linear EST  
 SWAMC44A12SK Brugia malayi adult male cDNA (SAW94NL-Bt  
 malayi cDNA clone SWAMC44A12 5', mRNA sequence.  
 AW140195  
 AW140195.1 GI:6159913  
 EST.  
 Brugia malayi  
 Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Fi  
 Onchocercidae; Brugia.  
 1 (bases 1 to 35)  
 Williams, S.A.  
 Genes expressed in adult males of Brugia malayi  
 Unpublished (1995)  
 Contact: Steven A. Williams  
 Molecular Parasitology  
 Smith College Department of Biological Sciences  
 Department of Biological Sciences, Clark Science Center,  
 College, Northampton, MA, 01063, USA  
 Tel: 4135853786  
 Fax: 4135853786  
 Email: genome@smith.edu  
 Seq primer: pBluescript SK  
 Location/Qualifiers  
 1. .35  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /strain="TRS Labs"  
 /db\_xref="taxon:6279"  
 /clone="SWAMC44A12"  
 /lab\_host="XLI-Blue MRF"  
 /clone\_lib="Brugia malayi adult male cDNA (SAW9  
 /note="Vector: lambda Unizap XR; Site 1: EcoR I  
 Xho I; Lymphatic filarial nematode parasite of  
 mRNA was prepared from adult males of Brugia ma  
 isolated from jirds and converted to double str  
 using reverse transcriptase and oligo(dT) follc  
 RNase H and DNAPol I. The library had 4.6 x 10E  
 independent recombinants and average insert siz  
 base pairs. The library was constructed by Noe  
 The library is available from Dr. S.A. Williams  
 genome@smith.edu."

Query Match 66.0%; Score 13.2; DB 10; Length 35;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTGTGCTCCTCCACGGGTT 20  
 |||||

Db 13 CGTGTCTCCTCCTGCTT 30

RESULT 5  
 BH851251/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

BH851251 45 bp DNA linear GSS  
 SALK\_072736.23.80.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_072736.23.80.x,  
 survey sequence.  
 BH851251  
 BH851251.1 GI:21422122  
 GSS.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 45)

iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
m,P., Zimmerman,J., and Ecker,J.R.  
Sequence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
ublished (2001)

act: Joseph R. Ecker  
c Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 538 6379  
il: ecker@salk.edu

s is single pass sequence recovered from the left border of

ts: TDNA tagged.

Location/Qualifiers

1. 45

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_072736.23.80.x"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

ilarity 66.0%; Score 13.2; DB 28; Length 45;

Conservative 83.3%; Pred. No. 1.7e+05;

0; Mismatches 3; Indels 0; Gaps 0;

2CTGTGCTCCACCGGGT 19

|||||

CTTATCCACCGCGGT 27

11234 49 bp mRNA linear EST 30-AUG-1996  
#06.r1 Soares\_fetal heart NBH19W Homo sapiens cDNA clone  
#E:376259 5' similar to PIR:A54211 A54211 H+transporting ATP  
#ase ; mRNA sequence.

11234

11234.1 GI:1517468

sapiens (human)

sapiens

ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

alia; Euthera; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 49)

ier.L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

ian,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,

sons,J., Rafkin,L., Rohlfing,T., Soares,M., Tan,F.,

askis,B., Waterston,R., Williamson,A., Wohlmann,P. and

on,R.

WashU-Merck EST Project

ublished (1995)

act: Wilson RK

ington University School of Medicine

Forest Park Parkway, Box 8501, St. Louis, MO 63108

314 286 1800

314 286 1810

il: estwatson.wustl.edu

s clone is available royalty-free through LNL ; contact the

SE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

re considered overall poor quality

ible reversed clone; similarity on wrong strand

primer: -28M13 rev2 from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1. 49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1284515"

/db\_xref="taxon:9606"

/clone="IMAGE:376259"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal heart NBH19W"

/note="Organ: heart; Vector: pT73D (Pharmacia)

modified polylinker; Site 1: Not I; Site 2: Eco

strand cDNA was primed with a Not I - oligo(dT)

TGTTACCAATCTGAAGTCGAGCGCGCATCTTTTCTTTT

double-stranded cDNA was size selected, ligate

adapters (Pharmacia), digested with Not I and

the Not I and Eco RI sites of a modified pT73

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed

M.Fatima Bonaldo. This library was constructed

same fetus as the fetal lung library, Soares f

NBH19W."

ORIGIN

Query Match

Best Local Similarity 66.0%; Score 13.2; DB 9; Length 49;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTGCTCCACCGGT 19

|||||

DB 18 TTCTGTGCTCCACGTGT 1

RESULT 7

AA180620

LOCUS

DEFINITION

malayi cDNA clone AFGCIB10 5', mRNA sequence.

ACCESSION

AA180620

VERSION

AA180620.1 GI:1763812

KEYWORDS

EST.

SOURCE

Brugia malayi

Brugia malayi

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F;

Onchocercidae; Brugia.

REFERENCE

1 (bases 1 to 49)

Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,I

Jones,S.J.

Genes expressed in adult female Brugia malayi

Unpublished (1996)

CONTACT: Blaxter ML

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashtworth Labs, King's Buildings, West Mains Road, Edinbu

3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at

<http://www.sanger.ac.uk/brugia/AF/MBACGIB1073.html> This

full sequence of the cDNA clone. The polyA tail has been

and is excluded from this sequence

Seq primer: T3.

Location/Qualifiers

1...49

/organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/clone="AFGIB10"

/sex="female"

/dev\_stage="adult"

FEATURES

source



/lab\_host="XLI-Blue MRF"  
 /clone lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BmaF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase H and DNA  
 pol I. The library has 5 x 10<sup>5</sup> independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The  
 library is available from Dr.S.A.Williams, email:  
 genome@smith.edu."

66.0%; Score 13.2; DB 9; Length 49;  
 Similarity 83.3%; Pred. No. 1.7e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
 |||||  
 TTGTCTGCACGGGTT 47

1635 50 bp mRNA linear EST 17-DEC-1996  
 2G0A07T3 Brugia malayi adult female cDNA (SAW96MLW-BmaF) Brugia  
 (i) cDNA clone AFCG0A07 5', mRNA sequence.

1635.1 GI:1737665

Brugia malayi  
 Brugia malayi  
 Cytota: Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 Oecercidae; Brugia.  
 bases 1 to 50)  
 -er.M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and  
 S.S.J.  
 3 expressed in adult female Brugia malayi  
 3 published (1996)  
 3 Contact: Blaxter ML  
 3 Institute of Cell, Animal and Population Biology  
 3 University of Edinburgh  
 3 North Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
 UK.

+44 131 650 6760  
 +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk  
 The ABI trace of this sequence can be viewed at  
 http://www.sanger.ac.uk/bugia/AFC/MBAPCG0A07T3.html  
 primer: T3.

Location/Qualifiers  
 1. 50  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="AFCG0A07"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="XLI-Blue MRF"  
 /clone lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BmaF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase H and DNA  
 pol I. The library has 5 x 10<sup>5</sup> independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The

library is available from  
 genome@smith.edu."

66.0%; Score 13.2; DB 9; Length 50;  
 Similarity 83.3%; Pred. No. 1.7e+05;  
 Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTTGTCTCCACGGGTT 20  
 |||||  
 Db 31 CGTTGTCTCCACGGGTT 48

RESULT 9  
 AA406799  
 LOCUS  
 DEFINITION  
 MAFCAZ4G10T3 Brugia malayi adult female cDNA (SAW96MLW-B  
 malayi cDNA clone AFCZ4G10 5', mRNA sequence.

AA406799  
 VERSION  
 AA406799.1 GI:2064791  
 KEYWORDS  
 EST.  
 SOURCE  
 Brugia malayi  
 ORGANISM

REFERENCE  
 1 (bases 1 to 51)

AUTHORS  
 Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L  
 Jones,S.J.

TITLE  
 Genes expressed in adult female Brugia malayi  
 JOURNAL  
 Unpublished (1996)

COMMENT  
 Contact: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
 3,UT, UK.

Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at  
 http://www.sanger.ac.uk/bugia/AFC/MBAPCAZ4G10T3.html The  
 full sequence of the cDNA clone. The polyA tail has been  
 and is excluded from this sequence  
 Seq primer: T3.

FEATURES  
 source  
 Location/Qualifiers

1. 51  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="AFCZ4G10"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="XLI-Blue MRF"  
 /clone lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BmaF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco R  
 Xho I; Lymphatic filarial nematode parasite of  
 mRNA was prepared from approximately 50 adult f  
 isolated from the peritoneal cavity of jirds a  
 converted to double-stranded cDNA using  
 transcriptase and oligo(dT) followed by RNase H  
 pol I. The library has 5 x 10<sup>5</sup> independent rec  
 and the average insert size is ~900bp. The libra  
 constructed by Michelle Lizotte-Waniew  
 library is available from  
 genome@smith.edu."

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 51;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTTGTCTCCACGGGTT 20  
 |||||

GTGTGCTGCACCTGGTT 49

54424 53 bp mRNA linear EST 05-JUN-1997  
 FCX1D10T3 Brugia malayi adult female cDNA (SAW96MLW-BMAF) Brugia  
 ay1 cDNA clone AFCX1D10 5', mRNA sequence.  
 54424  
 54424.1 GI:2168093  
 Gia malayi  
 Gia malayi  
 hoceridae; Brugia.  
 (bases 1 to 53)  
 xter:M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and  
 es,S.J.  
 es expressed in adult female Brugia malayi  
 ublished (1996)  
 tact: Blaxter ML  
 titute of Cell, Animal and Population Biology  
 versity of Edinburgh  
 worth labs, King's Buildings, West Mains Road, Edinburgh, EH9  
 , UK.  
 : +44 131 650 6760  
 : +44 131 670 5450  
 il: mark.blaxter@ed.ac.uk  
 ABI trace of this sequence can be viewed at  
 p://www.sanger.ac.uk/brugia/AFC/MBFAFCX1D10T3.html  
 primer: T3:  
 Location/Qualifiers  
 1..53  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="AFCX1D10"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="X11-Blue MRF"  
 /clone\_lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BMAF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase  
 pol I. The library has 5 x 10E6 independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The  
 library is available from Dr.S.A.Williams,  
 genome@smith.edu."

Location/Qualifiers

1..53  
 /organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/clone="AFCX1D10"

/sex="female"

/dev\_stage="adult"

/lab\_host="X11-Blue MRF"

/clone\_lib="Brugia malayi adult female cDNA

(SAW96MLW-BMAF)"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:

Xho I; Lymphatic filarial nematode parasite of humans.

mRNA was prepared from approximately 50 adult females

isolated from the peritoneal cavity of jirds and

converted to double-stranded cDNA using reverse

transcriptase and oligo(dT) followed by RNase H and DNA

pol I. The library has 5 x 10E6 independent recombinants

and the average insert size is ~900bp. The library was

constructed by Michelle Lizotte-Waniewski. The

library is available from Dr.S.A.Williams, email:

genome@smith.edu."

66.0%; Score 13.2; DB 9; Length 53;

ilarity 83.3%; Pred.No.1.8e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTGCTGCACCTGGTT 20

|||||

GTGTGCTGCACCTGGTT 51

89356 54 bp mRNA linear EST 12-DEC-1996  
 FCAS5SK Brugia malayi adult female cDNA (SAW96MLW-BMAF) Brugia  
 ay1 cDNA clone SWAFCA55 5', mRNA sequence.  
 89356  
 89356.1 GI:1634835

Gia malayi

# ORGANISM

Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F  
 Onchocercidae; Brugia.

1 (bases 1 to 54)

Williams,S.A.

Genes expressed in adult females of Brugia malayi

Unpublished (1996)

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

1..54

/organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/clone="SWAFCA55"

/sex="female"

/dev\_stage="adult"

/lab\_host="X11-Blue MRF"

/clone\_lib="Brugia malayi adult female cDNA

(SAW96MLW-BMAF)"

/note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco

Xho I; Lymphatic filarial nematode parasite of

mRNA was prepared from approximately 50 adult

isolated from the peritoneal cavity of jirds

converted to double-stranded cDNA using

transcriptase and oligo(dT) followed by RNase

pol I. The library has 5 x 10E6 independent re

and the average insert size is ~900bp. The libr

constructed by Michelle Lizotte-Wanie

library is available from Dr.S.A.Williams

genome@smith.edu."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 54;

Best Local Similarity 83.3%; Pred.No.1.8e+05;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CTTGTGCTGCACCTGGTT 20

|||||

Db 32 CTTGTGCTGCACCTGGTT 49

RESULT 12

LOCUS

AV955284

DEFINITION

AV955284 Nori Satoh unpublished cDNA library, cleavage :

Ciona intestinalis cDNA clone c109n01 5', mRNA sequen

EST.

ACCESSION

AV955284

VERSION

AV955284.1 GI:19443583

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; I

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 54)

Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

```

1. .54
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"
/clone="cic109n01"
/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
stage embryo"

66.0%; Score 13.2; DB 9; Length 54;
ilarity 83.3%; Pred. No. 1.8e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGTT 20
|||||
TTGTCTCTCGACAGGAT 20

7148
35G10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
e UUGC1M0035G10 R, genomic survey sequence.
7148
7148.1 GI:10365669

musculus (house mouse)
musculus
ryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
bases 1 to 55)
,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
m.H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
ly,M., Rose,M., Stokes,R., Tingey,A., von
erhausen,A. and Wright,D., Weiss,R.
e whole genome scaffolding with paired end reads from 10kb
mid inserts
ished (2000)
act: Robert B. Weiss
ersity of Utah Genome Center
ersity of Utah
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
2. USA
801 585 5606
801 585 7177
l: ddm@genetics.utah.edu
rt Length: 10000 Std Error: 0.00
e: 0035 row: G column: 10
primer: CACACAGGAACACGTATGACC
s: plasmid ends
quality sequence stop: 55.
Location/Qualifiers
1. .55
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035G10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from of pWD42 [gi|4732114|gb|AF129072.1], a copy-nu inducible derivative of plasmid R1. The vector with adaptors complementary to the insert adap purified. The sheared, adaptor mouse DNA was adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Strata) and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 28; Length 55;  
Best Local Similarity 83.3%; Pred. No. 1.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTGTCTCTCCACGGGTT 20  
|||||  
DB 20 CCTTCTCTTCCACTGGTT 3

## RESULT 14

AA406768  
LOCUS MAFPCZ4B07T3 Brugia malayi adult female cDNA (SAW96MLW-1)  
DEFINITION malayi cDNA clone AFCZ4B07 5', mRNA sequence.  
ACCESSION AA406768  
VERSION AA406768.1 GI:2064734  
KEYWORDS EST.  
SOURCE Brugia malayi  
ORGANISM Brugia malayi  
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F;  
Onchocercidae; Brugia.  
1 (bases 1 to 60)  
Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,I  
Jones,S.J.  
Genes expressed in adult female Brugia malayi  
Unpublished (1996)  
Contact: Blaxter ML  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
3JT, UK.  
Tel: +44 131 650 6760  
Fax: +44 131 670 5450  
Email: mark.blaxter@ed.ac.uk  
The ABI trace of this sequence can be viewed at  
<http://www.sanger.ac.uk/brugia/AFC/MAFPCZ4B07T3.html>  
Seq primer: T3

## FEATURES

Location/Qualifiers  
1. .60  
/organism="Brugia malayi"  
/mol\_type="mrna"  
/db\_xref="taxon:6279"  
/clone="AFCZ4B07"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="XL1-Blue MRF"  
/clone\_lib="Brugia malayi adult female cDNA  
(SAW96MLW-BMAF)"  
/notes="Vector: Lambda Uni-ZAP XR, Site 1: Eco R  
Xho I; Lymphatic filarial nematode parasite of  
mRNA was prepared from approximately 50 adult f  
isolated from the peritoneal cavity of jirds a  
converted to double-stranded cDNA using  
transcriptase and oligo(dT) followed by RNase H  
pol I. The library has 5 x 10<sup>8</sup> independent rec  
and the average insert size is ~900bp. The libra  
constructed by Michelle Lizotte-Waniew  
library is available from Dr.S.A.Williams,  
genome@smith.edu."

## ORIGIN

Query Match

66.0%; Score 13.2; DB 9; Length 60;

milarity 83.3%; Pred. No. 1.8e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 :CTTGCTCCACGGGTT 20  
 :TTTGCTCGACTGGTT 58  
 .031  
 :0d12.sl Stratagene liver (#937224) Homo sapiens cDNA clone  
 GE:84119 3' similar to gb:X00570 APOLIPOPROTEIN C-I PRECURSOR  
 MAN); mRNA sequence.  
 .031  
 .031.1 GI:685552  
 .  
 no sapiens (human)  
 no sapiens  
 :aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 :malia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 (Bases 1 to 60)  
 :lier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
 :scoe,S., Dietrich,N., DuBuque,T., Favell,A., Gish,W.,  
 :kins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,  
 :dis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,  
 :lfling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierzy-Meg,J.,  
 :vaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,  
 :Marra,M.  
 :eration and analysis of 280,000 human expressed sequence tags  
 :ome Res. 6 (9), 807-828 (1996)  
 44478  
 9549  
 :tact: Wilson RK  
 :hington University School of Medicine  
 :4 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 : 314 286 1800  
 : 314 286 1810  
 :il: est@watson.wustl.edu  
 :ert Size: -19  
 :ert Size: 409  
 :h quality sequence starts: 1  
 :h quality sequence stops: 1  
 :rce: IMAGE Consortium, LNL  
 :s clone is available royalty-free through LNL; contact the  
 :GE Consortium (info@image.lnl.gov) for further information.  
 :ce considered overall poor quality  
 :primer: -21ml3  
 :h quality sequence stop: 1.  
 :Location/Qualifiers  
 : 1..60  
 :/organism="Homo sapiens"  
 :/mol\_type="mRNA"  
 :/db\_xref="GDB:501176"  
 :/db\_xref="taxon:9606"  
 :/clone="IMAGE:84119"  
 :/sex="male"  
 :/dev\_stage="49 years old"  
 :/lab\_host="SOLR cells (kanamycin resistant)"  
 :/clone\_lib="Stratagene liver (#937224)"  
 :/notes="Organ: liver; Vector: pBluescript SK; Site 1:  
 :EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 :Oligo dT. Hepatectomy from normal male caucasian. Average  
 :insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor  
 :sequence: 5' GAATTCGGCAG 3' -3' adaptor sequence: 5'  
 :CTCGAGTTTCTTTTCTTTTCTTTT 3'"

milarity 66.0%; Score 13.2; DB 14; Length 60;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 :CTTGCTCCACGGGTT 20

Db

RESULT 16  
 W77719/c

LOCUS  
 DEFINITION

ACCSSION  
 W77719

VERSION  
 W77719.1

KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

REFERENCE  
 AUTHORS

1 (bases 1 to 49)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,  
 Geise,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moor  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R.,  
 Waterston,R.  
 The WashU-HMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; con  
 IMAGE Consortium (info@image.lnl.gov) for further info  
 MGI:246057  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:402289"  
 /sex="unknown"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse embryo NbME13.5 14.5"  
 /note="Vector: pT73D-Pac (Pharmacia) with a m  
 polylinker; Site1: Not 1; Site 2: Eco RI; 1st  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTCGCGCGCGCGGAATTTTTTTTTT  
 T 3'], on equal amounts of mRNA from 2 13.5dpc  
 14.5dpc embryos [total RNA provided by Minoru  
 State Univ., from 2]; double-stranded cDNA wa  
 Eco RI adaptors (Pharmacia), digested with the  
 cloned into the Not I and Eco RI sites of the  
 pT73 vector. Library went through one round of  
 normalization, and was constructed by Bento Soa  
 M.Fatima Bonaldo."

TITLE  
 JOURNAL

COMMENT

FEATURES  
 source

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CCTTGCTCCAC 15  
 DB 29 CCTTGCTCCAC 17

ORIGIN

38464 40 bp mRNA linear EST 18-AUG-1997  
 3809.s1 NCI CGAP Pr8 Homo sapiens cDNA clone IMAGE:957305  
 ilar to TR:G547185 G547185 ELFO-ATP SYNTHASE COMPLEX FO MEMBRANE  
 AIN F SUBUNIT. ; mRNA sequence.

38464 40 bp mRNA linear EST 18-AUG-1997  
 3809.s1 NCI CGAP Pr8 Homo sapiens cDNA clone IMAGE:957305  
 ilar to TR:G547185 G547185 ELFO-ATP SYNTHASE COMPLEX FO MEMBRANE  
 AIN F SUBUNIT. ; mRNA sequence.

38464.1 GI:2245967  
 sapiens (human)  
 sapiens  
 anyota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 -CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 r Gene Index  
 blished (1997)  
 act: Robert Strausberg, Ph.D.  
 li: cgapbs-r@mail.nih.gov  
 sue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,  
 .; Michael R. Emmert-Buck, M.D., Ph.D.  
 VA Library Preparation: David B. Krizman, Ph.D.  
 VA Library Arrayed by: Greg Lennon, Ph.D.  
 Sequencing by: Washington University Genome Sequencing Center  
 ne distribution: NCI-CGAP clone distribution information can be  
 id through the I.M.A.G.E. Consortium/LLNL at:  
 .bio.llnl.gov/bbrp/image/image.html

re considered overall poor quality  
 rt Length: 520 Std Error: 0.00  
 primer: -40m13 fwd. ET from Amersham  
 i quality sequence stop: 1.  
 Location/Qualifiers  
 1. 40  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:957305"  
 /sex="male"  
 /tissue\_type="prostate"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr8"  
 /note="Vector: PAMP10; mRNA made from invasive prostate  
 tumor, cDNA made by oligo-dT priming. Non-directionally  
 cloned. Size-selected on agarose gel, average insert  
 size 600 bp."

64.0%; Score 12.8; DB 9; Length 40;  
 ilarity 87.5%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0;  
 Gaps 0;  
 TGTCTCCACGGGT 19  
 |||||  
 TGTCTTCACGGT 1

8783 49 bp mRNA linear EST 23-OCT-1998  
 d05.s1 Soares NHPu S1 Homo sapiens cDNA clone IMAGE:1661769  
 ilar to TR:O14923 O14923 REGULATOR OF G PROTEIN SIGNALING  
 2. ; mRNA sequence.

8783 49 bp mRNA linear EST 23-OCT-1998  
 d05.s1 Soares NHPu S1 Homo sapiens cDNA clone IMAGE:1661769  
 ilar to TR:O14923 O14923 REGULATOR OF G PROTEIN SIGNALING  
 2. ; mRNA sequence.

8783.1 GI:3701953  
 sapiens (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LLNL ; con  
 IMAGE Consortium (info@image.llnl.gov) for further info  
 Trace considered overall poor quality  
 Insert Length: 387 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1661769"  
 /tissue\_type="Pooled human melanocyte, fetal h  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares NHPu S1"  
 /note="Organ: mixed (see below); Vector: pT7T3;  
 (pharmacia) with a modified polylinker; Site 1  
 Site 2: Eco RI; Equal amounts of plasmid DNA f  
 normalized libraries (melanocyte 2NBHM, pregna  
 NbHPu, and fetal heart NbHH19W) were mixed, an  
 were made in vitro. Following HAP purification  
 was used as tracer in a subtractive hybridizat  
 reaction. The driver was PCR-amplified cDNAs f  
 5,000 clones made from the same 3 libraries. T  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

Query Match 64.0%; Score 12.8; DB 9; Length 49;  
 Best Local Similarity 87.5%; Pred. No. 2.5e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;  
 QY 4 CTTGCTCCACGGGT 19  
 |||||  
 Db 8 CTTGCTCTTCGGGT 23

RESULT 19  
 AAL161672  
 LOCUS  
 DEFINITION  
 AAL161672  
 malayi cDNA clone AFG0E08 5', mRNA sequence.  
 AAL161672.1 GI:1737702  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Brugia malayi  
 Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Fi  
 Onchocercidae; Brugia.  
 1 (bases 1 to 60)  
 Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, I  
 Jones, S.J.  
 Genes expressed in adult female Brugia malayi  
 Unpublished (1996)  
 Contact: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
 3UT, UK.  
 Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk  
 The ABI trace of this sequence can be viewed at  
 http://www.sanger.ac.uk/brugia/AF0/MBAF0G0E08r3.html  
 Seq primer: 13.  
 Location/Qualifiers

```

1. .56
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="AFG0E08"
/sex="female"
/dev_stage="adult"
/lab_host="XU-Blue MRF"
/clone_lib="Brugia malayi adult female cDNA
(SAW96MLW-BmaF)"
/notes="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 50 adult females
isolated from the peritoneal cavity of jirds and
converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 5 x 108 independent recombinants
and the average insert size is ~900bp. The library was
constructed by Michelle Lizotte-Waniewski. The
library is available from Dr.S.A.Williams, email:
genome@smith.edu."

```

```

64.0%; Score 12.8; DB 9; Length 60;
milarity 87.5%; Pred. No. 2.7e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

TGTCTCCACGGGTT 20
|||||
TGTCTGCAGTGGT 16

```

```

395
1c11.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328724 3'
ilar to gb:213009_rnal EPITHELIAL-CADHERIN PRECURSOR (HUMAN);
A sequence.
395
395.1 GI:1329476

```

```

o sapiens (human)
o sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 56)
lier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
ssoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
kins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
dis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
ling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
vaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
Marra,M.
eration and analysis of 280,000 human expressed sequence tags
One Res. 6 (9), 807-828 (1996)
4478
9549

```

```

tact: Wilson RK
ington University School of Medicine
4 Forest Park Parkway, Box 8501, St. Louis, MO 63108
: 314 286 1800
: 314 286 1810

```

```

i: est@wustl.edu
s clone is available royalty-free through LNL; contact the
GE Consortium (info@image.llnl.gov) for further information.
sible reversed clone: polyT not found
primer: mob REGA+ET.

```

```

Location/Qualifiers
1. .56
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1262928"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:328724"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Pancreatic Islet"
/notes="Organ: pancreas; Vector: pBluescript SK
EcoRI; Site 2: XhoI; Reference: Hum Mol Gen 2,
Takeda et al. Cloned unidirectionally. Primer:
-5' adaptor sequence: 5' GAATTCGACGAG 3' -3'
sequence: 5' CTCGAGTTTTTTTTTTTTT 3'"

```

## ORIGIN

```

Query Match 63.0%; Score 12.6; DB 14; Length 56;
Best Local Similarity 78.9%; Pred. No. 3.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

```

```

QY 1 ATCCTTGTCTCCACGGGT 19
|||||
Db 3 AGCCTTGTCTCCACGGCT 21
|||||

```

## RESULT 21

```

AA680800
LOCUS
DEFINITION
58 bp mRNA linear EST
LmfrAm0338 Leishmania major Amastigote Lambda Zap II 11
Leishmania major cDNA clone M87 5', mRNA sequence.
AA680800
ACCESSION
VERSION
AA680800.1 GI:2662805
KEYWORDS
EST.
SOURCE
Leishmania major
Leishmania major
Leishmania major
Leishmania major
Leishmania major
Leishmania.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae
Leishmania.

```

```

REFERENCE
1 (bases 1 to 58)
AUTHORS
Norrish,A.R., Dyall,S.D., Smith,D.F. and Blackwell,J.M.
TITLE
Analysis of Leishmania Major Amastigote Expressed Sequ
JOURNAL
Unpublished (1997)
COMMENT
Contact: Blackwell JM
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hi
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk
PCR Primers
FORWARD: GTAAACGACGCGCCAGT
BACKWARD: GGAACAGCTATGACCATG
Seq primer: AATTACCTCTACTAAGGG
High quality sequence stop: 58.

```

## FEATURES

```

source
1. .58
Location/Qualifiers
/organism="Leishmania major"
/mol_type="mRNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="M87"
/cell_type="Amastigote"
/clone_lib="Leishmania major Amastigote Lambda
library"
/notes="Vector: Lambda Zap II; Site 1: XhoI; Si

```

## ORIGIN

```

Query Match 63.0%; Score 12.6; DB 9; Length 58;
Best Local Similarity 78.9%; Pred. No. 3.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

```

```

QY 2 TCCTTGTCTCCACGGGTT 20
|||||
Db 20 TCCCTCTCTGCAGGTGT 38
|||||

```

## RESULT 22

```

H98532/c
LOCUS
H98532
44 bp mRNA linear EST

```

1d03.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone  
 SE:250661 3' similar to gb:M9178 ALPHA-ACTININ 1, CYTOSKELETAL  
 FORM (HUMAN); mRNA sequence.

332  
 332.1 GI:1123182

> sapiens (human)  
 > sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 44)  
 GenBank accession: U00001.1  
 Author: L. Clark, N. Dubuque, T. Elliston, K., Hawkins, M.,  
 Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trivaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

WashU-Merck EST Project  
 Published (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 1 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 : 314 286 1800  
 : 314 286 1810

1. est@wustl.edu  
 1 quality sequence starts: 1  
 1 quality sequence stops: 1  
 Note: IMAGE Consortium, LNLN  
 This clone is available royalty-free through LNLN; contact the  
 3E Consortium (info@image.llnl.gov) for further information.  
 The considered overall poor quality  
 The reverse cloned: polyT not found  
 Site Length: 747 Std Error: 0.00

Primer: Promega -21m13  
 1 quality sequence stop: 1.

Location/Qualifiers

1. 44  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3868367"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:250661"  
 /sex="Male"  
 /tissue\_type="melanocyte"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares melanocyte 2NBHM"  
 /note="Vector: pT73D (Pharmacia) with a modified  
 polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTACCATCTGAGTGGAGCGGCGCGAGTTTCTTTTCTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M. Fatima Bonaldo. RNA from normal foreskin melanocytes  
 (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 62.0%; Score 12.4; DB 14; Length 44;  
 Best Local Similarity 92.9%; Pred. No. 3.6e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTGTGCTCTCCACGG 17  
 |||||  
 CNTGTCTCTCCACNG 22

13207  
 1d08.s1 NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1147959 3'  
 similar to SW:AFAR\_RAT P38918 AFLATOXIN B1 ALDEHYDE REDUCTASE ;  
 a sequence.  
 13207

AA633207.1 GI:2556621  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 52)  
 GenBank accession: U00001.1  
 Author: NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgpbs-remail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmer  
 M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequen  
 Clone distribution: NCI-CGAP clone distribution inform  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.

FEATURES  
 source

1. 52  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1147959"  
 /tissue\_type="colon tumor RER+"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Co9"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharm  
 modified polylinker; 1st strand cDNA was prepa  
 RER+ colon tumor, and was then primed with a N  
 oligo(dT) primer. Double-stranded cDNA was lig  
 RI adaptors (Pharmacia), digested with Not I a  
 into the Not I and Eco RI sites of the modified  
 vector. Library is not normalized. Library wa  
 constructed by Bento Soares and M. Fatima Bona  
 (Soares4)."

ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 52;  
 Best Local Similarity 92.9%; Pred. No. 3.8e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 1 ATCCCTGTCTCCCA 14  
 |||||  
 DB 2 ATCCTGTCTCCAA 15

RESULT 24

R95728/c

LOCUS

R95728 55 bp mRNA linear EST  
 Yq47g09.r1 Soares fetal liver spleen INFLS Homo sapiens  
 IMAGE:198976 5' similar to gb:M91036 rna2 HEMOGLOBIN GA  
 GAMMA-G CHAINS (HUMAN); mRNA sequence.

R95728.1 GI:981388  
 EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 55)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 55)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trivaskis, E., Waterston, R., Williamson, A., Wohlmann, P.,  
 Wilson, R.

The WashU-Merck EST Project  
 Unpublished (1995)

TITLE

JOURNAL

act: Wilson RK  
 ington University School of Medicine  
 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 314 286 1800  
 314 286 1810  
 rt Size: 1338  
 quality sequence starts: 1  
 quality sequence stops: 1  
 ce: IMAGE Consortium, LNL  
 clone is available royalty-free through LNL; contact the  
 Consortium (info@image.lnl.gov) for further information.  
 rt Length: 1338 Std Error: 0.00  
 primer: M13RPI  
 quality sequence stop: 1.  
 Location/Qualifiers  
 1..55  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3768026"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:198976"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)  
 with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 15' AACGGGAAGATTAATTAAGATCTTTTTTTTTTTT 3',  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified p7T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

ilarity 62.0%; Score 12.4; DB 14; Length 55;  
 Conservativity 0; Mismatches 2; Indels 0; Gaps 0;  
 TTGTCTCCACGG 17  
 |||||  
 TTGTCTCCACGTG 19

18197 32 bp DNA linear GSS 13-JUN-2002  
 067630.51.80.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_067630.51.80.x, genomic  
 rey sequence.  
 18197  
 18197.1 GI:21419068  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 alyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 (bases 1 to 32)  
 nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 rinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 nn,P., Zimmerman,J. and Ecker,J.R.  
 sequence-Indexed Library of Insertion Mutations in the  
 idopsis Genome  
 ublished (2001)  
 tact: Joseph R. Ecker  
 k Institute Genomic Analysis Laboratory (SIGNAL)  
 Salk Institute for Biological Studies  
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 : 858 453 4100 x1/52

Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bot  
 TDNA. This sequence lies within an annotated exon of At1  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..32  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_067630.51.80.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thaliana  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic sec  
 the site of insertion. Details of the protocol  
 be found at http://signal.salk.edu/tdna\_protoc

ORIGIN  
 Query Match 61.0%; Score 12.2; DB 28; Length 32;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 4 CTGTCTCCACGGGTT 20  
 |||||  
 Db 30 CTGTCTCCACGTGTT 14

RESULT 26  
 CC583588  
 LOCUS  
 DEFINITION  
 CH240 379P17.TARBA13P2 CHORI-240 Bos taurus genomic cl  
 CC583588 53 bp DNA linear GSS  
 CH240 379P17, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Bos taurus (cow)  
 Bos taurus  
 Eukaryota; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora,  
 Bovidae; Bovinae; Bos.

REFERENCE  
 AUTHORS  
 Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabl  
 Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.  
 Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.  
 Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.  
 Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.  
 Dairympie,B.P. and Tellam,R.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES  
 Unpublished (2003)  
 Other GSSs: CH240 379P17.T7  
 Contac: Rob Holt

TITLE  
 JOURNAL  
 COMMENT

Sequencing  
 The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5  
 Tel: 604-877-6085  
 Fax: 604-877-6276  
 Email: rholt@bccgc.ca

Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). For BAC lib  
 availability, please contact Pieter de Jong (pdejong@mac  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.html).  
 was undertaken as part of the International Bovine BAC  
 Consortium (IBBMC) by CSIRO Livestock Industries, Austr  
 British Columbia Genome Sciences Centre, Canada.  
 Plate: 379 row: P column: 17  
 Seq primer: SP6  
 Class: BAC ends

FEATURES  
 Location/Qualifiers  
 1..53



```

/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_379P17"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

61.0%; Score 12.2; DB 29; Length 53;
larity 82.4%; Pred. No. 4.6e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTTGTCCTCCACGGG 18
|||||
TTATCTCCACGGG 22

3798 54 bp DNA linear GSS 14-FEB-2002
J24H12.1EL_x1 1008 - RescueMu Grid I Zea mays genomic, genomic
3798
3798.1 GI:186663266

nays
nays
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
a; Panicoideae; Andropogoneae; Zea.
cases 1 to 54)
37.V.
a genomic sequences found using engineered RescueMu transposon
shished (2001)
act: Walbot V
rtment of Biological Sciences
ford University
California Ave, Palo Alto, CA 94304, USA
650 723 2227
650 725 8221
l: walbot@stanford.edu
probable ligation site of ends cut by single endonuclease.
rse complemented post-ligation sequence from source sequence.
a: 1008024 row: 10
s: transposon-tagged.
Location/Qualifiers
1. 54
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

```

Query Match 61.0%; Score 12.2; DB 28; Length 54;
Best Local Similarity 82.4%; Pred. No. 4.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 3 CTTGTCTCCACGGGT 19
|||||
Db 17 CTTGTCTCCACGGGT 33

RESULT 28
AA862784/c
LOCUS AA862784 59 bp mRNA linear EST
OH41066.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:14
similar to gb:J04810 DIVERGENT UPSTREAM PROTEIN (HUMAN);
sequence.
ACCESSION AA862784
VERSION AA862784.1 GI:2955263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Eute
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Hom
REFERENCE 1 (bases 1 to 59)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequenc
Clone distribution: NCI-CGAP clone distribution informa
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 872 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES
Location/Qualifiers
1. 59
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1469171"
/tissue_type="pooled germ cell tumors"
/lab host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: p77N3D-Pac (Pharmacia) with a mo
polylinker; 1st strand cDNA was prepared from 3
germ cell tumors, and was then primed with a No
oligo(dT) primer. Double-stranded cDNA was ligo
RI adaptors (Pharmacia), digested with Not I an
into the Not I and Eco RI sites of the modified
vector. Library is normalized. Library was con
Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match 61.0%; Score 12.2; DB 9; Length 59;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 3 CTTGTCTCTCCACGGGT 19
|||||
Db 37 CTTCTCTCTCCACAGGT 21

RESULT 29
CA913675
LOCUS CA913675 59 bp mRNA linear EST
DEFINITION PCS18719 Scarlet Runner Bean Suspensor Region Triplex2
coccineus cDNA 5' similar to sb07g10.y1 Gm-ci004 Glycine

```

sequence.  
 3675  
 3675.1 GI:27400667

neolus coccineus  
 neolus coccineus  
 tryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 neolus.  
 (bases 1 to 59)  
 A.Q.; Le, B.H.; Weterings, K.; Bi, Y.-P.; Choi, J.-S.;  
 Iroy, K.E.; Choi, P.S.; Harada, J.J.; Fischer, R.L. and  
 Iberg, R.B.  
 Activity in Different Regions of a Post-Fertilization Plant  
 Published (2002)  
 act: Goldberg, R.B.  
 artment of Molecular, Cell, & Developmental Biology  
 versity of California, Los Angeles  
 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA  
 : 310 825 3270  
 : 310 825 8201  
 il: bob@ucla.edu  
 primer: 5' Triplex  
 7A=No.

Location/Qualifiers  
 1. .59  
 /organism="Phaseolus coccineus"  
 /mol\_type="rRNA"  
 /cultivar="Hammond's Dwarf Scarlet"  
 /db\_xref="taxon:3886"  
 /dev\_stage="6-days post-pollination"  
 /clone\_lib="Scarlet Runner Bean Suspensor Region Triplex2"  
 /note="Organ: Suspensor Region of Globular-Stage Embryos;  
 Vector: Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Suspensor  
 regions were micro-dissected from globular-stage embryos  
 six days after pollination from greenhouse-grown plants  
 [Weterings et al., Plant Cell 13, 2409-2425 (2001)].  
 Double-stranded cDNA was synthesized from suspensor mRNA  
 using the SMART cDNA Library Construction Kit according to  
 the manufacturer (Clontech). The suspensor cDNA fragments  
 were directionally ligated into the SfiI restriction site  
 of the lambda Triplex2 vector (Clontech), and the  
 recombinant cDNAs were transformed into E. coli XL1-Blue  
 cells (Clontech). Suspensor cDNA plasmids used for  
 directional sequencing were obtained by in vivo excision  
 from the lambda Triplex2 recombinants in E. coli BM25.8  
 cells (Clontech)."

61.0%; Score 12.2; DB 14; Length 59;  
 nilarity 82.4%; Pred. No. 4.7e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTGTCTCTCCACGG 17  
 |||||  
 TCCTGTGGCTCCATGG 13

202 60 bp mRNA linear EST 05-OCT-1995  
 8c03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
 3E:204676 5' similar to gb:X54150 Inal IMMUNOGLOBULIN ALPHA FC  
 EPTOR PRECURSOR (HUMAN); mRNA sequence.  
 202.1 GI:1010034

sapiens (human)  
 sapiens  
 ariota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 60)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, I.  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar-  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Travaskis, E., Waterston, R., Williamson, A., Wohldmann, P.  
 Wilson, R.

TITLE  
JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1551  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; con-  
 IMAGE Consortium (info@image.llnl.gov) for further info:  
 Trace considered overall poor quality  
 Insert Length: 1551 Std Error: 0.00  
 Seq primer: M13Rp1  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

source

1. .60  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
 /db\_xref="GDB:3773807"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:204676"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: pT7T3D  
 with a modified polylinker; Site\_1: Pac I; Site  
 1st strand cDNA was primed with a Pac I - oligo  
 15' AACGGAAGATTAATTAAGATCTTTTCTTTTCTTTT  
 double-stranded cDNA was ligated to Eco RI ada-  
 (Pharmacia), digested with Pac I and cloned in  
 and Eco RI sites of the modified pT7T3 vector.  
 went through one round of normalization. Libra-  
 constructed by Bento Soares and M.Fatima Bonali

## ORIGIN

Query Match 61.0%; Score 12.2; DB 14; Length 60;  
 Best Local Similarity 82.4%; Pred. No. 4.7e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 4 CTTGTCTCTCCACGGTTT 20

|||||  
 28 CTTGACCTCCAGGAGTT 12

## RESULT 31

AU014006

LOCUS

DEFINITION

AU014006 Schizosaccharomyces pombe late log phase cDNA

Schizosaccharomyces pombe cDNA clone spc08993, mRNA seq

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schizosaccharomyces pombe (fission yeast)

Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

1 (bases 1 to 37)

Morimyo, M. and Mita, K.

Identification of expressed sequence tags of Schizosaccl

pombe

Unpublished (1998)

ct: Mitsuoki Morimyo  
 ne Research Group  
 nal Institute of Radiological Sciences  
 Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
 l: morimyo@nirs.go.jp.  
 Location/Qualifiers  
 1. 37  
 /organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc08993"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA  
 sequences was not always from 5' to 3'. The cDNA data of  
 Schizosaccharomyces pombe are available for searching on  
 the World Wide Web. (URL, http://www.nirs.go.jp)"

60.0%; Score 12; DB 9; Length 37;  
 ilarity 75.0%; Pred. No. 5.1e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CTCTGTCTCCACGGGTT 20  
 |||||  
 ACTAGTGTCCAGGGGAT 28

4014  
 4014 Schizosaccharomyces pombe late log phase cDNA  
 Schizosaccharomyces pombe cDNA clone spc09002, mRNA sequence.  
 4014  
 4014.1 GI:3368805  
 Schizosaccharomyces pombe (fission yeast)  
 Schizosaccharomyces pombe  
 cyota; Fungi; Ascomycota; Schizosaccharomycetes;  
 Schizosaccharomycetales; Schizosaccharomycetaceae;  
 Schizosaccharomycetes.  
 bases 1 to 37)  
 Morimyo, M. and Mita, K.  
 Identification of expressed sequence tags of Schizosaccharomycetes  
 ublished (1998)  
 ct: Mitsuoki Morimyo  
 ne Research Group  
 nal Institute of Radiological Sciences  
 Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
 l: morimyo@nirs.go.jp.  
 Location/Qualifiers  
 1. 37  
 /organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc09002"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA  
 sequences was not always from 5' to 3'. The cDNA data of  
 Schizosaccharomyces pombe are available for searching on  
 the World Wide Web. (URL, http://www.nirs.go.jp)"

60.0%; Score 12; DB 9; Length 37;  
 ilarity 75.0%; Pred. No. 5.1e+05;

Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCTTGTCTCTCCACGGGTT 20  
 |||||  
 Db 9 ATACTAGTGTCTCCAGGGGAT 28

RESULT 33  
 AU014025  
 LOCUS  
 DEFINITION  
 AU014025 Schizosaccharomyces pombe late log phase cDNA  
 Schizosaccharomyces pombe cDNA clone spc09020, mRNA sequ  
 AU014025  
 AU014025.1 GI:3368816  
 EST.  
 Schizosaccharomyces pombe (fission yeast)  
 Schizosaccharomyces pombe  
 Schizosaccharomycetes;  
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 Schizosaccharomycetales; Schizosaccharomycetaceae;  
 Schizosaccharomycetes.  
 1 (bases 1 to 37)  
 Morimyo, M. and Mita, K.  
 Identification of expressed sequence tags of Schizosacch  
 pombe  
 ublished (1998)  
 Contact: Mitsuoki Morimyo  
 Genome Research Group  
 National Institute of Radiological Sciences  
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, J  
 Email: morimyo@nirs.go.jp.  
 Location/Qualifiers  
 1. 37  
 /organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc09020"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomyces pombe late log  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloni  
 into the SmaI site of M13mp19 DNA and the direc  
 sequences was not always from 5' to 3'. The cDN  
 Schizosaccharomyces pombe are available for sea  
 the World Wide Web. (URL, http://www.nirs.go.jp)

ORIGIN  
 Query Match 60.0%; Score 12; DB 9; Length 37;  
 Best Local Similarity 75.0%; Pred. No. 5.1e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCTTGTCTCTCCACGGGTT 20  
 |||||  
 Db 9 ATACTAGTGTCTCCAGGGGAT 28

RESULT 34  
 AU188695  
 LOCUS  
 DEFINITION  
 AU188695 46 bp mRNA linear EST  
 clone IMAGE:1723359 3' similar to TR:015304 015304 CD27B  
 sequence.  
 AU188695  
 AU188695.1 GI:3739904  
 EST.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom  
 1 (bases 1 to 46)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index

```

blished (1997)
act: Robert Strausberg, Ph.D.
l: cgapbs-remail.nih.gov
clone is available royalty-free through LNL; contact the
E Consortium (info@image.lnl.gov) for further information.
e considered overall poor quality
rt Length: 790 Std Error: 0.00
primer: -40UP from Gibco
quality sequence stop: 1.
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1723359"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placentae 8to9weeks_2NBHP8to9W"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

60.0%; Score 12; DB 9; Length 46;
ilarity 75.0%; Pred. No. 5.4e+05;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCTTGTCTCTCCACGGGTT 20
|||||
TCTTATCCACACGTGTT 30

30301 47 bp DNA linear GSS 17-DEC-2002
1_1_27_1_B01_1BL_x_1 3590 - RescueMu Grid M Zea mays genomic,
omic survey sequence.
30301
30301.1 GI:27215362
mays
mays
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
le; Panicoideae; Andropogoneae; Zea.
(bases 1 to 47)
ot,V.
ze genomic sequences found using engineered RescueMu transposon
blished (2001)
-act: Walbot V
artment of Biological Sciences
iford University
California Ave, Palo Alto, CA 94304, USA
: 650 723 2227
: 650 725 8221
il: walbot@stanford.edu
y probable ligation site of ends cut by single endonuclease.
erse complemented post-ligation sequence from source sequence.
te: 3590.1-27.1 column: 5
ss: transposon-tagged.
Location/Qualifiers
1..47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"

```

```

/tissue_type="leaf"
/dev_stage="adult"
/clone_lib="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered
pBlueScript backbone); Site 1: BamHI; Site 2: E
RescueMu is a 4.9 kb, modified maize Mu transp
designed to allow plasmid rescue from total ge
Mu elements insert preferentially into transcri
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the link
'RescueMu.' Grid M was grown at University of
2001. DNA was extracted from leaf punches, douk
using BamHI and BglII, and ligated to form circ
plasmids. DH10B cells were transformed and ther
on LB plates with ampicillin."

ORIGIN

Query Match 60.0%; Score 12; DB 28; Length 47;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCCTTGTCTCTCCACGGGTT 20
|||||
DB 29 ATCCTTGTCTCTCCACGGGTT 10
|||||

RESULT 36
CG710925
LOCUS 49 bp DNA linear GSS
DEFINITION 1119019D08.2EL_x1 1119 - RescueMu Grid AA Zea mays genom
survey sequence.
ACCESSION CG710925
VERSION CG710925.1 GI:37736831
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
Walbot V.
Maize genomic sequences found using engineered RescueMu
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endon
Reverse complemented post-ligation sequence from source
Plate: 1119019 row: 25
Class: transposon-tagged.
Location/Qualifiers
1..49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/clone_lib="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered
pBlueScript backbone); Site 1: BamHI; Site 2: E
RescueMu is a 4.9 kb, modified maize Mu transp
designed to allow plasmid rescue from total ge
Mu elements insert preferentially into transcri
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the link
'RescueMu.' Grid AA was grown at UC San Diego

```

was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

60.0%; Score 12; DB 29; Length 49;  
ilarity 75.0%; Pred. No. 5.5e+05;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CCTTGTCTCCACGGGTT 20  
|||||  
CATTGCTCGAGGACTT 37

33694 49 bp DNA linear GSS 03-APR-2001  
nodium chabaudi genome survey sequence, clone PC9h11.pit,  
nic survey sequence.

3694 GI:11140201  
genome survey sequence.  
nodium chabaudi  
nodium chabaudi  
ryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
cases 1 to 49)  
sen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D.,  
an, S., Phillips, R.S. and Turner, C.M.  
discovery in Plasmodium chabaudi by genome survey sequencing  
Biochem. Parasitol. 113 (2), 251-260 (2001)

2558

5179  
cases 1 to 49)

sen, C.S.

ct Submmission

itted (06-NOV-2000) Division of Infection & Immunity,  
arsity of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  
s 122 to 170 (QL to QR).

Location/Qualifiers

1. 49  
/organism="Plasmodium chabaudi"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:5825"  
/clone="PC9h11.pit"

60.0%; Score 12; DB 29; Length 49;  
ilarity 75.0%; Pred. No. 5.5e+05;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CCTTGTCTCCACGGGTT 20  
|||||  
CAGAGTACACACGGGTT 20

9714 51 bp mRNA linear EST 20-DEC-2001  
9c06.y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLONE ID:  
1075-3563 5', mRNA sequence.

9714

9714.1 GI:17962959

ine max (soybean)

ine max

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
ine.

bases 1 to 51)

maker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,  
na, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B.,  
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., H  
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Card  
McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp  
South Memorial Parkway Huntsville, AL 35801 For further  
call: (800)-533-4363 or contact: ccu@resgen.com web site

www.resgen.com

Putative full length read

vector to vector length is 52

Seq primer: -40RP from Gibco.

Location/Qualifiers

source

1. 51  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="SOYBEAN CLONE ID: Gm-cl075-3563"  
/tissue\_type="differentiating somatic embryos c  
MSM6AC"

/lab host="DH10B"

/clone lib="Gm-cl075"

/note="Vector: pBluescript II SK+; Site 1: EcoR  
XhoI; The cDNA library was constructed from mRN  
from differentiating somatic embryos cultured

The library was prepared using the Stratagene  
II SK(+) library construction kit. Complementary  
synthesized from mRNA using a primer consisting

poly(GT) sequence with an XhoI restriction sit  
adaptors were ligated to the blunt-ended cDNA  
followed by XhoI digestion. The cDNA fragments  
directionally cloned into the EcoRI-XhoI restr

of the pBluescript vector. The ligated cDNA fr  
were transformed into E.coli ElectroMax DH10B h  
tissue culture and library construction were pe

Francoise Thibaud-Nissen and Anu Khana (Lila Vo  
University of Illinois)."

ORIGIN

Query Match 60.0%; Score 12; DB 12; Length 51;  
Best Local Similarity 75.0%; Pred. No. 5.5e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCCTTGTCTCCACGGGTT 20

|||||

Db 31 ATATTTTCTCAATGGGTT 12

RESULT 39

CB225675/c

LOCUS

DEFINITION CB225675 52 bp mRNA linear EST  
1RT19B10 Bos taurus Reticulum #1 library Bos taurus cDNA  
ribosomal protein L21 (EC 2.3.8.-) - GO terms: structura  
constituent of ribosome (0003735); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;

Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 52)  
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,  
Gordon, P.M.K. and Moore, S.S.

e Expression Profiling of the Bovine Gastrointestinal Tract  
 ublished (2002)  
 tact: Dr. Stephen Moore  
 f Genomics Laboratory  
 t of AFNS, University of Alberta  
 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 : 780 492 0369  
 : 780 492 4265  
 il: stephen.moore@ualberta.ca  
 ert Length: 52 Std Error: 0.00  
 YA=No.

## Location/Qualifiers

1. 52  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="Smooth muscle"  
 /cell\_type="Stratified squamous epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueWRF strain"  
 /clone\_lib="Bos taurus Reticulum #1 library"  
 /note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site\_1:  
 EcoRI; Site\_2: Xho I"

60.0%; Score 12; DB 14; Length 52;  
 nilarity 75.0%; Pred. No. 5.6e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCCTTGTCCTCCACGGGTT 20  
 |||||  
 TCATTTTCTTCACAGTT 2

10472 55 bp DNA linear GSS 01-APR-2003  
 1\_139\_1\_C11.1EL\_x\_1 3591 - RescueMu Grid P Zea mays genomic,  
 omic survey sequence.

10472  
 10472.1 GI:29455363

mays  
 mays

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 re; Panicoideae; Andropogoneae; Zea.  
 (bases 1 to 55)

ot,V.

ze genomic sequences found using engineered RescueMu transposon

ublished (2001)

-act: Walbot V

artment of Biological Sciences

ford University

California Ave, Palo Alto, CA 94304, USA

: 650 723 2227

: 650 723 8221

li: walbot@stanford.edu

y probable ligation site of ends cut by single endonuclease.

arse complemented post-ligation sequence from source sequence.

-e: 3591.1.139.1 row: 30

as: transposon-tagged:

Location/Qualifiers

1. 55

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="PH10B"

/clone\_lib="3591 - RescueMu Grid P"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site\_1: BamHI; Site\_2:  
 RescueMu is a 4.9 kb, modified maize Mu transp  
 designed to allow plasmid rescue from total ge  
 Mu elements insert preferentially into transcr  
 units. For more information on RescueMu, go to  
 site 'www.zmndb.iastate.edu' and follow the lin  
 'RescueMu.' Grid P was grown at Molokai in 200  
 extracted from leaf strips, double digested us  
 and BglII, and ligated to form circular plasm  
 cells were transformed and then screened on LB  
 ampicillin."

## ORIGIN

Query Match 60.0%; Score 12; DB 28; Length 55;  
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCCTTGTCCTCCACGGGTT 20

|||||

Db 1 ATCCTTTCTTCCTTCCTCCGTT 20

|||||

RESULT 41

BX661950

LOCUS

DEFINITION

BX661950 57 bp DNA linear GSS  
 Arabidopsis thaliana T-DNA flanking sequence GK-681H02-  
 genomic survey sequence.

ACCESSION

BX661950

VERSION

BX661950.1 GI:37618372

KEYWORDS

GSS

SOURCE

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr

Spermatophyta; Magnoliophyta; eudicotyledons; core eudi

rosids; eurosids II; Brassicales; Brassicaceae; Arabido

Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K.,

and Weisshaar,B.

A pipeline for automated high-throughput generation of

(flanking sequence tags) from Arabidopsis thaliana T-DN

transformed lines

Unpublished

REFERENCE

2

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and W

A new Arabidopsis thaliana T-DNA mutagenised population

for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 57)

Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.

Direct Submission

Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institi

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 5082

This sequence is recovered from the left border of the

indicates an insertion close to or within gene At3g0408

sequences are generated at the MPI for Plant Breeding R

the context of the GABI-Kat project. GABI-Kat is part o

Plant Genomics program designated 'GABI'. Information o

availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. 57

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-681H02-023045"

/note="PCR was performed on DNA from Arabidops

plants (T1) which were transformed with the T-I

vector pAC161. The lines contain one or more T

insertions. The DNA fragment(s) resulting from

were directly sequenced to determine the genom

flanking the insertion. Sequences displaying s

## FEATURES

source

similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

60.0%; Score 12; DB 29; Length 57;  
 ilarity 75.0%; Pred. No. 5.7e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 'CCTTGCTCTCCACGGGTT 20  
 |||||  
 'CCTCGCTTCTACTGGTT 54

3UMR 59 bp DNA linear GSS 01-SEP-2000  
 aodon nigroviridis genome survey sequence PUC-ORI end of clone  
 08 of library G from Tetraodon nigroviridis, genomic survey  
 ence.  
 1324  
 1324.1 GI:7982949  
 genome survey sequence.  
 aodon nigroviridis  
 aodon nigroviridis  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 notepygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 thomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 adontoidea; Tetraodontidae; Tetraodon.

t Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 ot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F.,  
 in, W., and Weissenbach, J.  
 mate of human gene number provided by genome-wide analysis  
 g Tetraodon nigroviridis DNA sequence  
 Genet. 25 (2), 235-238 (2000)  
 6633  
 5645

t Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,  
 mes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
 in, W., Bernot, A., and Weissenbach, J.  
 acterization and repeat analysis of the compact genome of the  
 water pufferfish Tetraodon nigroviridis  
 me Res. 10 (7), 939-949 (2000)

9337  
 9143  
 bases 1 to 59)  
 scope.  
 ct Submission  
 itted (12-APR-2000) Genoscope - Centre National de Sequencage :  
 91 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 b : www.genoscope.cns.fr)  
 e clone-end sequencing project of the Tetraodon nigroviridis  
 me. For more information, please take a look at  
 ://www.genoscope.cns.fr/Tetraodon.  
 Location/Qualifiers

1. .59  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="059G08"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : CORG059BD04SP1-end :  
 PUC-ORI"

60.0%; Score 12; DB 29; Length 59;  
 ilarity 75.0%; Pred. No. 5.7e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CCTTGCTCTCCACGGGTT 20

Db 57 ACCCTGGACCTCCACGGGCT 38

RESULT 43  
 CF296469/c  
 LOCUS  
 DEFINITION  
 30DGS--06-N14.g1 Rice leaf plasmid cDNA library I (30DG;  
 sativa cDNA clone 30DGS--06-N14, mRNA sequence.

ACCESSION  
 CF296469  
 VERSION  
 CF296469.1  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shi  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 COMMENT  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.;  
 of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bbnahm@bio.com, bbnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .60  
 Location/Qualifiers  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="30DGS--06-N14"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (3  
 /note="Vector: PCR4-TOBO; Site 1: EcoRI; mRNA w  
 with oligoribonucleotides and then used as temp  
 RT-PCR."

ORIGIN  
 Query Match 60.0%; Score 12; DB 14; Length 60;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;  
 Qy 1 ATCTCTGCTCTCCACGGGTT 20  
 |||||  
 Db 40 ATCTGCTACTCCATGGAT 21

RESULT 44  
 AZ650525  
 LOCUS  
 DEFINITION  
 IM0520F13R Mouse 10kb plasmid UUGCIM library Mus musculus  
 clone UUGCIM0520F13 R, genomic survey sequence.  
 ACCESSION  
 AZ650525  
 VERSION  
 AZ650525.1  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
 1 (bases 1 to 22)

REFERENCE  
 AUTHORS  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads fro  
 plasmid inserts

published (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 112, USA  
 t: 801 585 5606  
 f: 801 585 7177  
 e: rdunn@genetics.utah.edu  
 insert Length: 10000 Std Error: 0.00  
 size: 0520 row: F column: 13  
 primer: CACACAGGAACAGCTATGACC  
 as: plasmid ends  
 th quality sequence stop: 22.

Location/Qualifiers  
 1. 22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U061M0520F13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U061M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [gil4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid RL. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Similarity 59.0%; Score 11.8; DB 28; Length 22;  
 Similarity 86.7%; Pred. No. 5.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCCTTGCTCTCCAC 15  
 |||||  
 TCCTTGCTCTCCAC 20

99801 34 bp mRNA linear EST 05-JUN-1998  
 1c11.s1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1607924 3,  
 ilar to TR:Q28298 Q28298 RIBOSOME RECEPTOR. ; mRNA sequence.

99801 GI:3190356

sapiens (human)  
 sapiens  
 aryoata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 34)  
 -CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 or Gene Index  
 ublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 l: cgapps@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution infor  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

Location/Qualifiers  
 1. 34  
 source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1607924"  
 /sex="female, pooled"  
 /tissue\_type="breast"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Br2"  
 /note="Vector: PT73D-Pac (Pharmacia) with a  
 polylinker; 1st strand cDNA was prepared from  
 breast tumor tissue, and was then primed with  
 oligo(dt) primer. Double-stranded cDNA was lig  
 RI adaptors (Pharmacia), digested with Not I &  
 into the Not I and Eco RI sites of the modifie  
 vector. This library is the normalized versio  
 NCI CGAP Br1.1. Library was constructed by Ber  
 and M. Fatima Bonaldo."

## ORIGIN

Query Match 59.0%; Score 11.8; DB 9; Length 34;  
 Best Local Similarity 86.7%; Pred. No. 6.1e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACG 16  
 |||||  
 Db 9 TCCTTGCTCTCCACG 23

Search completed: February 29, 2004, 11:20:44  
 Job time : 1545.3 secs



1 09:38:22 2004

us-10-090-326-16.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

cleic search, using sw model

February 29, 2004, 08:42:24 ; Search time 561.974 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

US-10-090-326-16

18  
1 ctcatttgaatttgc 18

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl:\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pla.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_man.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Descript
C 1	14.8	82.2	52	6	AX802710	AX802710
C 2	14.8	82.2	52	6	AX803056	AX803056
C 3	14	77.8	20	6	AR299374	AR299374
C 4	13.4	74.4	17	6	AR039529	AR039529
C 5	13.4	74.4	21	6	BD223828	BD223828
C 6	13.4	74.4	21	6	BD223838	BD223838
C 7	13.2	73.3	30	6	AR088737	AR088737
C 8	13.2	73.3	30	6	AR095464	AR095464
C 9	13.2	73.3	30	6	AR112465	AR112465
C 10	13.2	73.3	30	6	BD070730	BD070730
C 11	13.2	73.3	30	6	BD070756	BD070756
C 12	13.2	73.3	43	6	AR218439	AR218439
C 13	13.2	73.3	43	6	AR308225	AR308225
C 14	13.2	73.3	53	6	AR360210	AR360210
C 15	13	72.2	24	6	AX487503	AX487503
C 16	13	72.2	25	6	AX115740	AX115740
C 17	13	72.2	50	6	AX165018	AX165018
C 18	13	72.2	51	6	AX115741	AX115741
C 19	13	72.2	51	6	AX203928	AX203928
C 20	12.8	71.1	17	6	AR143576	AR143576
C 21	12.8	71.1	17	6	AR142578	AR142578
C 22	12.8	71.1	17	6	E49169	E49169
C 23	12.8	71.1	17	6	E49171	E49171
C 24	12.8	71.1	19	6	AR212683	AR212683
C 25	12.8	71.1	21	6	AX802543	AX802543
C 26	12.8	71.1	21	6	AX803055	AX803055
C 27	12.8	71.1	21	6	AX803276	AX803276
C 28	12.8	71.1	22	6	AR152786	AR152786
C 29	12.8	71.1	22	6	AX460279	AX460279
C 30	12.8	71.1	22	6	BD134242	BD134242
C 31	12.8	71.1	29	6	BD107065	BD107065
C 32	12.8	71.1	30	6	E49553	E49553
C 33	12.8	71.1	30	6	AX791284	AX791284
C 34	12.8	71.1	30	6	AX792291	AX792291
C 35	12.8	71.1	30	6	BD000721	BD000721
C 36	12.8	71.1	30	6	BD176724	BD176724
C 37	12.8	71.1	44	6	A23713	A23713
C 38	12.8	71.1	51	6	AX161257	AX161257
C 39	12.8	71.1	51	6	AX161258	AX161258
C 40	12.8	71.1	51	6	AX199396	AX199396
C 41	12.8	71.1	60	6	AX612397	AX612397
C 42	12.4	68.9	17	6	AR039527	AR039527
C 43	12.4	68.9	17	6	AX722776	AX722776
C 44	12.4	68.9	27	6	AX197327	AX197327
C 45	12.4	68.9	30	6	AX791288	AX791288
C 46	12.4	68.9	30	6	AX792109	AX792109
C 47	12.4	68.9	30	6	AX792504	AX792504
C 48	12.4	68.9	30	6	AX792638	AX792638
C 49	12.4	68.9	36	6	BD187098	BD187098
C 50	12.4	68.9	36	6	BD187099	BD187099
C 51	12.4	68.9	41	6	AX515933	AX515933
C 52	12.4	68.9	41	6	AX517373	AX517373
C 53	12.4	68.9	60	6	AX612395	AX612395
C 54	12.4	68.9	60	6	AX612396	AX612396
C 55	12.2	67.8	17	6	BD258527	BD258527
C 56	12.2	67.8	20	6	AR158757	AR158757
C 57	12.2	67.8	20	6	AR158758	AR158758
C 58	12.2	67.8	20	6	AR158759	AR158759
C 59	12.2	67.8	20	6	AR158760	AR158760
C 60	12.2	67.8	20	6	BD182366	BD182366
C 61	12.2	67.8	22	6	AR275223	AR275223
C 62	12.2	67.8	22	6	AR339881	AR339881
C 63	12.2	67.8	34	6	AR093100	AR093100
C 64	12.2	67.8	34	6	BD009924	BD009924
C 65	12.2	67.8	36	6	AR026172	AR026172

67.8	36	6	AR026252	Sequence	AR026252	Sequence	C 139	11.6	64.4	30	6	E64516
67.8	36	6	AR026289	Sequence	AR026289	Sequence	C 140	11.6	64.4	36	6	AR031680
67.8	36	6	AR026293	Sequence	AR026293	Sequence	C 141	11.6	64.4	36	6	I90298
67.8	36	6	I82914	Sequence 16	I82914	Sequence 16	C 142	11.6	64.4	41	6	A10955
67.8	36	6	I82994	Sequence 96	I82994	Sequence 96	C 143	11.6	64.4	43	6	AX483395
67.8	36	6	I83031	Sequence 13	I83031	Sequence 13	C 144	11.6	64.4	46	5	XELBETA6
67.8	36	6	I83035	Sequence 13	I83035	Sequence 13	C 145	11.6	64.4	48	6	AR011223
67.8	36	6	AR431100	Sequence	AR431100	Sequence	C 146	11.6	64.4	48	6	I17861
67.8	36	6	AR431180	Sequence	AR431180	Sequence	C 147	11.6	64.4	50	6	AR103103
67.8	36	6	AR431217	Sequence	AR431217	Sequence	C 148	11.6	64.4	50	6	AR139719
67.8	36	6	AR431221	Sequence	AR431221	Sequence	C 149	11.6	64.4	50	6	AR169834
67.8	36	6	AX828893	Sequence	AX828893	Sequence	C 150	11.6	64.4	50	6	AR391898
67.8	36	6	AX828973	Sequence	AX828973	Sequence	C 151	11.6	64.4	50	6	AX161129
67.8	36	6	AX829010	Sequence	AX829010	Sequence	C 152	11.6	64.4	51	6	AX159880
67.8	36	6	AX829014	Sequence	AX829014	Sequence	C 153	11.6	64.4	51	6	AX161723
67.8	39	6	AX024135	Sequence	AX024135	Sequence	C 154	11.6	64.4	51	6	AX161724
67.8	40	6	AX695305	Sequence	AX695305	Sequence	C 155	11.6	64.4	51	6	AX161725
67.8	42	8	ATH521719	Sequence	ATH521719	Sequence	C 156	11.6	64.4	51	6	AX161727
67.8	43	6	AX683986	Sequence	AX683986	Sequence	C 157	11.6	64.4	52	6	AR360214
67.8	50	6	AX011756	Sequence	AX011756	Sequence	C 158	11.6	64.4	59	9	AB010679
67.8	50	6	I15869	Sequence 19	I15869	Sequence 19	C 159	11.4	63.3	15	6	BD235742
67.8	51	6	HUMFIRC	Human nucle	HUMFIRC	Human nucle	C 160	11.4	63.3	17	6	AX727163
67.8	51	6	AX159515	Sequence	AX159515	Sequence	C 161	11.4	63.3	17	6	AX739421
67.8	51	6	AX159516	Sequence	AX159516	Sequence	C 162	11.4	63.3	18	6	AR039705
67.8	58	3	DROPTIS7	Sequence	D12605 D. melanoga	Sequence	C 163	11.4	63.3	19	6	E51982
67.8	58	3	AR269015	Sequence	AR269015	Sequence	C 164	11.4	63.3	19	6	E51983
67.8	59	8	ATH52349	Sequence	ATH52349	Sequence	C 165	11.4	63.3	20	6	AR158761
67.8	60	6	AX269016	Sequence	AX269016	Sequence	C 166	11.4	63.3	20	6	AR158762
66.7	17	6	AR039531	Sequence	AR039531	Sequence	C 167	11.4	63.3	20	6	AR158763
66.7	22	6	AR307393	Sequence	AR307393	Sequence	C 168	11.4	63.3	20	6	AR158764
66.7	22	6	BD070842	Method to	BD070842	Method to	C 169	11.4	63.3	20	6	BD248791
66.7	36	6	AX183680	Sequence	AX183680	Sequence	C 170	11.4	63.3	20	6	AR257161
66.7	37	6	AX183678	Sequence	AX183678	Sequence	C 171	11.4	63.3	20	6	AR313819
66.7	53	6	AR356620	Sequence	AR356620	Sequence	C 172	11.4	63.3	21	6	A49119
65.6	17	6	AX673592	Sequence	AX673592	Sequence	C 173	11.4	63.3	21	6	AR298039
65.6	17	6	AX673601	Sequence	AX673601	Sequence	C 174	11.4	63.3	21	6	AX154108
65.6	17	6	AX732265	Sequence	AX732265	Sequence	C 175	11.4	63.3	22	6	E26542
65.6	17	6	AX760467	Sequence	AX760467	Sequence	C 176	11.4	63.3	23	6	AR049795
65.6	20	6	AX154268	Sequence	AX154268	Sequence	C 177	11.4	63.3	23	6	AR149689
65.6	20	6	E32854	Sequence	E32854	Sequence	C 178	11.4	63.3	23	6	AR404818
65.6	21	6	A91603	Sequence 13	E32854 GidA1. 1/20	Sequence 13	C 179	11.4	63.3	24	6	AX488314
65.6	21	6	AX096796	Sequence	A91603	Sequence	C 180	11.4	63.3	25	6	AR287646
65.6	21	6	BD023385	Method fo	AX096796	Method fo	C 181	11.4	63.3	25	6	AX114999
65.6	22	8	ATH520143	Sequence	BD023385	Sequence	C 182	11.4	63.3	25	6	AX197276
65.6	27	6	AR178597	Sequence	ATH520143	Sequence	C 183	11.4	63.3	25	6	AX15476
65.6	27	6	AX117650	Sequence	AJ520143	Sequence	C 184	11.4	63.3	25	6	BD133804
65.6	27	6	AX742001	Sequence	AR178597	Sequence	C 185	11.4	63.3	29	6	AX163906
65.6	27	6	AX742002	Sequence	AX117650	Sequence	C 186	11.4	63.3	29	6	AX163914
65.6	27	6	AX742003	Sequence	AX742001	Sequence	C 187	11.4	63.3	29	6	AX163928
65.6	31	6	AX236643	Sequence	AX742002	Sequence	C 188	11.4	63.3	30	6	A23714
65.6	38	6	AX236643	Sequence	AX236643	Sequence	C 189	11.4	63.3	30	6	A23715
65.6	38	6	AX222780	Sequence	AX236643	Sequence	C 190	11.4	63.3	30	6	AR122678
65.6	38	6	AX424219	Sequence	AX222780	Sequence	C 191	11.4	63.3	30	6	AX766990
65.6	38	6	AX581545	Sequence	AX424219	Sequence	C 192	11.4	63.3	30	6	AX792262
65.6	51	6	AX160341	Sequence	AX581545	Sequence	C 193	11.4	63.3	30	6	AX792836
65.6	51	6	AX160342	Sequence	AX160341	Sequence	C 194	11.4	63.3	30	6	BD000562
65.6	51	6	AX160343	Sequence	AX160342	Sequence	C 195	11.4	63.3	31	6	E48925
65.6	51	6	AX160345	Sequence	AX160343	Sequence	C 196	11.4	63.3	31	6	E48925
65.6	51	6	AX160346	Sequence	AX160345	Sequence	C 197	11.4	63.3	31	6	BD094837
65.6	55	6	I22466	Sequence 15	AX160346	Sequence	C 198	11.4	63.3	35	6	AR083987
65.6	55	6	I45542	Sequence 15	AX164861	Sequence	C 199	11.4	63.3	35	6	AX521778
65.6	59	8	ATH522061	Sequence	I22466	Sequence	C 200	11.4	63.3	36	6	AX411833
64.4	20	6	BD090250	Sequence	I45542	Sequence	C 201	11.4	63.3	36	6	AX058129
64.4	20	6	BD176328	A method	AJ522061	Arabidops	C 202	11.4	63.3	37	6	BD131641
64.4	23	6	AX802019	Sequence	BD090250	A method	C 203	11.4	63.3	38	6	AR118806
64.4	24	6	AX164280	Sequence	BD176328	A method	C 204	11.4	63.3	38	6	AX766976
64.4	24	6	AX555508	Sequence	AX802019	Sequence	C 205	11.4	63.3	38	8	AJ595611
64.4	24	6	BD012870	Sequence	AX164280	Sequence	C 206	11.4	63.3	41	6	A42975
64.4	25	6	AX467435	Sequence	AX555508	Sequence	C 207	11.4	63.3	41	6	A45521
64.4	25	6	AX487091	Sequence	BD012870	Nucleus 1	C 208	11.4	63.3	41	6	AR030793
64.4	28	6	AX554106	Sequence	AX467435	Sequence	C 209	11.4	63.3	41	6	AR082130
					AX487091	Sequence	C 210	11.4	63.3	41	6	AX516624
					AX554106	Sequence	C 211	11.4	63.3	41	6	AX518795
							C 211	11.4	63.3	42	6	A97026

63.3	42	6	A97032	A97032 Sequence 9	C 285	11.2	62.2	40	6	BD177307	BD177307
63.3	42	6	AR166711	AR166711 Sequence	C 286	11.2	62.2	40	8	ATH529715	AJ529715
63.3	42	6	BD086303	BD086303 CD8 as ce	C 287	11.2	62.2	41	6	AR003331	AR003331
63.3	42	6	BD086309	BD086309 CD8 as ce	C 288	11.2	62.2	41	6	AR109119	AR109119
63.3	43	6	AX484594	AX484594 Sequence	C 289	11.2	62.2	41	6	AR200774	AR200774
63.3	43	6	AR289704	AR289704 Sequence	C 290	11.2	62.2	42	6	AR009122	AR009122
63.3	47	6	AR290479	AR290479 Sequence	C 291	11.2	62.2	42	6	AR028096	AR028096
63.3	47	6	AX194770	AX194770 Sequence	C 292	11.2	62.2	42	6	AR031539	AR031539
63.3	48	10	MMCRV83	X79969 M.musculus	C 293	11.2	62.2	42	6	AR052833	AR052833
63.3	51	6	AX115477	AX115477 Sequence	C 294	11.2	62.2	42	6	AR127985	AR127985
63.3	51	6	AX203929	AX203929 Sequence	C 295	11.2	62.2	42	6	AR175210	AR175210
63.3	53	8	AJ589857	AJ589857 Arabidops	C 296	11.2	62.2	42	6	AR267930	AR267930
63.3	56	12	SYNCRPBSA	M33417 Synthetic E	C 297	11.2	62.2	42	6	AR288145	AR288145
63.3	56	12	SYNCRPBSA	M33417 Synthetic E	C 298	11.2	62.2	42	6	AR302754	AR302754
63.3	60	9	S72312	S72312 phosphofruct	C 299	11.2	62.2	42	6	AR408330	AR408330
62.2	17	6	AR142560	AR142560 Sequence	C 300	11.2	62.2	42	6	AX068052	AX068052
62.2	17	6	AR142562	AR142562 Sequence	C 301	11.2	62.2	42	6	AX078773	AX078773
62.2	17	6	AR142572	AR142572 Sequence	C 302	11.2	62.2	42	6	AX328126	AX328126
62.2	17	6	AR142574	AR142574 Sequence	C 303	11.2	62.2	42	6	AX589713	AX589713
62.2	17	6	AR142577	AR142577 Sequence	C 304	11.2	62.2	42	6	AX703578	AX703578
62.2	17	6	AR142579	AR142579 Sequence	C 305	11.2	62.2	42	6	AX838876	AX838876
62.2	17	6	BD258528	BD258528 Regulatio	C 306	11.2	62.2	42	8	AJ587913	AJ587913
62.2	17	6	E49153	E49153 Coccidiosis	C 307	11.2	62.2	44	6	AX463220	AX463220
62.2	17	6	E49155	E49155 Coccidiosis	C 308	11.2	62.2	45	6	AR003330	AR003330
62.2	17	6	E49165	E49165 Coccidiosis	C 309	11.2	62.2	47	6	AR284609	AR284609
62.2	17	6	E49167	E49167 Coccidiosis	C 310	11.2	62.2	47	6	AR284748	AR284748
62.2	17	6	E49170	E49170 Coccidiosis	C 311	11.2	62.2	47	6	AR288602	AR288602
62.2	17	6	E49172	E49172 Coccidiosis	C 312	11.2	62.2	47	6	AR289172	AR289172
62.2	17	6	AR188289	AR188289 Sequence	C 313	11.2	62.2	47	6	AR289329	AR289329
62.2	17	6	AR324142	AR324142 Sequence	C 314	11.2	62.2	47	6	AR289765	AR289765
62.2	17	6	AR328768	AR328768 Sequence	C 315	11.2	62.2	47	6	AR290560	AR290560
62.2	18	6	AR098820	AR098820 Sequence	C 316	11.2	62.2	47	6	AR291008	AR291008
62.2	20	6	AR073972	AR073972 Sequence	C 317	11.2	62.2	47	6	AR291110	AR291110
62.2	20	6	AR158756	AR158756 Sequence	C 318	11.2	62.2	47	6	AR291135	AR291135
62.2	20	6	AR215996	AR215996 Sequence	C 319	11.2	62.2	47	6	AX463213	AX463213
62.2	20	6	AR262268	AR262268 Sequence	C 320	11.2	62.2	48	6	BD002301	BD002301
62.2	20	6	AR275220	AR275220 Sequence	C 321	11.2	62.2	51	6	AX158257	AX158257
62.2	20	6	AR316186	AR316186 Sequence	C 322	11.2	62.2	51	6	AX160095	AX160095
62.2	20	6	AR339878	AR339878 Sequence	C 323	11.2	62.2	51	6	AX160096	AX160096
62.2	20	6	BD090197	BD090197 A method	C 324	11.2	62.2	51	6	AX160259	AX160259
62.2	20	6	BD176275	BD176275 A method	C 325	11.2	62.2	51	6	AX193395	AX193395
62.2	22	6	A99112	A99112 Sequence 16	C 326	11.2	62.2	51	6	AX204267	AX204267
62.2	22	6	BD074921	BD074921 Peroxisom	C 327	11.2	62.2	56	4	AY240935	AY240935
62.2	24	6	AR271760	AR271760 Sequence	C 328	11.2	62.2	56	4	AY240936	AY240936
62.2	28	6	I49813	I49813 Sequence 37	C 329	11.2	62.2	59	6	AX011428	AX011428
62.2	29	6	BD253026	BD253026 Regulatio	C 330	11.2	62.2	59	6	BD225719	BD225719
62.2	29	6	BD253505	BD253505 Regulatio	C 331	11.2	62.2	60	6	AR098097	AR098097
62.2	29	6	BD258156	BD258156 Regulatio	C 332	11.2	62.2	60	6	AX612338	AX612338
62.2	29	6	AX328910	AX328910 Sequence	C 333	11.2	62.2	60	6	AR174176	AR174176
62.2	29	6	AX339538	AX339538 Sequence	C 334	11.2	62.2	60	6	AR039533	AR039533
62.2	29	6	AX350086	AX350086 Sequence	C 335	11.2	62.2	60	6	AX496095	AX496095
62.2	29	6	BD197148	BD197148 Method an	C 336	11.2	62.2	60	6	DOGP40001	DOGP40001
62.2	29	6	AR055772	AR055772 Homo sapi	C 337	11.2	62.2	60	6	E09057	E09057
62.2	30	6	E49556	E49556 Glucose deh	C 338	11.2	62.2	60	6	AX587381	AX587381
62.2	30	6	AX063325	AX063325 Sequence	C 339	11.2	62.2	60	6	BD089304	BD089304
62.2	30	6	BD000724	BD000724 Process f	C 340	11.2	62.2	60	6	BD090148	BD090148
62.2	31	6	AR145957	AR145957 Sequence	C 341	11.2	62.2	60	6	BD176226	BD176226
62.2	31	6	AR180848	AR180848 Sequence	C 342	11.2	62.2	60	6	AX020516	AX020516
62.2	34	6	AR089708	AR089708 Sequence	C 343	11.2	62.2	60	6	AR048837	AR048837
62.2	35	8	AJ596491	AJ596491 Arabidops	C 344	11.2	62.2	60	6	AR050432	AR050432
62.2	37	6	AR360598	AR360598 Sequence	C 345	11.2	62.2	60	6	AR203958	AR203958
62.2	38	6	AR046040	AR046040 Sequence	C 346	11.2	62.2	60	6	E64771	E64771
62.2	38	6	AR046198	AR046198 Sequence	C 347	11.2	62.2	60	6	AR427849	AR427849
62.2	38	6	AR047279	AR047279 Sequence	C 348	11.2	62.2	60	6	AX711391	AX711391
62.2	38	6	I53092	I53092 Sequence 83	C 349	11.2	62.2	60	6	ATH526504	ATH526504
62.2	38	6	I53250	I53250 Sequence 99	C 350	11.2	62.2	60	6	BD176716	BD176716
62.2	38	6	I54331	I54331 Sequence 20	C 351	11.2	62.2	60	6	E31439	E31439
62.2	38	6	AX218648	AX218648 Sequence	C 352	11.2	62.2	60	6	BD144785	BD144785
62.2	38	6	AX219812	AX219812 Sequence	C 353	11.2	62.2	60	6	AR037057	AR037057
62.2	38	6	AX424934	AX424934 Sequence	C 354	11.2	62.2	60	6	AR272284	AR272284
62.2	38	6	AX580554	AX580554 Sequence	C 355	11.2	62.2	60	6	AR288719	AR288719
62.2	38	6	AJ529728	AJ529728 Arabidops	C 356	11.2	62.2	60	6	AR289989	AR289989
62.2	40	6	I30557	I30557 Sequence 5	C 357	11.2	62.2	60	6	AX378238	AX378238

61.1	48	6	AX236719	Sequence	431	10.8	60.0	27	6	AX349861	AX349861
61.1	51	6	AX159813	Sequence	432	10.8	60.0	27	6	AX402782	AX402782
61.1	51	6	AX159814	Sequence	433	10.8	60.0	27	6	BD093331	BD093331
61.1	51	6	AX160334	Sequence	C 434	10.8	60.0	28	6	AX383898	AX383898
61.1	51	6	AX160930	Sequence	435	10.8	60.0	28	6	BD094261	BD094261
61.1	54	6	AX355589	Sequence	436	10.8	60.0	29	6	AR118023	AR118023
60.0	17	6	BD241483	Sequence	C 437	10.8	60.0	29	6	I13961	I13961
60.0	17	6	BD258529	Regulation	C 438	10.8	60.0	29	6	AR274501	AR274501
60.0	17	6	AR188288	Sequence	C 439	10.8	60.0	29	6	AX183968	AX183968
60.0	17	6	AR190627	Sequence	C 440	10.8	60.0	29	6	BD132548	BD132548
60.0	17	6	AR190628	Sequence	441	10.8	60.0	30	6	AR241590	AR241590
60.0	17	6	AR324141	Sequence	442	10.8	60.0	30	6	AR254546	AR254546
60.0	17	6	AR325550	Sequence	443	10.8	60.0	30	6	AX790893	AX790893
60.0	17	6	AR325551	Sequence	444	10.8	60.0	30	6	AX791133	AX791133
60.0	17	6	AX733501	Sequence	445	10.8	60.0	30	6	AX791941	AX791941
60.0	17	6	AX738060	Sequence	446	10.8	60.0	30	6	AX791942	AX791942
60.0	17	6	AX759529	Sequence	C 447	10.8	60.0	30	6	AX792274	AX792274
60.0	17	6	AX762675	Sequence	448	10.8	60.0	30	6	AX792408	AX792408
60.0	17	6	BD201687	Method an	449	10.8	60.0	30	6	AX792962	AX792962
60.0	17	6	BD201688	Method an	C 450	10.8	60.0	30	6	AX793057	AX793057
60.0	17	6	BD201689	Method an	C 451	10.8	60.0	30	6	AX793237	AX793237
60.0	18	6	AR93350	Sequence 14	452	10.8	60.0	30	6	AX793472	AX793472
60.0	18	6	AR016620	Sequence	C 453	10.8	60.0	30	6	AX793498	AX793498
60.0	18	6	I68607	Sequence 36	454	10.8	60.0	30	6	AX793605	AX793605
60.0	18	6	I85514	Sequence 36	C 455	10.8	60.0	30	6	BD016378	BD016378
60.0	18	6	AR181133	Sequence	456	10.8	60.0	30	6	BD211612	BD211612
60.0	18	6	AR181154	Sequence	C 457	10.8	60.0	31	6	AR222852	AR222852
60.0	18	6	AX119348	Sequence	C 458	10.8	60.0	31	6	AX137110	AX137110
60.0	18	6	AX119361	Sequence	C 459	10.8	60.0	32	6	AX452020	AX452020
60.0	18	6	BD066863	An antise	C 460	10.8	60.0	32	6	AX538809	AX538809
60.0	19	6	AX060748	Sequence	461	10.8	60.0	32	6	BD009811	BD009811
60.0	19	6	AX060927	Sequence	462	10.8	60.0	33	6	BD261380	BD261380
60.0	20	6	AR066943	Sequence	463	10.8	60.0	33	6	AR368996	AR368996
60.0	20	6	AR159096	Sequence	464	10.8	60.0	33	6	AX350102	AX350102
60.0	20	6	AR159097	Sequence	465	10.8	60.0	33	6	BD011028	BD011028
60.0	20	6	AR159098	Sequence	466	10.8	60.0	35	6	AR049421	AR049421
60.0	20	6	AR159099	Sequence	C 467	10.8	60.0	35	6	I86673	I86673
60.0	20	6	AR159100	Sequence	C 468	10.8	60.0	35	11	C75880	C75880
60.0	20	6	AR159101	Sequence	C 469	10.8	60.0	36	6	AR075056	AR075056
60.0	20	6	AR159102	Sequence	C 470	10.8	60.0	36	6	AR141874	AR141874
60.0	20	6	AR266137	Sequence	C 471	10.8	60.0	37	6	AR219999	AR219999
60.0	20	6	AR305377	Sequence	C 472	10.8	60.0	37	6	AR220716	AR220716
60.0	20	6	AR309481	Sequence	C 473	10.8	60.0	37	6	AX683735	AX683735
60.0	20	6	AR313467	Sequence	C 474	10.8	60.0	37	6	BD137085	BD137085
60.0	20	6	AR359572	Sequence	C 475	10.8	60.0	38	6	AR045648	AR045648
60.0	20	6	AR371915	Sequence	C 476	10.8	60.0	38	6	AR046695	AR046695
60.0	20	6	AX057892	Sequence	C 477	10.8	60.0	38	6	I52700	I52700
60.0	20	6	AX802817	Sequence	C 478	10.8	60.0	38	6	I53747	I53747
60.0	20	6	BD106288	Novel LDL	C 479	10.8	60.0	38	6	AR330030	AR330030
60.0	21	6	AR297838	Sequence	C 480	10.8	60.0	38	6	AR331643	AR331643
60.0	21	6	AX059443	Sequence	C 481	10.8	60.0	38	6	AR335878	AR335878
60.0	21	6	BD105567	Estrogen	C 482	10.8	60.0	38	6	AX218749	AX218749
60.0	21	8	AF501764	Arabidops	C 483	10.8	60.0	38	6	AX228358	AX228358
60.0	22	6	I12740	Sequence 38	C 484	10.8	60.0	38	6	AX228503	AX228503
60.0	22	6	AX553627	Sequence	C 485	10.8	60.0	39	6	AX273352	AX273352
60.0	22	6	BD089361	Sequence	486	10.8	60.0	40	6	AX554068	AX554068
60.0	22	12	AB068996	Synthetic	C 487	10.8	60.0	41	6	AX514825	AX514825
60.0	23	6	AX117406	Method	C 488	10.8	60.0	41	6	AX516305	AX516305
60.0	24	6	E30987	Hyaluronic	C 489	10.8	60.0	41	6	AX516978	AX516978
60.0	24	6	I12739	Sequence 37	490	10.8	60.0	41	6	AX518092	AX518092
60.0	24	6	AX455497	Sequence	491	10.8	60.0	41	6	AX518701	AX518701
60.0	25	6	AR049778	Sequence	492	10.8	60.0	41	6	AX518452	AX518452
60.0	25	6	AR149672	Sequence	493	10.8	60.0	41	6	AX519489	AX519489
60.0	25	6	AR182666	Sequence	494	10.8	60.0	41	6	AX519489	AX519489
60.0	25	6	AR404801	Sequence	C 495	10.8	60.0	42	6	AX253580	AX253580
60.0	25	6	AX207466	Sequence	496	10.8	60.0	44	6	AX826942	AX826942
60.0	26	6	AX697976	Sequence	497	10.8	60.0	45	6	AR066029	AR066029
60.0	26	6	AX003453	Sequence	C 498	10.8	60.0	45	6	BD237155	BD237155
60.0	26	6	BD087069	Erythrovi	C 499	10.8	60.0	45	6	I28424	I28424
60.0	27	6	AR044530	Sequence	500	10.8	60.0	45	6	AR302918	AR302918
60.0	27	6	E49888	Analysis me	C 501	10.8	60.0	45	6	AR410149	AR410149
60.0	27	6	AR189817	Sequence	502	10.8	60.0	47	6	AR284621	AR284621
60.0	27	6	AR370335	Sequence	503	10.8	60.0				

60.0	47	6	AR288536	AR288536 Sequence	C 577	10.6	58.9	25	6	AX609052
60.0	47	6	AR288782	AR288782 Sequence	C 578	10.6	58.9	26	6	E15564
60.0	47	6	AR289922	AR289922 Sequence	C 579	10.6	58.9	26	6	AR240238
60.0	47	6	AR291477	AR291477 Sequence	C 580	10.6	58.9	26	6	BD143552
60.0	47	6	AX040147	AX040147 Sequence	C 581	10.6	58.9	26	6	BD167781
60.0	49	6	E15442	E15442 PCR primer	C 582	10.6	58.9	27	6	AR184983
60.0	49	8	AJ595839	AJ595839 Arabidops	C 583	10.6	58.9	27	6	AR189066
60.0	50	6	AR282093	AR282093 Sequence	C 584	10.6	58.9	27	6	AR191151
60.0	50	6	AR282197	AR282197 Sequence	C 585	10.6	58.9	27	6	AR402596
60.0	50	6	AR356357	AR356357 Sequence	C 586	10.6	58.9	27	6	BD068096
60.0	50	9	HSTFE31AS	X84970 H.sapiens t	C 587	10.6	58.9	27	11	EX295821
60.0	51	6	AX159208	AX159208 Sequence	C 588	10.6	58.9	28	6	AR090169
60.0	51	6	AX160260	AX160260 Sequence	C 589	10.6	58.9	28	6	AR197204
60.0	51	6	AX160750	AX160750 Sequence	C 590	10.6	58.9	28	6	AR259358
60.0	51	6	AX165498	AX165498 Sequence	C 591	10.6	58.9	28	6	BD012175
60.0	51	6	AX165640	AX165640 Sequence	C 592	10.6	58.9	28	6	BD012175
60.0	51	6	AX204272	AX204272 Sequence	C 593	10.6	58.9	28	12	SYNANVAX
60.0	51	10	D85557	D85557 Rattus norv	C 594	10.6	58.9	30	6	AR126679
60.0	52	14	ADY1TR	M17114 Avian egg d	C 595	10.6	58.9	30	6	AR162856
60.0	54	8	AY201320	AY201320 Arabidops	C 596	10.6	58.9	30	6	I74339
60.0	57	6	AR355550	AR355550 Sequence	C 597	10.6	58.9	30	6	AR302243
60.0	57	8	ATH530139	ATH530139 Arabidops	C 598	10.6	58.9	30	6	AX080326
60.0	57	8	ATH530157	ATH530157 Arabidops	C 599	10.6	58.9	30	6	AX793051
60.0	58	6	I80917	I80917 Sequence 3	C 600	10.6	58.9	30	6	AX793651
60.0	59	1	HEA38NU2	M33439 H.influenza	C 601	10.6	58.9	30	6	BD000563
60.0	59	6	AR023542	AR023542 Sequence	C 602	10.6	58.9	30	6	BD190380
60.0	59	6	AR023543	AR023543 Sequence	C 603	10.6	58.9	31	6	BD002344
60.0	59	6	AR082650	AR082650 Sequence	C 604	10.6	58.9	31	6	BD082896
60.0	59	6	AR082651	AR082651 Sequence	C 605	10.6	58.9	31	6	BD160819
60.0	59	6	AR156177	AR156177 Sequence	C 606	10.6	58.9	32	6	AR090186
60.0	59	6	AR156178	AR156178 Sequence	C 607	10.6	58.9	32	6	AR090186
60.0	59	6	AR381059	AR381059 Sequence	C 608	10.6	58.9	32	6	AR197221
60.0	59	6	AR381060	AR381060 Sequence	C 609	10.6	58.9	32	6	AR197223
60.0	59	6	AR183563	AR183563 Sequence	C 610	10.6	58.9	32	6	AR259375
60.0	59	8	ATH52896S	AJ52896S Arabidops	C 611	10.6	58.9	32	6	AR259377
60.0	60	6	AR221653	AR221653 Sequence	C 612	10.6	58.9	32	6	AR262196
60.0	60	6	BD022884	BD022884 Vascular	C 613	10.6	58.9	33	6	AR022055
58.9	17	6	AR039381	AR039381 Sequence	C 614	10.6	58.9	33	6	AR095481
58.9	17	6	BD256711	BD256711 Regulatio	C 615	10.6	58.9	33	6	I92845
58.9	19	6	AR295557	AR295557 Sequence	C 616	10.6	58.9	33	6	AR203899
58.9	19	6	AR295603	AR295603 Sequence	C 617	10.6	58.9	33	6	AX062285
58.9	19	6	AX699172	AX699172 Sequence	C 618	10.6	58.9	33	6	BD078599
58.9	20	6	AR062651	AR062651 Sequence	C 619	10.6	58.9	33	6	BD169044
58.9	20	6	AR104754	AR104754 Sequence	C 620	10.6	58.9	33	6	BD185507
58.9	20	6	AR105576	AR105576 Sequence	C 621	10.6	58.9	33	8	AJ590027
58.9	20	6	AR123103	AR123103 Sequence	C 622	10.6	58.9	35	6	AX825025
58.9	20	6	AR123238	AR123238 Sequence	C 623	10.6	58.9	35	6	AR026188
58.9	20	6	I20653	I20653 Sequence 51	C 624	10.6	58.9	35	6	AR026268
58.9	20	6	I33346	I33346 Sequence 51	C 625	10.6	58.9	35	6	I82930
58.9	20	6	AR294702	AR294702 Sequence	C 626	10.6	58.9	35	6	I83010
58.9	20	6	AR370576	AR370576 Sequence	C 627	10.6	58.9	35	6	AR431116
58.9	20	6	AX712122	AX712122 Sequence	C 628	10.6	58.9	35	6	AR431116
58.9	20	6	AX712124	AX712124 Sequence	C 629	10.6	58.9	35	6	AX685946
58.9	20	6	AX712137	AX712137 Sequence	C 630	10.6	58.9	35	6	AX828909
58.9	20	6	AX712138	AX712138 Sequence	C 631	10.6	58.9	35	6	AX828989
58.9	21	6	A76292	A76292 Sequence 15	C 632	10.6	58.9	35	11	C75722
58.9	21	6	AR293217	AR293217 Sequence	C 633	10.6	58.9	35	11	C75861
58.9	21	6	AX657324	AX657324 Sequence	C 634	10.6	58.9	35	11	C75889
58.9	21	6	BD061256	BD061256 A method	C 635	10.6	58.9	36	6	AR264637
58.9	22	6	AX014712	AX014712 Sequence	C 636	10.6	58.9	39	6	A00609
58.9	22	6	BD204638	BD204638 Novel mem	C 637	10.6	58.9	39	6	A00613
58.9	24	6	AR234729	AR234729 Sequence	C 638	10.6	58.9	40	6	A00610
58.9	24	6	AR381899	AR381899 Sequence	C 639	10.6	58.9	40	6	A00614
58.9	24	6	AR381891	AR381891 Sequence	C 640	10.6	58.9	41	6	A00611
58.9	24	6	AX001262	AX001262 Sequence	C 641	10.6	58.9	41	6	A00615
58.9	24	6	AX001264	AX001264 Sequence	C 642	10.6	58.9	41	6	AR036778
58.9	24	6	AX057416	AX057416 Sequence	C 643	10.6	58.9	41	6	AX515801
58.9	24	6	AX290524	AX290524 Sequence	C 644	10.6	58.9	41	6	AX518396
58.9	24	6	AX488231	AX488231 Sequence	C 645	10.6	58.9	42	6	AX520851
58.9	24	6	AX483338	AX483338 Sequence	C 646	10.6	58.9	42	6	A00612
58.9	25	6	BD245731	BD245731 Developme	C 647	10.6	58.9	43	6	A00616
58.9	25	6	AX370553	AX370553 Sequence	C 648	10.6	58.9	43	6	A00617
58.9	25	6	AX548337	AX548337 Sequence	C 649	10.6	58.9	43	6	A00618
					C 649	10.6	58.9	43	6	AR218440

58.9	43	6	AR218443	Sequence	723	10.4	57.8	17	6	AX649100
58.9	43	6	AR218446	Sequence	724	10.4	57.8	17	6	AX649101
58.9	43	6	AR218456	Sequence	c 725	10.4	57.8	17	6	AX674002
58.9	43	6	AR308226	Sequence	c 726	10.4	57.8	17	6	AX722741
58.9	43	6	AR308229	Sequence	c 727	10.4	57.8	17	6	AX761546
58.9	43	6	AR308232	Sequence	728	10.4	57.8	18	6	AR183142
58.9	43	6	AR308242	Sequence	729	10.4	57.8	18	6	AR203279
58.9	44	6	A00619	B.amyloliqu	730	10.4	57.8	18	6	AX277053
58.9	44	6	A00620	B.amyloliqu	731	10.4	57.8	18	6	AX599396
58.9	45	5	DOU16146	Discopyge o	732	10.4	57.8	18	6	AX796280
58.9	45	6	EL13951	PCR primer	c 733	10.4	57.8	18	6	AX796412
58.9	45	6	AR341050	Sequence	735	10.4	57.8	18	6	AX804444
58.9	45	6	AX362633	Sequence	736	10.4	57.8	18	6	AX823044
58.9	45	6	AX590407	Sequence	737	10.4	57.8	18	6	AX826684
58.9	45	6	AX590408	Sequence	738	10.4	57.8	19	6	E51984
58.9	45	6	AX743227	Sequence	c 739	10.4	57.8	19	6	AX082024
58.9	45	6	AX743228	Sequence	740	10.4	57.8	19	6	AX082025
58.9	47	6	BD063368	Streptoco	c 741	10.4	57.8	19	6	AX706732
58.9	47	6	AR284459	Sequence	742	10.4	57.8	19	6	AX706733
58.9	47	6	AR284650	Sequence	c 743	10.4	57.8	19	6	AX707662
58.9	47	6	AR288466	Sequence	c 744	10.4	57.8	19	6	AX707663
58.9	47	6	AR289844	Sequence	c 745	10.4	57.8	19	6	BD090367
58.9	47	6	AR292052	Sequence	746	10.4	57.8	19	6	BD176445
58.9	48	6	I68157	Sequence 1	747	10.4	57.8	20	6	A30627 S
58.9	49	6	AR076906	Sequence	748	10.4	57.8	20	6	AR076881
58.9	49	6	AR167297	Sequence	749	10.4	57.8	20	6	AR119536
58.9	49	6	AX147850	Sequence	750	10.4	57.8	20	6	AR131572
58.9	49	6	AX521899	Sequence	751	10.4	57.8	20	6	AR158765
58.9	50	3	GIAC260	STS of NotI	752	10.4	57.8	20	6	AR171017
58.9	51	6	AX018945	Sequence	753	10.4	57.8	20	6	AR173029
58.9	51	6	AX115789	Sequence	c 754	10.4	57.8	20	6	AR199506
58.9	51	6	AX159905	Sequence	c 755	10.4	57.8	20	6	AR200977
58.9	51	6	AX159906	Sequence	c 756	10.4	57.8	20	6	AR266147
58.9	51	6	AX189966	Sequence	c 757	10.4	57.8	20	6	AR294660
58.9	51	6	AX189967	Sequence	c 758	10.4	57.8	20	6	AR359331
58.9	51	6	BD136656	Productio	c 759	10.4	57.8	20	6	AX419728
58.9	52	6	AR103101	Sequence	c 760	10.4	57.8	20	6	AX709266
58.9	52	6	AR139717	Sequence	c 761	10.4	57.8	20	6	BD012430
58.9	52	6	AR169832	Sequence	762	10.4	57.8	20	6	BD012443
58.9	52	6	AR391896	Sequence	763	10.4	57.8	20	6	BD084990
58.9	53	6	AX772346	Sequence	764	10.4	57.8	21	6	BD217353
58.9	54	6	AR355847	Sequence	765	10.4	57.8	21	6	AR011691
58.9	56	6	I22465	Sequence 14	766	10.4	57.8	21	6	AR016876
58.9	56	6	I45541	Sequence 14	767	10.4	57.8	21	6	AR092291
58.9	58	6	A42262	Sequence 12	768	10.4	57.8	21	6	AR119508
58.9	58	6	AR127029	Sequence	769	10.4	57.8	21	6	AR122425
58.9	58	6	AR220033	Sequence	770	10.4	57.8	21	6	AR171012
58.9	58	6	AR221316	Sequence	c 771	10.4	57.8	21	6	I33065 Se
58.9	58	6	AR374621	Sequence	c 772	10.4	57.8	21	6	AR293906
58.9	58	6	AR408166	Sequence	c 773	10.4	57.8	21	6	AX096046
58.9	58	6	AX430050	Sequence	c 774	10.4	57.8	21	6	AX539336
58.9	60	6	AR068210	Sequence	c 775	10.4	57.8	21	6	AX539337
58.9	60	6	AR076962	Sequence	c 776	10.4	57.8	21	6	AX706612
58.9	60	6	AR078795	Sequence	c 777	10.4	57.8	21	6	AX706613
58.9	60	6	AX522702	Sequence	778	10.4	57.8	21	6	AX707542
58.9	60	10	MWV1817X3	M.musculus	779	10.4	57.8	21	6	AX707543
58.9	12	6	BD080345	Methods o	c 780	10.4	57.8	21	8	BD217325
58.9	16	6	BD178667	Gene pane	781	10.4	57.8	21	8	ACE391689
58.9	17	6	AR039543	Sequence	782	10.4	57.8	22	6	AR072076
58.9	17	6	AR039545	Sequence	783	10.4	57.8	22	6	EL3120
58.9	17	6	BD256410	Regulatio	c 784	10.4	57.8	22	6	E29768
58.9	17	6	BD256858	Regulatio	c 785	10.4	57.8	22	6	AX511797
58.9	17	6	AR211598	Sequence	c 786	10.4	57.8	23	6	A38741 Se
58.9	17	6	AX328767	Sequence	c 787	10.4	57.8	23	6	AR102155
58.9	17	6	AX214955	Sequence	c 788	10.4	57.8	23	6	I12757 Se
58.9	17	6	AX216792	Sequence	c 789	10.4	57.8	23	6	I44506 Se
58.9	17	6	AX217131	Sequence	c 790	10.4	57.8	23	6	AR262782
58.9	17	6	AX217132	Sequence	c 791	10.4	57.8	23	6	AX115347
58.9	17	6	AX649096	Sequence	c 792	10.4	57.8	24	6	A36683 Se
58.9	17	6	AX649097	Sequence	c 793	10.4	57.8	24	6	A37121 Se
58.9	17	6	AX649098	Sequence	c 794	10.4	57.8	24	6	A41635 Se
58.9	17	6	AX649099	Sequence	795	10.4	57.8	24	6	AR025277
58.9	17	6	AX649099	Sequence	795	10.4	57.8	24	6	AR118808

57.8	24	6	AR128109	AR128109 Sequence	869	10.4	57.8	32	6	AR070924	AR070924
57.8	24	6	I35661	I35661 Sequence 4	870	10.4	57.8	32	6	AR157623	AR157623
57.8	24	6	AR235474	AR235474 Sequence	c 871	10.4	57.8	32	6	AR222498	AR222498
57.8	24	6	AR371602	AR371602 Sequence	c 872	10.4	57.8	32	6	AX046589	AX046589
57.8	24	6	AX391905	AX391905 Sequence	c 873	10.4	57.8	32	6	AX592754	AX592754
57.8	24	6	AX402779	AX402779 Sequence	c 874	10.4	57.8	32	6	BD063738	BD063738
57.8	24	6	BD089752	BD089752 A Method	c 875	10.4	57.8	32	6	BD063741	BD063741
57.8	24	6	AF501806	AF501806 Arabidopsis	c 876	10.4	57.8	32	6	BD182854	BD182854
57.8	24	12	AB068071	AB068071 Synthetic	c 877	10.4	57.8	33	6	AR7346 Se	AR7346 Se
57.8	25	6	AR094168	AR094168 Sequence	c 878	10.4	57.8	33	6	AX7584	AX7584
57.8	25	6	AR103012	AR103012 Sequence	c 879	10.4	57.8	33	6	AX081587	AX081587
57.8	25	6	AR105296	AR105296 Sequence	c 880	10.4	57.8	33	6	AX236751	AX236751
57.8	25	6	I80853	I80853 Sequence 16	c 881	10.4	57.8	33	6	AX374768	AX374768
57.8	25	6	AX650600	AX650600 Sequence	c 882	10.4	57.8	34	6	AR095871	AR095871
57.8	25	6	AX650601	AX650601 Sequence	c 883	10.4	57.8	34	6	AR106608	AR106608
57.8	25	6	AX650602	AX650602 Sequence	c 884	10.4	57.8	34	6	AR167226	AR167226
57.8	25	6	AX650603	AX650603 Sequence	c 885	10.4	57.8	34	6	AR361060	AR361060
57.8	25	6	AX650604	AX650604 Sequence	c 886	10.4	57.8	34	6	AX300426	AX300426
57.8	25	6	AX650605	AX650605 Sequence	c 887	10.4	57.8	34	11	C75800	C75800 H
57.8	25	6	AX650606	AX650606 Sequence	c 888	10.4	57.8	35	6	AX554163	AX554163
57.8	25	6	AX650607	AX650607 Sequence	c 889	10.4	57.8	35	6	BD176894	BD176894
57.8	25	6	AX650608	AX650608 Sequence	c 890	10.4	57.8	35	8	ATH526177	ATH526177
57.8	25	6	AX650609	AX650609 Sequence	c 891	10.4	57.8	36	6	BD232130	BD232130
57.8	25	6	AX650610	AX650610 Sequence	c 892	10.4	57.8	36	6	BD232131	BD232131
57.8	25	6	AX650611	AX650611 Sequence	c 893	10.4	57.8	36	6	E63403 In	E63403 In
57.8	25	6	AX650612	AX650612 Sequence	c 894	10.4	57.8	36	6	E63404 In	E63404 In
57.8	25	6	AX650613	AX650613 Sequence	c 895	10.4	57.8	36	6	E63405 In	E63405 In
57.8	27	6	AR2208	AR2208 Sequence 29	c 896	10.4	57.8	36	6	E63406 In	E63406 In
57.8	27	6	AR030703	AR030703 Sequence	c 897	10.4	57.8	36	6	AR374966	AR374966
57.8	27	6	AR164391	AR164391 Sequence	c 898	10.4	57.8	36	6	AR374967	AR374967
57.8	27	6	AR189409	AR189409 Sequence	c 899	10.4	57.8	36	6	AR374968	AR374968
57.8	27	6	AX488253	AX488253 Sequence	c 900	10.4	57.8	36	6	AR374969	AR374969
57.8	27	6	AX56386	AX56386 Sequence	c 901	10.4	57.8	36	6	AX010044	AX010044
57.8	27	6	BD132646	BD132646 Methods a	c 902	10.4	57.8	36	6	AX010046	AX010046
57.8	28	6	AR053467	AR053467 Sequence	c 903	10.4	57.8	36	6	AX010143	AX010143
57.8	28	6	AX593089	AX593089 Sequence	c 904	10.4	57.8	36	6	AX010145	AX010145
57.8	28	6	AX601424	AX601424 Sequence	c 905	10.4	57.8	36	6	AX464458	AX464458
57.8	29	6	A30635	A30635 Synthetic H	c 906	10.4	57.8	36	6	BD016620	BD016620
57.8	29	6	A30637	A30637 Synthetic H	c 907	10.4	57.8	36	6	BD084651	BD084651
57.8	29	6	A30639	A30639 Synthetic H	c 908	10.4	57.8	36	6	BD188170	BD188170
57.8	29	6	BD263086	BD263086 Vector. 7	c 909	10.4	57.8	36	6	BD226740	BD226740
57.8	29	6	E08922	E08922 Synthetic n	c 910	10.4	57.8	36	6	BD226741	BD226741
57.8	29	6	I04725	I04725 Sequence 49	c 911	10.4	57.8	37	6	E54938	E54938 V1
57.8	29	6	AX025032	AX025032 Sequence	c 912	10.4	57.8	37	6	AR362820	AR362820
57.8	29	6	BD200431	BD200431 Method an	c 913	10.4	57.8	37	6	AX183711	AX183711
57.8	30	6	AR003553	AR003553 Sequence	c 914	10.4	57.8	38	6	AR030712	AR030712
57.8	30	6	AR028243	AR028243 Sequence	c 915	10.4	57.8	38	6	AR059775	AR059775
57.8	30	6	AR083986	AR083986 Sequence	c 916	10.4	57.8	38	6	AR118807	AR118807
57.8	30	6	AR138646	AR138646 Sequence	c 917	10.4	57.8	38	6	AR167893	AR167893
57.8	30	6	BD269462	BD269462 Mitomycin	c 918	10.4	57.8	38	6	BD231844	BD231844
57.8	30	6	AR224181	AR224181 Sequence	c 919	10.4	57.8	38	6	AR332329	AR332329
57.8	30	6	AR266946	AR266946 Sequence	c 920	10.4	57.8	38	6	AR336282	AR336282
57.8	30	6	AX793439	AX793439 Sequence	c 921	10.4	57.8	38	6	AX019814	AX019814
57.8	30	6	BD022939	BD022939 Species-s	c 922	10.4	57.8	39	11	AX3322709	AX3322709
57.8	30	6	BD134759	BD134759 Thermoana	c 923	10.4	57.8	40	6	BD261349	BD261349
57.8	30	6	BD166353	BD166353 Oxidoredu	c 924	10.4	57.8	40	6	AR255726	AR255726
57.8	31	6	AR003551	AR003551 Sequence	c 925	10.4	57.8	41	6	AX008602	AX008602
57.8	31	6	AR102074	AR102074 Sequence	c 926	10.4	57.8	41	6	AX513840	AX513840
57.8	31	6	AR106610	AR106610 Sequence	c 927	10.4	57.8	41	6	AX514110	AX514110
57.8	31	6	AR106612	AR106612 Sequence	c 928	10.4	57.8	41	6	AX514180	AX514180
57.8	31	6	AR119388	AR119388 Sequence	c 929	10.4	57.8	41	6	AX514285	AX514285
57.8	31	6	BD268005	BD268005 Stereose	c 930	10.4	57.8	41	6	AX514329	AX514329
57.8	31	6	E10072	E10072 Primer. 9/1	c 931	10.4	57.8	41	6	AX515192	AX515192
57.8	31	6	AR183128	AR183128 Sequence	c 932	10.4	57.8	41	6	AX515864	AX515864
57.8	31	6	AR203265	AR203265 Sequence	c 933	10.4	57.8	41	6	AX516156	AX516156
57.8	31	6	AR240730	AR240730 Sequence	c 934	10.4	57.8	41	6	AX517660	AX517660
57.8	31	6	AR257476	AR257476 Sequence	c 935	10.4	57.8	41	6	AX517716	AX517716
57.8	31	6	AX081611	AX081611 Sequence	c 936	10.4	57.8	41	6	AX518510	AX518510
57.8	31	6	AX277039	AX277039 Sequence	c 937	10.4	57.8	41	6	AX519896	AX519896
57.8	31	6	AX374792	AX374792 Sequence	c 938	10.4	57.8	41	6	AX520211	AX520211
57.8	31	6	BD022745	BD022745 Live Heli	c 939	10.4	57.8	41	6	AX520259	AX520259
57.8	31	6	BD063733	BD063733 Fibrobias	c 940	10.4	57.8	41	6	AX520467	AX520467
57.8	31	6	BD134757	BD134757 Thermoana	c 941	10.4	57.8	41	6	AX521121	AX521121

```

57.8 42 6 AR138258 Sequence
57.8 45 6 AX817936 Sequence
57.8 46 6 AR003554 Sequence
57.8 46 6 BD134760 Thermoana
57.8 46 6 BD210999 Regulated
57.8 47 6 AR288486 Sequence
57.8 47 6 AR288824 Sequence
57.8 47 6 AR288997 Sequence
57.8 47 6 AR289107 Sequence
57.8 47 6 AR291345 Sequence
57.8 47 6 AR291629 Sequence
57.8 47 6 AR291664 Sequence
57.8 47 6 AR291793 Sequence
57.8 47 6 AR291836 Sequence
57.8 48 6 AR429764 Sequence
57.8 48 6 AR429765 Sequence
57.8 48 6 AX701394 Sequence
57.8 49 6 AJ596684 Arabidops
57.8 50 6 I42242 Sequence 55
57.8 50 6 AR200395 Sequence
57.8 50 6 AR420668 Sequence
57.8 50 6 AR422001 Sequence
57.8 50 6 AX159876 Sequence
57.8 50 6 BD014187 Probe for
57.8 50 6 BD116221 EST and e
57.8 50 6 BD117554 EST and e
57.8 50 6 BD223995 Near infr
57.8 51 6 AX118445 Sequence
57.8 51 6 AX159875 Sequence
57.8 53 6 AR003552 Sequence
57.8 53 6 AX419861 Sequence
57.8 53 6 BD134758 Thermoana
57.8 56 6 AR357271 Sequence
57.8 56 8 AJ590829 Arabidops
57.8 57 6 AR200397 Sequence
57.8 57 6 AR370332 Sequence
57.8 57 6 BD223997 Near infr
57.8 58 8 AJ595433 Arabidops
57.8 59 6 BD263083 Vector. 7
57.8 59 6 AX025029 Sequence
57.8 59 6 AX916520 Sequence
57.8 59 6 BD052053 Sequence
57.8 60 8 ATH531112 Arabidops
57.8 60 8 ATH531161 Arabidops
56.7 15 6 AR056020 Sequence
56.7 15 6 AR056021 Sequence
56.7 15 6 AR113778 Sequence
56.7 15 6 AR113779 Sequence
56.7 15 6 AX633118 Sequence
56.7 15 6 AX633120 Sequence
56.7 16 8 ATH526313 Arabidops
56.7 16 8 ATH527078 Arabidops
56.7 16 8 ATH527140 Arabidops
56.7 17 6 BD254691 Regulatio
56.7 17 6 BD259667 Regulatio
56.7 17 6 I36898 Sequence 5
56.7 17 6 AR328769 Sequence
56.7 17 6 AX578370 Sequence
56.7 17 6 AX578927 Sequence

02710 52 bp DNA linear PAT 24-NOV-2003
uence 220 from Patent WO03057914.
02710
02710.1 GI:38501408
thetic construct
thetic construct

artificial sequences.
1
REFERENCE 1
AUTHORS Karlsten,F.
TITLE Method for detecting human papillomavirus mRNA
JOURNAL Patent: WO 03057914-A 220 17-JUL-2003;
NORCHIP A/S (NO)
FEATURES location/Qualifiers
source 1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HPV NASBA primer"

ORIGIN
Query Match 82.2%; Score 14.8; DB 6; Length 52;
Best Local Similarity 88.9%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18
Db 47 CTCATTGGGAATCGTGCC 30

RESULT 2
AX803056/c
LOCUS AX803056 52 bp DNA linear PAT
DEFINITION Sequence 88 from Patent WO03057927.
ACCESSION AX803056
VERSION AX803056.1 GI:38501721
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Karlsten,F.
TITLE Detection of human papillomavirus e6 mRNA
JOURNAL Patent: WO 03057927-A 88 17-JUL-2003;
NORCHIP A/S (NO)
FEATURES location/Qualifiers
source 1..52
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

ORIGIN
Query Match 82.2%; Score 14.8; DB 6; Length 52;
Best Local Similarity 88.9%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18
Db 47 CTCATTGGGAATCGTGCC 30

RESULT 3
AR299374
LOCUS AR299374 20 bp DNA linear PAT
DEFINITION Sequence 11109 from patent US 6537751.
ACCESSION AR299374
VERSION AR299374.1 GI:31686658
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high densit
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11109 25-MAR-2003;
FEATURES location/Qualifiers
source 1..20
/organism="unknown"

```



1 09:38:22 2004

us-10-090-326-16.max.rge

/mol\_type="genomic DNA"

77.8%; Score 14; DB 6; Length 20;  
nilarity 100.0%; Pred. No. 3.6e+04; Indels 0; Gaps 0;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGAATTTG 16  
|||||  
ATTGGAATTTG 16

39529 17 bp DNA linear PAT 29-SEP-1999  
ence 377 from patent US 5807743.  
19529  
19529.1 GI:5958892

own.  
own.  
assified.  
(bases 1 to 17)  
hcomb,D.T. and McSwiggen,J.A.  
rleukin-2 receptor gamma-chain ribozymes  
nt: US 5807743-A 377 15-SEP-1998;  
Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

74.4%; Score 13.4; DB 6; Length 17;  
nilarity 93.3%; Pred. No. 7.7e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CAATTGGAATTTT 15  
|||||  
CAATTGGAATTTT 17

3828 21 bp DNA linear PAT 17-JUL-2003  
tification of microorganism causing acute respiratory tract  
ction (ARI).

3828  
3828.1 GI:33033598  
002526088-A/3.  
hctic construct  
hctic construct  
ficial sequences.  
bases 1 to 21)  
es,G. and Schmitt,H.J.  
tification of microorganism causing acute respiratory tract  
ction (ARI)  
nt: JP 2002526088-A 3 20-AUG-2002;  
GENETICS NV  
Artificial Sequence  
JP 2002526088-A/3  
20-AUG-2002  
22-SEP-1999 JP 2000574290  
24-SEP-1998 EP 98870203.1  
GEERT JANNES,HEINZ JOSEF SCHMITT  
Cl2N15/09,Cl2Q1/68,Cl2N15/00  
Description of Artificial Sequence:oligonucleotide PH Key  
Location/Qualifiers  
source 1..21  
/organism='Artificial Sequence'.  
Location/Qualifiers  
1..21  
/organism="synthetic construct"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 21;  
Best Local Similarity 93.3%; Pred. No. 7.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CTCATTTGGAATTTT 15  
|||||  
Db 15 CTCATTTGGAATTTT 1

RESULT 6  
BD223838/c

LOCUS BD223838 21 bp DNA linear PAT  
DEFINITION Identification of microorganism causing acute respirato  
infection (ARI).

ACCESSION BD223838  
VERSION BD223838.1 GI:33033608  
KEYWORDS JP 2002526088-A/13.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Jannes,G. and Schmitt,H.J.  
TITLE Identification of microorganism causing acute respirato  
infection (ARI)  
JOURNAL Patent: JP 2002526088-A 13 20-AUG-2002;  
INNOGENETICS NV

COMMENT OS Artificial Sequence  
PN JP 2002526088-A/13  
PD 20-AUG-2002  
PF 22-SEP-1999 JP 2000574290  
PR 24-SEP-1998 EP 98870203.1

PI GEERT JANNES,HEINZ JOSEF SCHMITT  
PC Cl2N15/09,Cl2Q1/68,Cl2N15/00  
CC Description of Artificial Sequence:oligonucleotide  
Location/Qualifiers  
FT source 1..21  
/organism='Artificial Sequence'.  
Location/Qualifiers  
1..21

FEATURES  
source

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 21;  
Best Local Similarity 93.3%; Pred. No. 7.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CTCATTTGGAATTTT 15  
|||||  
Db 15 CTCATTTGGAATTTT 1

RESULT 7  
AR088737/c

LOCUS AR088737 30 bp DNA linear PAT  
DEFINITION Sequence 33 from patent US 5990091.

ACCESSION AR088737  
VERSION AR088737.1 GI:10015500  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Tartaglia,J., Cox,W.I., Gettig,R.Robert., Martinez,H., P  
and Pincus,S.E.  
TITLE Vectors having enhanced expression, and methods of makir  
thereof  
JOURNAL Patent: US 5990091-A 33 23-NOV-1999;  
FEATURES Location/Qualifiers

L 09:38:22 2004

us-10-090-326-16.max.rge

1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;  
ilarity 83.3%; Pred. No. 9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTGGCC 18  
|||||  
ACTTTGGAATTGGCC 12

15464  
ence 18 from patent US 6004777.  
30 bp DNA linear PAT 08-SEP-2000  
15464  
15464.1 GI:10023359

own.  
own.  
classified.  
(bases 1 to 30)  
taglia,J., Jacobs,B.L., Goebel,S.J., Cox,W.I., Gettig,R.Robert.,  
us,S.E. and Paoletti,E.  
ors having enhanced expression, and methods of making and uses  
eof  
nt: US 6004777-A 18 21-DEC-1999;  
Location/Qualifiers  
1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;  
ilarity 83.3%; Pred. No. 9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTGGCC 18  
|||||  
TACTTTGGAATTGGCC 12

12465  
ence 33 from patent US 6130066.  
30 bp DNA linear PAT 16-MAY-2001  
12465  
12465.1 GI:14092365

own.  
own.  
classified.  
(bases 1 to 30)  
taglia,J., Cox,W.I., Gettig,R.Robert., Martinez,H., Paoletti,E.  
Pincus,S.E.  
ors having enhanced expression and methods of making and uses  
eof  
nt: US 6130066-A 33 10-OCT-2000;  
Location/Qualifiers  
1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;  
ilarity 83.3%; Pred. No. 9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTGGCC 18  
|||||

Db 29 CTACTTTGGAATTGGCC 12

RESULT 10  
BD070730/c

LOCUS  
DEFINITION  
30 bp DNA linear PAT  
Vectors having enhanced expression, and methods of makin  
thereof.

ACCESSION  
BD070730  
VERSION  
BD070730.1 GI:22616333  
KEYWORDS  
JP 2001514518-A/33.  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1 (bases 1 to 30)  
Tartaglia,J., Cox,W.I., Gettig,R.R., Martinez,H., Paolet  
Pincus,S.E.  
Vectors having enhanced expression, and methods of makin  
thereof

JOURNAL  
Patent: JP 2001514518-A 33 11-SEP-2001;

COMMENT  
VIROGENETICS CORP

OS Artificial Sequence

PN JP 2001514518-A/33

PD 11-SEP-2001

PF 13-FEB-1998 JP 1998539564

PR 12-MAR-1997 US 08/816155

PI JAMES TARTAGLIA,WILLIAM I COX,RUSSELL R

GETTIG,HECTOR MARTINEZ,

PI ENZO PAOLETTI,STEVEN E PINCUS

PC Cl2N15/64,Cl2N15/67,Cl2N15/86,A61K48/00

CC Vectors having enhanced expression, and methods of

uses thereof

CC Key Location/Qualifiers

FT source 1..30

/organism='Artificial Sequence'

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 30;  
Best Local Similarity 83.3%; Pred. No. 9e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCAATTGGAATTGGCC 18

|||||  
29 CTACTTTGGAATTGGCC 12

RESULT 11  
BD070756/c

LOCUS  
DEFINITION  
30 bp DNA linear PAT  
Vectors having enhanced expression, and methods of makin  
thereof.

ACCESSION  
BD070756

VERSION  
BD070756.1 GI:22616359

KEYWORDS  
JP 2001514519-A/17.

SOURCE  
Vaccinia virus

ORGANISM  
Vaccinia virus

Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chord

Orthopoxvirus.

REFERENCE  
1 (bases 1 to 30)

AUTHORS  
Tartaglia,J., Jacobs,B.L., Goebel,S.J., Cox,W.I., Gettig

Pincus,S.E. and Paoletti,E.

Vectors having enhanced expression, and methods of makin  
thereof

JOURNAL  
Patent: JP 2001514519-A 17 11-SEP-2001;

VIROGENETICS CORP,ARIZONA STATE UNIVERSITY

OS Vaccinia virus

PN JP 2001514519-A/17

PD 11-SEP-2001

25-FEB-1998 JP 1998539591  
 12-MAR-1997 US 08/815809  
 JAMES TARTAGLIA, BERTRAM L JACOBS, SCOTT J GOBBEL, WILLIAM I COX,  
 RUSSELL ROBERT GETTIG, STEVEN E PINCUS, ENZO PAOLETTI PC  
 15/63, A61K39/12, A61K39/285  
 Vectors having enhanced expression, and methods of making and  
 uses thereof  
 Key Location/Qualifiers  
 source 1..30  
 /organism="Vaccinia virus".  
 Location/Qualifiers  
 1..30  
 /organism="Vaccinia virus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10245"

73.3%; Score 13.2; DB 6; Length 30;  
 ilarity 83.3%; Pred. No. 9e+04; 3; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGGAATTTGCC 18  
 |||||  
 ACTTTGGGAATTTGCC 12

3439 43 bp DNA linear PAT 25-SEP-2002  
 ance 9 from patent US 6420113.  
 3439  
 3439.1 GI:23319216

own.  
 assified.  
 ases 1 to 43)  
 nler, J., Valkirs, G. and Gray, J.  
 eric polyclonal antibodies  
 nt: US 6420113-A 9 16-JUL-2002;  
 Location/Qualifiers  
 1..43  
 /organism="unknown"  
 /mol\_type="genomic DNA"

73.3%; Score 13.2; DB 6; Length 43;  
 ilarity 83.3%; Pred. No. 8.5e+04; 3; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGGAATTTGCC 18  
 |||||  
 CTATTGGGCTTTTGCC 11

3225 43 bp mRNA linear PAT 12-JUN-2003  
 ance 28 from patent US 6555310.  
 3225  
 3225.1 GI:31699617

own.  
 assified.  
 ases 1 to 43)  
 .J., Buechler, J. and Valkirs, G.  
 clonal libraries  
 nt: US 6555310-A 28 29-APR-2003;  
 Location/Qualifiers  
 1..43  
 /organism="unknown"  
 /mol\_type="mRNA"

## ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 8.5e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18  
 |||||  
 Db 28 CTCATTGGGCTTTTGCC 11

RESULT 14  
 AR360210/c  
 LOCUS AR360210 53 bp DNA linear PAT  
 DEFINITION Sequence 101 from patent US 6596279.  
 ACCESSION AR360210  
 VERSION AR360210.1 GI:33767091  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 53)  
 AUTHORS Paoletti, E.; Tartaglia, J., Cox, W. I., Gallo, R. and Franch  
 TITLE Immunodeficiency recombinant poxvirus  
 JOURNAL Patent: US 6596279-A 101 22-JUL-2003;  
 FEATURES Location/Qualifiers  
 source 1..53  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 53;  
 Best Local Similarity 83.3%; Pred. No. 8.3e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18  
 |||||  
 Db 47 CTACTTTGGGAATTTGCC 30

RESULT 15  
 AX487503/c  
 LOCUS AX487503 24 bp DNA linear PAT  
 DEFINITION Sequence 4803 from Patent WO02053728.  
 ACCESSION AX487503  
 VERSION AX487503.1 GI:22321651  
 KEYWORDS  
 SOURCE Candida albicans  
 ORGANISM Candida albicans  
 Candida albicans  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharo  
 Saccharomycetales; mitosporic Saccharomycetales; Candida

REFERENCE 1  
 AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K. L.  
 TITLE Gene disruption methodologies for drug target discovery  
 JOURNAL Patent: WO 02053728-A 4803 11-JUL-2002;  
 FEATURES Elitra Pharmaceuticals, Inc. (US)  
 Location/Qualifiers  
 source 1..24  
 /organism="Candida albicans"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:5476"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;

QY 5 TTGTGGGAATTTGCC 17  
 |||||  
 Db 14 TTGTGGGAATTTGCC 2

RESULT 16

15740 25 bp DNA linear PAT 11-MAY-2001  
 hence 863 from Patent WO0129262.  
 15740  
 15740.1 GI:14032682

thetic construct  
 thetic construct  
 ificial sequences.

ult-Newburg, L. and Pohl, M.  
 copying reagents, kits and methods of use thereof  
 ent: WO 0129262-A 863 26-APR-2001;  
 hid BioSciences, Inc. (US)

Location/Qualifiers  
 1. .25  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

72.2%; Score 13; DB 6; Length 25;

milarity 100.0%; Pred. NO. 1.2e+05; Length 25;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGGAATTTT 15  
 |||||  
 ATTGGGAATTTT 15

65018 50 bp DNA linear PAT 22-JUN-2001  
 hence 213 from Patent WO0138586.  
 65018  
 65018.1 GI:14545847

o sapiens (human)  
 o sapiens  
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

nkets, R.A. and Leach, M.  
 leic acids containing single nucleotide polymorphisms and  
 hods of use thereof  
 ent: WO 0138586-A 213 31-MAY-2001;  
 agen Corporation (US)

Location/Qualifiers

1. .50  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

re 25\_26  
 /note="Nucleotide deleted between bases 25 and 26"  
 Accession number cg43933591  
 26  
 /note="single nucleotide polymorphism"

72.2%; Score 13; DB 6; Length 50;  
 milarity 100.0%; Pred. NO. 1.1e+05; Length 50;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGGAATTTT 15  
 |||||  
 ATTGGGAATTTT 14

15741 51 bp DNA linear PAT 11-MAY-2001  
 hence 864 from Patent WO0129262.

ACCESSION AX115741  
 VERSION AX115741.1 GI:14032683  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho  
 1  
 Picoult-Newburg, L. and Pohl, M.  
 genotyping reagents, kits and methods of use thereof  
 Patent: WO 0129262-A 864 26-APR-2001;  
 Orchid BioSciences, Inc. (US)  
 FEATURES  
 source  
 1. .51  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

Query Match 72.2%; Score 13; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. NO. 1.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;

QY 3 CATTGGGAATTTT 15  
 |||||  
 Db 3 CATTGGGAATTTT 15

RESULT 19  
 AX203928/c  
 LOCUS AX203928 51 bp DNA linear PAT  
 DEFINITION Sequence 34 from Patent WO0148245.  
 ACCESSION AX203928  
 VERSION AX203928.1 GI:15393385  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

REFERENCE 1  
 AUTHORS Shimkets, R.A. and Leach, M.  
 TITLE Nucleic acids containing single nucleotide polymorphism  
 methods of use thereof  
 JOURNAL Patent: WO 0148245-A 34 05-JUL-2001;  
 Curagen Corporation (US)

FEATURES  
 source  
 1. .51  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

variation

26  
 /note="single nucleotide polymorphism"  
 Accession number cg43969076"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. NO. 1.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTCATTGGGAATT 13  
 |||||  
 Db 13 CTCATTGGGAATT 1

RESULT 20  
 AR142576  
 LOCUS AR142576 17 bp DNA linear PAT  
 DEFINITION Sequence 35 from patent US 6203801.  
 ACCESSION AR142576  
 VERSION AR142576.1 GI:15103862  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

<p>A61K39/21, PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/3 C07K14/455,C12N15/09, PC G01N33/569,C12N15/00 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers FT source 1..17 FT Location/Qualifiers           /organism='Unidentified'. 1..17 Location/Qualifiers /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'</p>					
<p>ORIGIN</p> <p>Query Match                 71.1%;      Score 12.8;   DB 6;   Length 17; Best Local Similarity   87.5%;   Pred. No. 1.6e+05; Matches   14;   Conservative   0;   Mismatches   2;   Indels   0;</p>					
<p>QY   2 TCATTGGGAATTTGTC 17                 DB   2 TCAATTGGGATTTGTC 17                </p>					
<p>RESULT 23</p> <p>E49171 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM</p> <p>E49171 Coccidiosis vaccine. E49171 E49171.1 GI:18629296 JP 2000219635-A/31. unidentified unclassified.</p>					
<p>REFERENCE AUTHORS TITLE JOURNAL COMMENT</p> <p>1 (bases 1 to 17) Schaepe,T.C., Kaiberu,K.M. and Fuerumuren,A.N. Coccidiosis vaccine Patent: JP 2000219635-A 31 08-AUG-2000; AKZO NOBEL NV OS Unidentified PN JP 2000219635-A/31 PD 08-AUG-2000 PF 01-OCT-1999 JP 1999281680 PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 9820345 THEODORUS CORNELIS SCHAEPE,KATARINA MARIA KAIBERU, PI A NICHOLAS FUERUMUREN PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K A61K39/21 PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02 C07K14/455,C12N15/09, PC G01N33/569,C12N15/00 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers FT source 1..17 FT Location/Qualifiers           /organism='Unidentified'. 1..17 Location/Qualifiers /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'</p>					
<p>FEATURES source</p> <p>ORIGIN</p> <p>Query Match                 71.1%;      Score 12.8;   DB 6;   Length 17; Best Local Similarity   87.5%;   Pred. No. 1.6e+05; Matches   14;   Conservative   0;   Mismatches   2;   Indels   0;</p>					
<p>QY   2 TCATTGGGAATTTGTC 17                 DB   2 TCAATTGGGATTTGTC 17                </p>					

12683  
ence 46 from patent US 6403089.  
12683  
12683.1 GI:23309470

town.  
town.  
classified.  
(bases 1 to 19)  
, G. and Clark, D.A.  
ods of modulating immune coagulation  
nt: US 6403089-A 46 11-JUN-2002;  
Location/Qualifiers  
1. .19  
/organism="unknown"  
/mol\_type="genomic DNA"

71.1%; Score 12.8; DB 6; Length 19;  
ilarity 87.5%; Pred. No. 1.5e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
ATTGGAATTTTGGC 18  
|||||  
ATTAGATTTTGGC 4

12543  
ence 53 from Patent WO03057914.  
2543  
2543.1 GI:38501241

helic construct  
helic construct  
ficial sequences.  
sen, F.  
od for detecting human papillomavirus mRNA  
nt: WO 03057914-A 53 17-JUL-2003;  
hip A/S (NO)  
Location/Qualifiers  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HPV primer"

71.1%; Score 12.8; DB 6; Length 21;  
ilarity 87.5%; Pred. No. 1.5e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CATTTGGGAATTTTG 16  
|||||  
CATTTGGGAATCGTG 1

3055  
ence 87 from Patent WO03057927.  
3055  
3055.1 GI:38501720

a papillomavirus  
a papillomavirus  
ses; dsDNA viruses, no RNA stage; Papillomaviridae;  
llomavirus.

REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
Norchip A/S (NO)  
FEATURES  
source  
1. .21  
Location/Qualifiers  
/organism="Human papillomavirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10566"

ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 1 CTCATTTGGGAATTTTG 16  
|||||  
Db 16 CTCATTTGGGAATCGTG 1

RESULT 27  
AX803276/c  
LOCUS AX803276 21 bp DNA linear PAT  
DEFINITION Sequence 308 from Patent WO03057927.  
ACCESSION AX803276  
VERSION AX803276.1 GI:38501941  
KEYWORDS  
SOURCE Human papillomavirus  
ORGANISM Human papillomavirus  
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
Norchip A/S (NO)  
FEATURES  
source  
1. .21  
Location/Qualifiers  
/organism="Human papillomavirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10566"

ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 1 CTCATTTGGGAATTTTG 16  
|||||  
Db 16 CTCATTTGGGAATCGTG 1

RESULT 28  
AR152786  
LOCUS AR152786 22 bp DNA linear PAT  
DEFINITION Sequence 66 from patent US 6235470.  
ACCESSION AR152786  
VERSION AR152786.1 GI:15120318  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Sidransky, D.  
TITLE Detection of neoplasia by analysis of saliva  
JOURNAL Patent: US 6235470-A 66 22-MAY-2001;  
FEATURES  
source  
1. .22  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"

```

71.1%; Score 12.8; DB 6; Length 22;
ilarity 87.5%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 2; Indels 0;
TTTGAATTGGCC 18
|||||
TCTTGAATTGGCC 21

2079          22 bp      DNA      linear      PAT 08-JUL-2002
ence 6 from Patent WO0208407.
2079
2079.1 GI:21725903
hctic construct
hctic construct
ficial sequences.
t.R.W., Reaume,A.G. and Dorfman,K.
-targeted non-human mammal with human fad presenilin mutation
generational offspring
nt: WO 0208407-A 6 31-JAN-2002;
ALON, INC. (US)
Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Novel Sequence"

71.1%; Score 12.8; DB 6; Length 22;
ilarity 87.5%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
CATTTGGAATTTTG 16
|||||
GATCTGGAATTTTG 22

4242          22 bp      DNA      linear      PAT 18-SEP-2002
tion of neoplasia by analysis of saliva.
4242
4242.1 GI:23229187
020505888-A/66.
hctic construct
hctic construct
ficial sequences.
ases 1 to 22)
anski,D.
tion of neoplasia by analysis of saliva
it: JP 2002505888-A 66 26-FEB-2002;
JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
Artificial Sequence
JP 2002505888-A/66
26-FEB-2002
10-MAR-1999 JP 2000535774
10-MAR-1998 US 09/038637
DAVID SIDLANSKI
C12N15/09,C12Q1/68,C12N15/00
nucleotide
Key
Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Location/Qualifiers
1..22
/organism="Artificial Sequence".

Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match
Best Local Similarity 71.1%; Score 12.8; DB 6; Length 22;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 3 CATTTGGAATTTTGCC 18
|||||
Db 6 CATCTGGAATTTTGCC 21

RESULT 31
BD107065
LOCUS
DEFINITION
Alpha 1-3 galactosyl transferase gene knockout cell and
constructing the same.
ACCESSION
BD107065
VERSION
BD107065.1 GI:23201883
KEYWORDS
JP 2002017360-A/4.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Sawada,T., Murakami,T., Yokoyama,N., Urakawa,M., Uruno,K
Aoyagi,T.
TITLE
Alpha 1-3 galactosyl transferase gene knockout cell and
constructing the same
JOURNAL
Patent: JP 2002017360-A 4 22-JAN-2002;
NATIONAL FEDERATION OF AGRICULTURAL COOPERATIVE ASSOCIAT
WOMEN'S MEDICAL COLLEGE
OS Artificial Sequence
PN JP 2002017360-A/4
PD 22-JAN-2002
PF 04-JUL-2000 JP 2000202748
PI TOKIHIKO SAWADA,TORU MURAKAMI,NACHIKO YOKOYAMA,MAMI
PI KATSUYOSHI URUNO,TAKAHITO AOYAGI
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,C12N15/00,C1
antisense primer for amplifying a DNA fragment by PCR du
construction
CC of targeting vector
FH Key Location/Qualifiers
FT source
1..29
/organism="Artificial Sequence".
FEATURES
source
1..29
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match
Best Local Similarity 71.1%; Score 12.8; DB 6; Length 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 3 CATTTGGAATTTTGCC 18
|||||
Db 9 CATTTGGAATTTTGAC 24

RESULT 32
E49553
LOCUS
DEFINITION
Glucose dehydrogenase.
ACCESSION
E49553
VERSION
E49553.1 GI:18622043
KEYWORDS
JP 2000350588-A/4.
SOURCE
Synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Hayade,K.
TITLE
Glucose dehydrogenase
JOURNAL
Patent: JP 2000350588-A 4 19-DEC-2000;

```

```

1
REFERENCE
AUTHORS Legrain,P., Rain,J.C., Colland,F., de Reuse,H. and Labi
TITLE Protein-protein interactions in Helicobacter pylori
JOURNAL Patent: WO 02066501-A 4755 29-AUG-2002;
Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
FEATURES
source
1..30
/organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 2 TCATTGGGAATTTGCC 17
|||||
DB 6 TCATTTGGAGTTTGC 21
|||||

RESULT 35
BD000721 30 bp DNA linear PAT
DEFINITION Process for producing glucose dehydrogenase.
ACCESSION BD000721
VERSION SD000721.1 GI:18623834
KEYWORDS JP 2000354495-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 30)
AUTHORS Hayade,K.
TITLE Process for producing glucose dehydrogenase
JOURNAL Patent: JP 2000354495-A 4 26-DEC-2000;
KOJI HAYADE
COMMENT
OS Artificial Sequence
PN JP 2000354495-A/4
PD 26-DEC-2000
PF 12-MAY-2000 JP 2000140344
PR KOJI HAYADE
PI
PC C12N15/09,C12N1/21,C12N9/04//C12Q1/32,C12Q1/54,(C1
C12R1:19),
PC (C12N9/04,C12R1:19),C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..30
/organism="Artificial Sequence".
FEATURES
source
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 30;
Best Local Similarity 87.5%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 3 CATTTGGGAATTTGCC 18
|||||
DB 1 CCATTGGGAATTTTCC 16
|||||

RESULT 36
BD176724 30 bp DNA linear PAT
DEFINITION Glucose dehydrogenase.
ACCESSION BD176724
VERSION BD176724.1 GI:29122434
KEYWORDS WO 02072839-A/5.
SOURCE synthetic construct

```

```

HAYADE
Artificial Sequence
JP 2000350588-A/4
19-DEC-2000
18-JAN-2000 JP 2000009152
KOJI HAYADE
C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/04, PC
21/54,C12N15/09,
C12N5/00
Key Location/Qualifiers
source
1..30
/organism="Artificial Sequence".
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
71.1%; Score 12.8; DB 6; Length 30;
milarity 87.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
ATTTGGGAATTTGCC 18
|||||
TTTGGGAATTTTCC 16
|||||

91284 30 bp DNA linear PAT 17-JUL-2003
uence 3748 from Patent WO02066501.
91284
91284.1 GI:32956731
icobacter pylori
icobacter pylori
teria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
icobacteraceae; Helicobacter.
rain,P., Rain,J.C., Colland,F., de Reuse,H. and Labigne,A.
tein-protein interactions in Helicobacter pylori
ent: WO 02066501-A 3748 29-AUG-2002;
rigenics (FR) ; INSTITUT PASTEUR (FR)
Location/Qualifiers
1..30
/organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
71.1%; Score 12.8; DB 6; Length 30;
milarity 87.5%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CATTTGGGAATTTGCC 17
|||||
CATATGGGAATTTTAC 21
|||||

792291 30 bp DNA linear PAT 17-JUL-2003
uence 4755 from Patent WO02066501.
792291
792291.1 GI:32957738
icobacter pylori
icobacter pylori
teria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
icobacteraceae; Helicobacter.

```



09:38:22 2004

us-10-090-326-16.max.rge

```
helic construct
ficial sequences.
bases 1 to 30)
,K. and Igarashi, S.
ose dehydrogenase
nt: WO 02072839-A 5 19-SEP-2002;
SODE,SATOSHI IGARASHI
Artificial Sequence
WO 02072839-A/5
19-SEP-2002
07-MAR-2002 WO 2002JP002124
13-MAR-2001 JP 01P 070413
KOJI SODE,SATOSHI IGARASHI
C12N15/53,C12N9/04,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/
32,G01N27/327
primer for point mutation
key Location/Qualifiers
source 1..30
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

71.1%; Score 12.8; DB 6; Length 30;
ilarity 87.5%; Pred.No.1.4e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGGAATTTGTC 18
|||||
TTTGGGAATTTTTC 16

'13 44 bp DNA linear PAT 05-JUL-2002
helic SIA1 PCR primer.
'13
'13.1 GI:23956600
helic construct
helic construct
ficial sequences.
(bases 1 to 44)
ant: GB 2256197-A 17 02-DEC-1992;
Location/Qualifiers
1..44
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

71.1%; Score 12.8; DB 6; Length 44;
ilarity 87.5%; Pred.No.1.4e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TATTGGGAATTTGTC 17
|||||
TATTTGAATTTCTGC 5

61257 51 bp DNA linear PAT 22-JUN-2001
uence 4585 from Patent WO0140521.
61257
61257.1 GI:14542588
sapiens (human)
sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1
REFERENCE Shimkets,R.A. and Leach,M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms
TITLE Methods of use thereof
JOURNAL Patent: WO 0140521-A 4585 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (4586 is other
Accession number cg43960464"
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred.No.1.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTGCC 18
|||||
16 CATTGGGAATCTTGCC 1
Db

RESULT 39
AX161258/c
LOCUS AX161258 51 bp DNA linear PAT
DEFINITION Sequence 4586 from Patent WO0140521.
ACCESSION AX161258
VERSION AX161258.1 GI:14542589
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1
REFERENCE Shimkets,R.A. and Leach,M.
AUTHORS Nucleic acids containing single nucleotide polymorphism:
TITLE Methods of use thereof
JOURNAL Patent: WO 0140521-A 4586 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (4585 is other
Accession number cg43960464"
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred.No.1.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTGCC 18
|||||
16 CATTGGGAATCTTGCC 1
Db

RESULT 40
AX199396
LOCUS AX199396 51 bp DNA linear PAT
DEFINITION Sequence 326 from Patent WO0151670.
ACCESSION AX199396
VERSION AX199396.1 GI:15389790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
```

alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 kets, R.A. and Leach, M.D.  
 eic acids containing single nucleotide polymorphisms and  
 ods of use thereof  
 nt: WO 0151670-A 326 19-JUL-2001;  
 gen Corporation (US)  
 Location/Qualifiers  
 1..51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 26  
 /note="2 of 2 allelic variants (325 is other entry)  
 Accession number C943946S70"  
 71.1%; Score 12.8; DB 6; Length 51;  
 milarity 87.5%; Pred. No. 1.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 CATTGGAATTTC 17  
 |||||  
 3AGTTGGAATTTC 36  
 12397 60 bp DNA linear PAT 17-FEB-2003  
 uence 3422 from Patent WO02072882.  
 12397  
 12397.1 GI:28407826  
 o sapiens (human)  
 sapiens  
 aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 len, P. and Seedorf, U.  
 onary chip  
 ent: WO 02072882-A 3422 19-SEP-2002;  
 AM GmbH (DE)  
 Location/Qualifiers  
 1..60  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 71.1%; Score 12.8; DB 6; Length 60;  
 milarity 87.5%; Pred. No. 1.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 TCATTGGAATTTC 16  
 |||||  
 TCATCTGGAATTTC 38  
 139527 17 bp DNA linear PAT 29-SEP-1999  
 uence 375 from patent US 5807743.  
 139527  
 139527.1 GI:5958890  
 nown.  
 nown.  
 lassified.  
 (bases 1 to 17)  
 nchcomb, D.T. and McSwiggen, J.A.  
 erleukin-2 receptor gamma-chain ribozymes  
 ent: US 5807743-A 375 15-SEP-1998;  
 Location/Qualifiers

source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 68.9%; Score 12.4; DB 6; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 1 CTCATTGGAAATTT 14  
 |||||  
 Db 4 CTGATTGGAAATTT 17  
 RESULT 43  
 AX722776 17 bp DNA linear PAT  
 LOCUS  
 DEFINITION  
 Sequence 463 from Patent WO03025176.  
 ACCESSION  
 AX722776  
 VERSION  
 AX722776.1 GI:30423277  
 KEYWORDS  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu  
 1  
 Telerman, A., Amson, R. and Tuijinder, M.  
 Sequences involved in phenomena of tumour suppression,  
 reversion, apoptosis and/or virus resistance and their  
 medicines  
 JOURNAL  
 Patent: WO 03025176-A 463 27-MAR-2003;  
 Molecular Engines Laboratories (FR)  
 Location/Qualifiers  
 1..17  
 /organism="Mus musculus"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:10090"  
 ORIGIN  
 Query Match 68.9%; Score 12.4; DB 6; Length 17;  
 Best Local Similarity 92.9%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 1 CTCATTGGAAATTT 14  
 |||||  
 Db 4 CTCATTGGAAATTT 17  
 RESULT 44  
 AX197327 27 bp DNA linear PAT  
 LOCUS  
 DEFINITION  
 Sequence 1034 from Patent WO0151627.  
 ACCESSION  
 AX197327  
 VERSION  
 AX197327.1 GI:15387533  
 KEYWORDS  
 SOURCE  
 Glycine max (soybean)  
 ORGANISM  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae;  
 Glycine.  
 1  
 Haughe, B.M., Wang, M.L., Parsons, J.D. and Parnell, L.D.  
 Nucleic acid molecules and other molecules associated w  
 cyst nematode resistance  
 Patent: WO 0151627-A 1034 19-JUL-2001;  
 MONSANTO COMPANY (US)  
 Location/Qualifiers  
 1..27  
 /organism="Glycine max"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:3847"  
 /note="Seq ID: 515002\_region\_G2\_70595\_13\_Reve

09:38:22 2004

us-10-090-326-16.max.rge

68.9%; Score 12.4; DB 6; Length 27;  
ilarity 92.9%; Pred. No. 2.4e+05;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ATTGGAATTTT 15  
|||||  
ATTGGAATTAT 27

1288 30 bp DNA linear PAT 17-JUL-2003  
ence 3752 from Patent WO02066501.

1288

1288.1 GI:32956735

cobacter pylori  
cobacter pylori  
eria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
cobacteraceae; Helicobacter.

ain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.  
ein-protein interactions in Helicobacter pylori  
nt: WO 02066501-A 3752 29-AUG-2002;

igenics (FR) ; INSTITUT PASTEUR (FR)

Location/Qualifiers

1. 30

/organism="Helicobacter pylori"

/mol\_type="unassigned DNA"

/db\_xref="taxon:210"

68.9%; Score 12.4; DB 6; Length 30;  
ilarity 92.9%; Pred. No. 2.3e+05;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ATTGGAATTTT 15  
|||||  
ATATGGAATTTT 19

.: February 29, 2004, 09:43:28  
74 secs

09:38:22 2004

us-10-090-326-16.max.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 07:46:14 ; Search time 153.584 Seconds  
(without alignments)  
497.886 Million cell updates/sec

JS-10-090-326-16

18

1 ctctatttggaattttgcc 18

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002s.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	18	6	ABQ82550	Abq82550	Glucuroni
100.0	22	6	ABQ82537	Abq82537	Beta-gluc
100.0	22	9	ADD68258	Add68258	PCR prime
82.2	52	9	ADD36583	Add36583	Human pap
82.2	52	9	ADD22161	Add22161	HPV E6 ge
77.8	20	2	AAX52730	Aax52730	Human gen
77.8	20	3	AAX276753	Aax276753	Human bla
76.7	41	4	AH49769	Aah49769	Human gro
74.4	17	2	AAV94759	Aav94759	Human II-
74.4	21	2	AAV65069	Aav65069	Parainflu
74.4	21	3	AAAL4173	Aaal4173	Piv-3 fus
74.4	21	3	AAAL4163	Aaal4163	Piv-3 fus
73.3	23	4	AAH27357	Aah27357	PCR prime
73.3	30	2	AAV58254	Aav58254	HIV Pol2
73.3	30	2	AAV60282	Aav60282	HIV-1 Pol
73.3	30	8	ABT44474	Abt44474	PCR prime
73.3	30	9	ADC21256	Adc21256	E. coli 1
73.3	33	6	ABV76515	Abv76515	Human cyt
73.3	41	6	ABV76517	Abv76517	Human cyt
73.3	43	6	ABS70690	Abs70690	Mouse imm
73.3	43	9	AAD61290	Aad61290	Mouse imm
73.3	51	4	AAL27046	Aal27046	Human SNP
73.3	53	2	AAT04743	Aat04743	PCR prime

24	13.2	73.3	60	6	ABN49959	Abn49959
25	13	72.2	13	5	ABF80741	Abf80741
26	13	72.2	13	5	ABF80740	Abf80740
27	13	72.2	24	6	ABZ30652	Abz30652
28	13	72.2	25	4	AAH38067	Aah38067
29	13	72.2	30	6	ABX03639	Abx03639
30	13	72.2	30	5	ABL00222	AbL00222
31	13	72.2	51	4	AAH38068	Aah38068
32	13	72.2	51	4	AAH79419	Aah79419
33	12.8	71.1	17	3	AAZ94932	Aaz94932
34	12.8	71.1	17	3	AAZ94930	Aaz94930
35	12.8	71.1	21	9	ADD36719	Add36719
36	12.8	71.1	21	9	ADD36940	Add36940
37	12.8	71.1	21	9	ADD22294	Add22294
38	12.8	71.1	21	9	ADD21998	Add21998
39	12.8	71.1	22	5	AAZ21716	Aaz21716
40	12.8	71.1	22	5	AAZ21716	Aaz21716
41	12.8	71.1	22	6	ABA95094	AbA95094
42	12.8	71.1	22	7	ACC72192	Acc72192
43	12.8	71.1	29	6	ABL49764	AbL49764
44	12.8	71.1	30	3	AAC63949	Aac63949
45	12.8	71.1	30	6	ABV73543	Abv73543
46	12.8	71.1	30	6	ABX67521	Abx67521
47	12.8	71.1	30	6	ABX68528	Abx68528
48	12.8	71.1	33	4	AAH49767	Aah49767
49	12.8	71.1	33	7	ABZ25658	Abz25658
50	12.8	71.1	44	2	AAQ31445	Aaq31445
51	12.8	71.1	44	2	AAQ66901	Aaq66901
52	12.8	71.1	51	4	AAI77645	Aai77645
53	12.8	71.1	51	4	AAI77644	Aai77644
54	12.8	71.1	51	4	AAH89545	Aah89545
55	12.8	71.1	60	6	ABN33965	Abn33965
56	12.8	71.1	60	6	ABN38239	Abn38239
57	12.4	68.9	17	2	AAV94758	Aav94758
58	12.4	68.9	17	7	ACC63216	Acc63216
59	12.4	68.9	20	7	ABZ89717	Abz89717
60	12.4	68.9	25	8	ACK05014	Ack05014
61	12.4	68.9	27	2	AAQ71057	Aaq71057
62	12.4	68.9	27	5	AAI62403	Aai62403
63	12.4	68.9	30	6	ABX67525	Abx67525
64	12.4	68.9	30	6	ABX68741	Abx68741
65	12.4	68.9	30	6	ABX68346	Abx68346
66	12.4	68.9	30	6	ABX68875	Abx68875
67	12.4	68.9	30	7	AAZ54100	Aaz54100
68	12.4	68.9	33	6	ABL58640	AbL58640
69	12.4	68.9	34	2	AAQ32964	Aaq32964
70	12.4	68.9	36	2	AAQ32964	Aaq32964
71	12.4	68.9	36	7	ABZ79662	Abz79662
72	12.4	68.9	36	7	ABZ79663	Abz79663
73	12.4	68.9	41	2	AAV47743	Aav47743
74	12.4	68.9	41	6	ABL58642	AbL58642
75	12.4	68.9	41	6	ABV76518	Abv76518
76	12.4	68.9	41	6	ABZ46787	Abz46787
77	12.4	68.9	41	6	ABZ45347	Abz45347
78	12.4	68.9	50	6	ABZ02952	Abz02952
79	12.4	68.9	50	6	ABZ00967	Abz00967
80	12.4	68.9	60	6	ABN49514	Abn49514
81	12.4	67.8	17	3	AAQ63229	Aaq63229
82	12.2	67.8	20	5	AAH80417	Aah80417
83	12.2	67.8	20	5	AAH80416	Aah80416
84	12.2	67.8	20	5	AAH80418	Aah80418
85	12.2	67.8	20	5	AAH80415	Aah80415
86	12.2	67.8	20	7	AAH80415	Aah80415
87	12.2	67.8	20	7	AAH80415	Aah80415
88	12.2	67.8	20	9	ADD81307	Add81307
89	12.2	67.8	20	9	ADD81308	Add81308
90	12.2	67.8	20	9	ADD81309	Add81309
91	12.2	67.8	20	9	ADD81306	Add81306
92	12.2	67.8	25	2	AAV09030	Aav09030
93	12.2	67.8	27	9	ADC26548	Adc26548
94	12.2	67.8	34	2	AAV22156	Aav22156
95	12.2	67.8	36	2	AAQ74588	Aaq74588
96	12.2	67.8	36	2	AAQ74580	Aaq74580

67.8	36	2	AAQ74576	AaQ74576 Helper pr	c 170	11.8	65.6	41	2	AAV51093	AAV51093
67.8	36	2	AAQ74584	AaQ74584 Helper pr	c 171	11.8	65.6	41	6	ABV77355	ABV77355
67.8	36	3	ACF80081	AcF80081 Baboon TA	172	11.8	65.6	42	3	AAc55139	AAc55139
67.8	39	3	AAa15334	AaA15334 PCR prime	c 173	11.8	65.6	50	6	ABZ06247	ABZ06247
67.8	39	8	ADA73939	AdA73939 Carcinoma	174	11.8	65.6	50	6	ABZ02614	ABZ02614
67.8	39	8	ADA02413	AdA02413 Mouse car	175	11.8	65.6	50	6	ABZ00917	ABZ00917
67.8	39	9	ADB72152	AdB72152 Mouse car	176	11.8	65.6	51	4	AAI76729	AAI76729
67.8	40	8	ADB99211	AdB99211 Human PSM	177	11.8	65.6	51	4	AAI76730	AAI76730
67.8	43	7	AAI51928	AaI51928 Bacillus	178	11.8	65.6	51	4	AAI76732	AAI76732
67.8	45	4	AAc82263	AaC82263 Human ret	179	11.8	65.6	51	4	AAI76733	AAI76733
67.8	49	2	AAI72047	AaI72047 Ribozyme	180	11.8	65.6	51	4	AAI76728	AAI76728
67.8	50	2	AAI13473	AaI13473 Chimeraic	181	11.8	65.6	51	5	ABL00065	ABL00065
67.8	50	6	ABZ03556	AbZ03556 Human leu	182	11.6	64.4	18	3	AAZ88117	AAZ88117
67.8	50	6	ABZ02584	AbZ02584 Human leu	c 183	11.6	64.4	18	3	AAZ88128	AAZ88128
67.8	50	6	ABZ05491	AbZ05491 Human leu	c 184	11.6	64.4	20	6	ABL45450	ABL45450
67.8	50	6	ABZ06640	AbZ06640 Human leu	c 185	11.6	64.4	20	6	ABZ93152	ABZ93152
67.8	50	6	ABZ07030	AbZ07030 Human leu	186	11.6	64.4	24	2	AAZ34207	AAZ34207
67.8	51	4	AAI75902	AaI75902 Human sil	187	11.6	64.4	24	2	AAZ34207	AAZ34207
67.8	51	4	AAI75903	AaI75903 Human sil	188	11.6	64.4	24	3	AAc58424	AAc58424
67.8	58	9	ADC26553	AdC26553 Plasmid p	189	11.6	64.4	24	3	AAc78822	AAc78822
67.8	59	2	AAV40092	AaV40092 Oligonuc	c 190	11.6	64.4	24	4	AAf87678	AAf87678
67.8	60	2	AAV40093	AaV40093 Oligonuc	c 191	11.6	64.4	24	5	AAH55866	AAH55866
67.8	60	6	ABN34531	AbN34531 Human spl	192	11.6	64.4	24	6	ABZ55214	ABZ55214
67.8	60	6	ABN47065	AbN47065 Human spl	193	11.6	64.4	24	7	ACd42740	ACd42740
66.7	12	5	ABII15340	AbI15340 Oligonuc	194	11.6	64.4	24	7	ACa63775	ACa63775
66.7	13	4	ABH33261	AbH33261 Oligonuc	195	11.6	64.4	24	7	ABV72419	ABV72419
66.7	13	5	ABH308644	AbH308644 Oligonuc	196	11.6	64.4	24	7	ACA71939	ACA71939
66.7	13	5	ABH33260	AbH33260 Oligonuc	197	11.6	64.4	24	7	ACX92579	ACX92579
66.7	13	5	ABH33260	AbH33260 Oligonuc	198	11.6	64.4	24	7	ACA66320	ACA66320
66.7	13	5	ABH33260	AbH33260 Oligonuc	199	11.6	64.4	24	8	ADA24911	ADA24911
66.7	13	5	ABH33260	AbH33260 Oligonuc	200	11.6	64.4	24	8	ACD29921	ACD29921
66.7	17	2	AAV94760	AaV94760 Human IL-	201	11.6	64.4	24	8	ADAI12572	ADAI12572
66.7	21	5	AAc62176	AAc62176 Oligomer	202	11.6	64.4	24	8	ACD29336	ACD29336
66.7	22	2	AAH57681	AaH57681 Exon 10 o	203	11.6	64.4	24	9	ADB73878	ADB73878
66.7	36	4	AAH91069	AaH91069 Human inf	204	11.6	64.4	24	9	ADB76594	ADB76594
66.7	37	4	AAH91066	AaH91066 Human inf	205	11.6	64.4	24	9	ADG44020	ADG44020
66.7	37	4	AAH91067	AaH91067 Human inf	206	11.6	64.4	24	9	ADG61780	ADG61780
66.7	37	4	AAH91067	AaH91067 Human inf	207	11.6	64.4	24	9	ADG63744	ADG63744
66.7	53	2	AAV77049	AaV77049 Staphyloc	208	11.6	64.4	24	9	ADG68968	ADG68968
66.7	60	6	ABN36812	AbN36812 Human spl	209	11.6	64.4	24	9	ADG63028	ADG63028
66.7	60	6	ABN37392	AbN37392 Human spl	210	11.6	64.4	24	9	ADG68093	ADG68093
65.6	17	7	ACC53279	AcC53279 Human tum	211	11.6	64.4	24	9	ADG41413	ADG41413
65.6	17	7	ACC53270	AcC53270 Human tum	212	11.6	64.4	24	9	ADG67468	ADG67468
65.6	17	7	ABT38262	AbT38262 Tumour su	213	11.6	64.4	24	9	ADG62404	ADG62404
65.6	17	9	ADB43465	AdB43465 Tumour su	214	11.6	64.4	24	9	ADG62404	ADG62404
65.6	19	9	ADE43547	AdE43547 Human IDE	215	11.6	64.4	24	9	ADG42037	ADG42037
65.6	20	2	AAV82076	AaV82076 PCR prime	216	11.6	64.4	24	9	ADG49406	ADG49406
65.6	20	2	AAZ02646	AaZ02646 PCR prime	217	11.6	64.4	24	9	ADG35460	ADG35460
65.6	21	2	AAV41028	AaV41028 Primer AL	218	11.6	64.4	24	9	ADE16574	ADE16574
65.6	21	2	AAV41028	AaV41028 Primer AL	219	11.6	64.4	24	9	ADG73189	ADG73189
65.6	22	2	AAV77010	AaV77010 Wheat mic	220	11.6	64.4	24	9	ADG72547	ADG72547
65.6	22	6	ABA99720	AbA99720 Human HLF	221	11.6	64.4	24	9	ADE17198	ADE17198
65.6	22	9	ADD21871	AdD21871 Protein t	222	11.6	64.4	24	10	ADE48706	ADE48706
65.6	23	8	ADG72991	AdG72991 PCR prime	223	11.6	64.4	24	10	ADE89807	ADE89807
65.6	25	8	ADA37097	AdA37097 Rat Gluta	224	11.6	64.4	24	10	ABL57480	ABL57480
65.6	27	4	AAH39977	AaH39977 SNP Spec	c 225	11.6	64.4	25	6	ABZ30240	ABZ30240
65.6	27	6	AAK98259	AaK98259 Caenorhab	226	11.6	64.4	25	6	ABZ30240	ABZ30240
65.6	27	7	AAZ55690	AaZ55690 CMI28 PCR	227	11.6	64.4	25	8	ACI15562	ACI15562
65.6	31	2	AAV55691	AaV55691 CMI29 PCR	c 228	11.6	64.4	25	8	ACI15495	ACI15495
65.6	31	2	AAV67542	AaV67542 Nucleotid	c 229	11.6	64.4	25	8	ACH52822	ACH52822
65.6	31	3	AAZ96692	AaZ96692 T cell an	c 230	11.6	64.4	27	3	AAa58403	AAa58403
65.6	31	5	AAZ44076	AaZ44076 Neisseria	c 231	11.6	64.4	28	3	AAZ95252	AAZ95252
65.6	32	8	ADA36995	AdA36995 Oligonuc	c 232	11.6	64.4	28	3	AAZ93878	AAZ93878
65.6	33	6	ABZ24923	AbZ24923 Cell divi	c 233	11.6	64.4	30	2	AAZ33234	AAZ33234
65.6	33	6	AAI50919	AaI50919 Human ner	c 234	11.6	64.4	31	2	AAV94909	AAV94909
65.6	33	6	ABV74701	AbV74701 Signal tr	c 235	11.6	64.4	32	2	AAV18041	AAV18041
65.6	35	9	ADD29057	AdD29057 BbVCI-R1	c 236	11.6	64.4	33	6	ABA95672	ABA95672
65.6	36	7	ABZ22462	AbZ22462 Human MTS	c 237	11.6	64.4	33	6	ABK12790	ABK12790
65.6	38	4	ABK08222	AbK08222 Human CD2	c 238	11.6	64.4	33	7	ABZ25877	ABZ25877
65.6	38	6	ABK19908	AbK19908 Human ERG	c 239	11.6	64.4	36	2	AAV16946	AAV16946
65.6	38	6	ABK59012	AbK59012 Human CLC	c 240	11.6	64.4	36	2	AAI16816	AAI16816
65.6	39	2	AAQ12322	AaQ12322 HPV type	c 241	11.6	64.4	39	6	ABK49529	ABK49529
65.6	39	2	AAI71182	AaI71182 HPV type	c 242	11.6	64.4	39	6	ABK49537	ABK49537
65.6	39	9	ADD71236	AdD71236 Mouse Et							

64.4	41	4	AAH47808	11.4	316	63.3	25	6	ABL50083	1
64.4	41	7	ABZ25879	11.4	317	63.3	25	8	ACK24090	1
64.4	42	2	AAX78675	11.4	318	63.3	26	7	ACC58107	1
64.4	42	2	AAX78676	11.4	319	63.3	27	3	AAA14283	1
64.4	42	2	AAV84727	11.4	320	63.3	27	4	AAH41087	1
64.4	43	3	ABZ26816	11.4	321	63.3	28	4	ABK11935	1
64.4	43	6	AAZ68522	11.4	322	63.3	29	4	AAO09015	1
64.4	47	3	AAQ35570	11.4	323	63.3	29	4	AAO08993	1
64.4	48	6	AAQ35570	11.4	324	63.3	29	4	AAO09001	1
64.4	48	6	AAQ35570	11.4	325	63.3	29	9	ADD14976	1
64.4	50	2	AAV40154	11.4	326	63.3	30	2	AAQ31448	1
64.4	50	4	AAI77516	11.4	327	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ02067	11.4	328	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ04559	11.4	329	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ04139	11.4	330	63.3	30	6	ABX69073	1
64.4	50	6	ABZ05325	11.4	331	63.3	30	6	ABX68499	1
64.4	51	2	ABX78694	11.4	332	63.3	30	7	ACC58544	1
64.4	51	4	AAI78112	11.4	333	63.3	31	3	AAH414274	1
64.4	51	4	AAI78111	11.4	334	63.3	31	4	AAH44286	1
64.4	51	4	AAI78110	11.4	335	63.3	31	4	AAH44286	1
64.4	51	4	AAI76267	11.4	336	63.3	32	7	ABZ77834	1
64.4	51	4	AAI78114	11.4	337	63.3	32	7	ABZ77834	1
64.4	52	2	AAI78114	11.4	338	63.3	34	2	AAV37944	1
64.4	52	2	AAI78114	11.4	339	63.3	34	2	AAV37944	1
64.4	56	3	AAI78697	11.4	340	63.3	34	2	AAV37944	1
64.4	56	3	AAI78697	11.4	341	63.3	34	2	AAV37944	1
64.4	56	3	AAI78697	11.4	342	63.3	34	2	AAV37944	1
64.4	57	2	AAI78696	11.4	343	63.3	35	6	AAV37944	1
64.4	60	6	ABN43584	11.4	344	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	345	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	346	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	347	63.3	37	2	AAV37944	1
64.4	60	6	ABN43584	11.4	348	63.3	38	7	AAV37944	1
64.4	60	6	ABN43584	11.4	349	63.3	39	9	AAV37944	1
64.4	60	6	ABN43584	11.4	350	63.3	39	9	AAV37944	1
64.4	60	6	ABN43584	11.4	351	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	352	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	353	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	354	63.3	41	6	ABZ48210	1
64.4	60	6	ABN43584	11.4	355	63.3	41	8	ADAI4244	1
64.4	60	6	ABN43584	11.4	356	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	357	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	358	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	359	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	360	63.3	43	6	ABZ27947	1
64.4	60	6	ABN43584	11.4	361	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	362	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	363	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	364	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	365	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	366	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	367	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	368	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	369	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	370	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	371	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	372	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	373	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	374	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	375	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	376	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	377	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	378	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	379	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	380	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	381	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	382	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	383	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	384	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	385	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	386	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	387	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	388	63.3	47	3	AAZ67092	1

62.2	17	3	Aaz294914	Eimeria t	C 462	11.2	62.2	42	2	AAT47616	Aat47616
62.2	17	3	Aaf06330	Hammerhea	C 463	11.2	62.2	42	2	AAV17709	Aav17709
62.2	18	3	Aaz293505	TRADD ant	C 464	11.2	62.2	42	2	AAV26985	Aav26985
62.2	20	2	Aat27521	Mouse and	C 465	11.2	62.2	42	2	AAV18808	Aav18808
62.2	20	2	Aaz11551	Mouse and	C 466	11.2	62.2	42	2	AAZ08491	Aaz08491
62.2	20	2	Aax03831	Regulator	C 467	11.2	62.2	42	4	AAF55028	Aaf55028
62.2	20	2	Aax97397	Primer us	C 468	11.2	62.2	42	4	AAF75821	Aaf75821
62.2	20	3	AAZ73529	Mouse and	C 469	11.2	62.2	42	4	AAF28311	Aaf28311
62.2	20	4	AAZ11554	Human gly	C 470	11.2	62.2	42	6	ABK15602	Abk15602
62.2	20	5	AH80414	Oligonucle	C 471	11.2	62.2	42	6	ABI98949	Abi98949
62.2	20	6	AB145397	Human chr	C 472	11.2	62.2	42	7	ABZ25307	Abz25307
62.2	20	6	AB145397	Mouse and	C 473	11.2	62.2	42	7	ABZ25442	Abz25442
62.2	20	6	AB145397	Human chr	C 474	11.2	62.2	42	8	AAZ55878	Aaz55878
62.2	20	7	ABZ88402	Human oli	C 475	11.2	62.2	42	8	ADD15071	Add15071
62.2	20	7	ACD42114	Antisense	C 476	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 477	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 478	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 479	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 480	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 481	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 482	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 483	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 484	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 485	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 486	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 487	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 488	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 489	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 490	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 491	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 492	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 493	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 494	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 495	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 496	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 497	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 498	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 499	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 500	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 501	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 502	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 503	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 504	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 505	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 506	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 507	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 508	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 509	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 510	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 511	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 512	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 513	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 514	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 515	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 516	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 517	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 518	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 519	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 520	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 521	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 522	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 523	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 524	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 525	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 526	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 527	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 528	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 529	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 530	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 531	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 532	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 533	11.2	62.2	42	9	ADD15019	Add15019
62.2	20	9	AD61626	PCR prime	C 534	11.2	62.2	42	9	ADD15019	Add15019

61.1	13	5	ABC52427	Abc52427 Oligonuc	608	10.8	60.0	17	2	AAx73365
61.1	13	5	ABC30524	Abc30524 Oligonuc	609	10.8	60.0	17	2	AAx73366
61.1	13	5	ABF08427	Abf08427 Oligonuc	c 610	10.8	60.0	17	2	AAx71026
61.1	13	5	ABC72794	Abc72794 Oligonuc	c 611	10.8	60.0	17	2	AAa21487
61.1	13	5	ABC72795	Abc72795 Oligonuc	c 612	10.8	60.0	17	2	AAa21488
61.1	13	5	ABC14978	Abc14978 Oligonuc	c 613	10.8	60.0	17	2	AAa21489
61.1	13	5	ABC85628	Abc85628 Oligonuc	c 614	10.8	60.0	17	3	AAa36335
61.1	13	5	ABF94613	Abf94613 Oligonuc	c 615	10.8	60.0	17	3	AAa36331
61.1	13	5	ABC85629	Abc85629 Oligonuc	c 616	10.8	60.0	17	3	AAf06331
61.1	13	5	ABF94612	Abf94612 Oligonuc	c 617	10.8	60.0	17	7	ABT39498
61.1	13	5	ABF08130	Abf08130 Oligonuc	c 618	10.8	60.0	17	7	ACD63081
61.1	13	5	ABC24019	Abc24019 Oligonuc	619	10.8	60.0	17	9	ACD59532
61.1	13	5	ABC52426	Abc52426 Oligonuc	620	10.8	60.0	17	9	ADB42527
61.1	13	5	ABC30525	Abc30525 Oligonuc	c 621	10.8	60.0	17	9	ADB45673
61.1	13	5	ABF08131	Abf08131 Oligonuc	c 622	10.8	60.0	18	2	AAV13362
61.1	13	5	ABF30369	Abf30369 Oligonuc	c 623	10.8	60.0	18	4	AAV37865
61.1	13	5	ABF01915	Abf01915 Oligonuc	624	10.8	60.0	18	4	AAa04918
61.1	13	5	ABF92185	Abf92185 Oligonuc	c 625	10.8	60.0	18	4	AAa04910
61.1	13	2	AAV94761	AAv94761 Human IL-	c 626	10.8	60.0	18	6	ABA94100
61.1	17	6	ABQ96210	Abq96210 Tumour su	627	10.8	60.0	18	6	ABA94121
61.1	17	6	AAQ84974	Aaq84974 E. coli P	628	10.8	60.0	20	2	AAQ12728
61.1	20	2	ABT13254	Abt13254 Fancoi a	c 629	10.8	60.0	20	2	AAQ82291
61.1	20	6	ABL45348	AbL45348 Human chr	c 630	10.8	60.0	20	2	AAV85914
61.1	20	6	ABL44504	AbL44504 Human chr	c 631	10.8	60.0	20	2	AAx94678
61.1	20	7	ABZ85718	Abz85718 Human oli	c 632	10.8	60.0	20	4	AAa90819
61.1	20	7	ABZ85199	Abz85199 Human oli	c 633	10.8	60.0	20	5	AAf24531
61.1	20	7	ABZ85200	Abz85200 Human oli	634	10.8	60.0	20	5	AAH80756
61.1	20	9	ADC42491	Adc42491 FANCD2 PC	635	10.8	60.0	20	5	AAH80757
61.1	21	2	AAZ18208	Aaz18208 Serine th	636	10.8	60.0	20	5	AAH80755
61.1	21	2	ABZ22860	Abz22860 Clonal T	637	10.8	60.0	20	5	AAH80759
61.1	23	2	AAV63028	AAv63028 D. immiti	638	10.8	60.0	20	5	AAH80758
61.1	23	2	AAV63316	AAv63316 Forward P	639	10.8	60.0	20	5	AAH80760
61.1	23	3	AAA58201	Aaa58201 Onchocerc	640	10.8	60.0	20	6	AAH80760
61.1	23	3	AAAL37887	Aal37887 Ankyrin c	c 641	10.8	60.0	20	6	AAH80760
61.1	23	6	ABT11220	Abt11220 TRC8 rela	642	10.8	60.0	20	7	ABD49273
61.1	23	6	ABK10442	Abk10442 Human TRC	c 643	10.8	60.0	20	7	ABD49273
61.1	24	6	AAa14957	AaL14957 Human cyc	c 644	10.8	60.0	20	9	ABT15787
61.1	27	3	AAa28444	Aaa28444 Synthetic	645	10.8	60.0	20	9	ADD36841
61.1	27	7	ABX13222	Abx13222 DNA encod	646	10.8	60.0	20	9	ADD81646
61.1	27	8	ADB39111	Adb39111 Human tum	647	10.8	60.0	20	9	ADD81645
61.1	29	6	ABS53583	Abs53583 Aminoketo	648	10.8	60.0	20	9	ADD81651
61.1	29	6	AAV69389	AAv69389 Human ATG	649	10.8	60.0	20	9	ADD81649
61.1	30	2	AAx34667	Aax34667 Human ATG	650	10.8	60.0	20	9	ADD81647
61.1	31	2	AAV67634	AAv67634 Nucleotid	651	10.8	60.0	20	9	ADD81650
61.1	34	2	AAf56219	Aaf56219 Candida C	652	10.8	60.0	21	2	AAx09855
61.1	34	3	AAZ08277	Aaz08277 PCR prime	653	10.8	60.0	21	2	AAV28008
61.1	34	3	AAZ57187	Aaz57187 Human DET	c 654	10.8	60.0	21	2	AAV74304
61.1	40	7	ABX94276	Abx94276 PCR prime	c 655	10.8	60.0	21	3	AAZ75217
61.1	40	9	ADD12872	Add12872 Fusion pr	c 656	10.8	60.0	21	3	AAf22270
61.1	41	4	AAI99689	Aai99689 Human TNF	c 657	10.8	60.0	21	4	AAf96459
61.1	41	4	AAI99690	Aai99690 Human TNF	c 658	10.8	60.0	21	4	AAf96459
61.1	41	6	ABA92437	AbA92437 Human L1	c 659	10.8	60.0	22	6	ABA98668
61.1	41	6	ABA92438	AbA92438 Human L1	660	10.8	60.0	22	6	AAQ29594
61.1	42	3	AAZ55060	Aaz55060 Neisseria	c 661	10.8	60.0	22	6	AAQ35488
61.1	42	3	AAZ55062	Aaz55062 Neisseria	c 662	10.8	60.0	22	6	ABL44561
61.1	45	8	ACF05705	Acf05705 Tyrosinas	c 663	10.8	60.0	23	3	AAf47308
61.1	47	6	ABK40779	Abk40779 Human obe	c 664	10.8	60.0	23	3	AAc64188
61.1	48	5	AAa44152	Aaa44152 Neisseria	c 665	10.8	60.0	24	4	AAH39733
61.1	50	6	ABZ00825	Abz00825 Human leu	666	10.8	60.0	24	2	AAQ35487
61.1	50	6	ABZ02713	Abz02713 Human leu	c 667	10.8	60.0	24	3	AAZ88215
61.1	51	4	ABZ28523	Abz28523 Human SNP	c 668	10.8	60.0	24	4	AAH75679
61.1	51	4	AAI76721	Aai76721 Human sil	669	10.8	60.0	24	6	ABK48760
61.1	51	4	AAI77317	Aai77317 Human sil	670	10.8	60.0	24	7	ABZ24992
61.1	51	4	AAI76201	Aai76201 Human sil	c 671	10.8	60.0	24	8	ACA04405
61.1	51	4	AAI76200	Aai76200 Human sil	c 672	10.8	60.0	24	9	ADD71237
61.1	54	2	AAV76018	AAv76018 Staphyloc	c 673	10.8	60.0	25	2	AAQ45056
61.1	60	6	ABN36322	Abn36322 Human spl	674	10.8	60.0	25	2	AAT47885
61.1	60	6	ABN42302	Abn42302 Human spl	c 675	10.8	60.0	25	2	AAT58816
61.1	60	6	ABN45336	Abn45336 Human spl	676	10.8	60.0	25	2	AAV42180
61.1	60	6	ABN41847	Abn41847 Human spl	677	10.8	60.0	25	2	AAV67046
61.1	60	6	ABN32590	Abn32590 Human spl	678	10.8	60.0	25	8	ACI43493
61.1	60	6	ABN46342	Abn46342 Human spl	679	10.8	60.0	25	8	ACI59517
61.1	15	4	AAf98036	AAf98036 Human IGE	680	10.8	60.0	25	8	ACI70546



60.0	25	8	ACI03292	Acio3292 Human mic	754	10.8	60.0	37	2	AAZ20421
60.0	25	8	ACI48766	AcI48766 Human mic	755	10.8	60.0	37	7	ABX12321
60.0	25	8	ACI37164	AcI37164 Human mic	C 756	10.8	60.0	38	4	AAT81823
60.0	25	8	ACI51074	AcI51074 Human mic	C 757	10.8	60.0	38	4	AAH96661
60.0	25	8	ACI81790	AcI81790 Human mic	C 758	10.8	60.0	38	4	AAH96516
60.0	25	8	ACI59107	AcI59107 Human mic	C 759	10.8	60.0	38	4	ABK04191
60.0	25	8	ACI54715	AcI54715 Human mic	C 760	10.8	60.0	38	4	ABK04191
60.0	25	8	ACK05015	ACK05015 Human mic	761	10.8	60.0	39	2	AAQ98268
60.0	25	8	ACI93271	ACI93271 Human mic	762	10.8	60.0	39	7	ABV93840
60.0	25	8	ACI54714	ACI54714 Human mic	763	10.8	60.0	39	7	ABV93536
60.0	25	8	ACH51672	ACH51672 DNA targe	764	10.8	60.0	40	3	AAZ48355
60.0	26	2	AAV37565	AAV37565 L. welshi	C 765	10.8	60.0	41	3	AAA95683
60.0	26	2	AAV37565	AAV37565 PCR prime	C 766	10.8	60.0	41	3	ABV77356
60.0	26	2	AAQ81619	AAQ81619 sense deg	767	10.8	60.0	41	6	ABL58643
60.0	27	2	AAQ74398	AAQ74398 sense deg	C 768	10.8	60.0	41	6	ABZ49883
60.0	27	2	AAQ72555	AAQ72555 Mouse flk	769	10.8	60.0	41	6	ABZ49883
60.0	27	2	AAQ86063	AAQ86063 PCR prime	770	10.8	60.0	41	6	ABZ43699
60.0	27	3	AAQ73600	AAQ73600 Reverse p	771	10.8	60.0	41	6	ABZ47506
60.0	27	4	AAH19584	AAH19584 PCR prime	C 772	10.8	60.0	41	6	ABZ43743
60.0	27	5	AAF29341	AAF29341 PCR prime	C 773	10.8	60.0	41	6	ABZ44239
60.0	27	6	ABL91377	ABL91377 Chlamydia	C 774	10.8	60.0	41	6	ABA05969
60.0	27	6	ABK29293	ABK29293 Candida d	C 775	10.8	60.0	41	6	ABA05970
60.0	28	4	AAH19816	AAH19816 Antisense	C 776	10.8	60.0	41	7	ACC59104
60.0	28	6	AD31897	AD31897 Borrelia	C 777	10.8	60.0	42	4	AAI13888
60.0	28	6	AD31954	AD31954 Human can	C 778	10.8	60.0	42	6	AAI13888
60.0	29	2	AAQ98233	AAQ98233 Primer us	C 779	10.8	60.0	44	4	AAI13888
60.0	29	2	AAQ98233	AAQ98233 Secreted	C 780	10.8	60.0	44	7	AAI13888
60.0	29	2	AAV02220	AAV02220 Oligonucle	781	10.8	60.0	45	2	AAQ61685
60.0	29	2	AAQ02845	AAQ02845 B. subtil	782	10.8	60.0	45	2	AAQ61685
60.0	29	2	AAV70822	AAV70822 PCR prime	783	10.8	60.0	45	2	AAV30775
60.0	29	2	AAV70568	AAV70568 PCR prime	784	10.8	60.0	45	2	AAV30775
60.0	29	3	AAQ04677	AAQ04677 Polymorph	C 785	10.8	60.0	45	2	AAV80380
60.0	29	3	AAQ69977	AAQ69977 VEGF-bind	C 786	10.8	60.0	45	3	AAI12600
60.0	29	4	AAH91395	AAH91395 Human inf	787	10.8	60.0	45	4	AAQ62826
60.0	30	2	AAI13835	AAI13835 Leptospir	788	10.8	60.0	46	2	AAQ34187
60.0	30	3	AAZ54846	AAZ54846 Neisseria	C 789	10.8	60.0	47	3	AAZ68859
60.0	30	3	AAZ55600	AAZ55600 Canine IL	790	10.8	60.0	47	3	AAZ66170
60.0	30	6	ABX67130	ABX67130 Novel Hel	791	10.8	60.0	47	3	AAZ67310
60.0	30	6	ABX69709	ABX69709 Novel Hel	C 792	10.8	60.0	47	3	AAZ69172
60.0	30	6	ABX68179	ABX68179 Novel Hel	793	10.8	60.0	47	3	AAZ65924
60.0	30	6	ABX68511	ABX68511 Novel Hel	C 794	10.8	60.0	47	3	AAZ65924
60.0	30	6	ABX67370	ABX67370 Novel Hel	C 795	10.8	60.0	47	3	AAZ65924
60.0	30	6	ABX68645	ABX68645 Novel Hel	796	10.8	60.0	48	6	AAZ65924
60.0	30	6	ABX69474	ABX69474 Novel Hel	C 797	10.8	60.0	49	2	AAV20544
60.0	30	6	ABX69735	ABX69735 Novel Hel	C 798	10.8	60.0	50	2	AAV76786
60.0	30	6	ABX68178	ABX68178 Novel Hel	C 799	10.8	60.0	50	2	AAZ52064
60.0	30	6	ABX69199	ABX69199 Novel Hel	800	10.8	60.0	50	2	AAZ52064
60.0	30	6	ABX69842	ABX69842 Novel Hel	C 801	10.8	60.0	50	6	ABZ02871
60.0	30	6	ABX69294	ABX69294 Novel Hel	C 802	10.8	60.0	50	6	ABZ02871
60.0	30	7	AAZ55142	AAZ55142 Goat beta	803	10.8	60.0	50	6	ABZ02871
60.0	31	2	AAV67520	AAV67520 Nucleotid	804	10.8	60.0	50	6	ABZ02871
60.0	31	2	AAZ39181	AAZ39181 Human gen	C 805	10.8	60.0	50	6	ABZ02871
60.0	31	2	AAZ39334	AAZ39334 Human gen	806	10.8	60.0	50	6	ABZ02871
60.0	31	4	AAF58281	AAF58281 Primer #3	C 807	10.8	60.0	50	6	ABZ02871
60.0	32	2	AAQ53457	AAQ53457 PLRV inte	808	10.8	60.0	50	6	ABZ02871
60.0	32	2	AAV04290	AAV04290 Fibrinoge	809	10.8	60.0	50	6	ABZ02871
60.0	32	6	AAZ44056	AAZ44056 tRNA-L-P	810	10.8	60.0	50	6	ABZ02871
60.0	32	6	ABT09738	ABT09738 Human PAL	811	10.8	60.0	50	6	ABZ02871
60.0	32	6	ABT09735	ABT09735 Human PAL	C 812	10.8	60.0	51	3	AAA77114
60.0	32	6	ABA00201	ABA00201 Probe TRN	C 813	10.8	60.0	51	3	AAA77114
60.0	33	2	AAQ34492	AAQ34492 pFOG301 p	814	10.8	60.0	51	4	AAI130828
60.0	33	2	AAQ46746	AAQ46746 HIV captu	C 815	10.8	60.0	51	4	AAI130828
60.0	33	2	AAQ89522	AAQ89522 Human imm	816	10.8	60.0	51	4	AAI130828
60.0	33	3	AAZ7020	AAZ7020 Chlamydia	817	10.8	60.0	51	4	AAI130828
60.0	33	3	AAH84184	AAH84184 Human cel	818	10.8	60.0	51	4	AAI130828
60.0	33	6	ABQ78898	ABQ78898 Human zin	C 819	10.8	60.0	51	4	AAI130828
60.0	33	6	ABL91618	ABL91618 Chlamydia	C 820	10.8	60.0	51	5	ABL00702
60.0	33	6	AAI51736	AAI51736 Heparin b	821	10.8	60.0	51	5	ABL00702
60.0	33	6	AAI99808	AAI99808 Human mic	C 822	10.8	60.0	57	2	AAV75979
60.0	34	2	AAZ91936	AAZ91936 Porphorym	823	10.8	60.0	58	2	AAZ91936
60.0	35	2	AAZ47872	AAZ47872 5' primer	824	10.8	60.0	58	4	AAZ47872
60.0	35	3	AAZ57882	AAZ57882 Glucose-6	C 825	10.8	60.0	59	2	AAZ57882
60.0	36	2	AAV11876	AAV11876 Synthetic	C 826	10.8	60.0	59	2	AAZ57882

60.0	59	2	AAZ233040	Aaz233040	Seq ID No	900	10.6	58.9	24	2	AAZ07539	C
60.0	59	2	AAZ233041	Aaz233041	Seq ID No	C 901	10.6	58.9	24	5	AAF23836	F
60.0	59	4	AAF90150	Aaf90150	Nucleotid	C 902	10.6	58.9	24	6	ABT03741	F
60.0	59	4	AAF90149	Aaf90149	Nucleotid	C 903	10.6	58.9	24	6	ABL40235	F
60.0	59	4	AAH90949	Aah90949	Human inf	C 904	10.6	58.9	24	6	ABZ31312	C
60.0	59	6	ABK47205	Abk47205	Nucleic a	C 905	10.6	58.9	24	6	ABZ31312	C
60.0	59	6	ABK47206	Abk47206	Nucleic a	C 906	10.6	58.9	24	6	ABZ31312	C
60.0	60	3	AAAC69871	Aac69871	VEGF-bind	C 907	10.6	58.9	24	7	ACC74479	C
60.0	60	6	ABN41167	Abn41167	Human spl	C 908	10.6	58.9	24	7	ACC74479	C
60.0	60	6	ABN47974	Abn47974	Human spl	C 909	10.6	58.9	24	7	ACC74483	C
60.0	60	6	ABN43256	Abn43256	Human spl	C 910	10.6	58.9	24	7	ACC74483	C
60.0	60	6	ABN44659	Abn44659	Human spl	C 911	10.6	58.9	24	7	ACC74483	C
60.0	60	6	ABN46537	Abn46537	Human spl	C 912	10.6	58.9	25	3	AA668707	F
60.0	60	6	ABN33165	Abn33165	Human spl	C 913	10.6	58.9	25	6	ABN11131	F
60.0	60	6	ABN39655	Abn39655	Human spl	C 914	10.6	58.9	25	6	ABN11125	F
60.0	60	6	ABN40657	Abn40657	Human spl	C 915	10.6	58.9	25	6	ABN11124	F
60.0	60	6	ABN43881	Abn43881	Human spl	C 916	10.6	58.9	25	6	ABN11123	F
60.0	60	6	ABN59416	Abn59416	Human spl	C 917	10.6	58.9	25	6	ABN11128	F
60.0	60	6	ABN45043	Abn45043	Human spl	C 918	10.6	58.9	25	6	ABN11130	F
60.0	60	6	ABN45816	Abn45816	Human spl	C 919	10.6	58.9	25	6	ABN11126	F
60.0	60	6	ABN32726	Abn32726	Human spl	C 920	10.6	58.9	25	6	ABN11127	F
60.0	60	6	ABN49703	Abn49703	Human spl	C 921	10.6	58.9	25	6	ABN11129	F
60.0	60	6	ABN38965	Abn38965	Human spl	C 922	10.6	58.9	25	6	ABT03740	F
60.0	60	6	ABN44217	Abn44217	Human spl	C 923	10.6	58.9	25	7	ABK16400	F
58.9	13	5	ABH38242	Abh38242	Oligonucl	C 924	10.6	58.9	25	7	ACA90090	C
58.9	13	5	ABF81610	Abf81610	Oligonucl	C 925	10.6	58.9	25	8	AD47127	F
58.9	13	5	ABF93804	Abf93804	Oligonucl	C 926	10.6	58.9	25	8	ACI60975	F
58.9	13	5	ABF93805	Abf93805	Oligonucl	C 927	10.6	58.9	25	8	ACI19470	F
58.9	13	5	ABF81611	Abf81611	Oligonucl	C 928	10.6	58.9	25	8	ACI14718	F
58.9	13	5	ABH38243	Abh38243	Oligonucl	C 929	10.6	58.9	25	8	ACI42001	F
58.9	17	2	AAV94685	Aav94685	Human IL-	C 930	10.6	58.9	25	8	ACI19471	F
58.9	17	6	AAFO4513	Aaf04513	Hammerhea	C 931	10.6	58.9	25	8	ACI95656	F
58.9	17	6	ABNO6221	Abn06221	Human GDM	C 932	10.6	58.9	25	8	ACI60289	F
58.9	18	6	ABK94520	Abk94520	Human BRC	C 933	10.6	58.9	25	8	ACI35893	F
58.9	19	3	AAZ72936	Aaz72936	Human bia	C 934	10.6	58.9	25	8	ACK15714	F
58.9	19	3	AAZ72982	Aaz72982	Human bia	C 935	10.6	58.9	25	8	ACK15714	F
58.9	20	2	AAQ44556	Aaq44556	Antisense	C 936	10.6	58.9	25	8	ACI51157	F
58.9	20	2	AAO1802	Aat01802	Peptide n	C 937	10.6	58.9	25	8	ACH59223	I
58.9	20	2	AAZ03069	Aat33069	Antisense	C 938	10.6	58.9	25	8	ACH59097	I
58.9	20	2	AAZ05977	Aaz05977	PCR prime	C 939	10.6	58.9	25	8	ACH59728	I
58.9	20	3	AAZ94937	Aaz94937	Eimeria t	C 940	10.6	58.9	25	9	ADC21668	F
58.9	20	3	AAZ72081	Aaz72081	Human bia	C 941	10.6	58.9	25	9	ADC58032	F
58.9	20	3	AAZ48959	Aaz48959	Human VCA	C 942	10.6	58.9	25	9	ADC58032	F
58.9	20	4	AAZ72125	Aaf72125	Human MEX	C 943	10.6	58.9	26	2	AAV28383	F
58.9	20	7	ACC49082	Acc49082	Human apo	C 944	10.6	58.9	26	6	ABK86257	F
58.9	20	7	ACC49098	Acc49098	Human apo	C 945	10.6	58.9	26	9	ABK49903	F
58.9	20	7	ACC49084	Acc49084	Human apo	C 946	10.6	58.9	26	9	AD61701	F
58.9	20	7	ACC49097	Acc49097	Human apo	C 947	10.6	58.9	26	9	AD85914	S
58.9	21	2	AAQ33226	Aaq33226	PCR prime	C 948	10.6	58.9	27	2	AAK67721	F
58.9	21	2	AAQ48948	Aaq48948	Human HT6	C 949	10.6	58.9	27	2	AAK71804	F
58.9	21	2	AAQ80615	Aaq80615	Primer fo	C 950	10.6	58.9	27	2	AAK73889	F
58.9	21	2	AAZ95650	Aat95650	Primer fo	C 951	10.6	58.9	28	2	AAV98156	F
58.9	21	2	AAZ72766	Aat72766	Corn kern	C 952	10.6	58.9	28	6	ABK66201	F
58.9	21	2	AAZ96264	Aat96264	Primer fo	C 953	10.6	58.9	28	6	ABL41272	I
58.9	21	2	AAV56547	Aav56547	Human DP2	C 954	10.6	58.9	29	2	AAZ19907	I
58.9	21	3	AAZ71862	Aaz71862	B. cereus	C 955	10.6	58.9	29	2	AAZ19907	I
58.9	21	3	AAZ70596	Aaz70596	Human bia	C 956	10.6	58.9	30	2	AAQ95026	F
58.9	21	4	AAZ933549	Aaz933549	Human APC	C 957	10.6	58.9	30	2	AAZ93277	I
58.9	21	4	AAZ97209	Aaf97209	Human gen	C 958	10.6	58.9	30	2	AAV33696	F
58.9	21	4	AAZ95907	Aaf95907	Human gen	C 959	10.6	58.9	30	3	AAA48381	F
58.9	21	6	ABK65777	Abk65777	Human sin	C 960	10.6	58.9	30	5	AAZ27968	F
58.9	21	6	ABK67230	Abk67230	DPI, SRPI	C 961	10.6	58.9	30	6	ABX03627	F
58.9	21	7	ABZ79350	Abz79350	Acetyl-Co	C 962	10.6	58.9	30	6	ABX69888	F
58.9	21	7	ACA64567	Acc64567	C. elegans	C 963	10.6	58.9	30	6	ABX69888	F
58.9	22	2	AAQ72555	Aaq72555	Adenonato	C 964	10.6	58.9	30	7	ACC44836	N
58.9	22	2	AAZ28071	Aaz28071	Ataxia te	C 965	10.6	58.9	30	7	ABZ70624	N
58.9	22	2	AAZ28818	Aaz28818	Rac membr	C 966	10.6	58.9	31	2	AAZ70624	N
58.9	23	2	AAZ01025	Aat01025	Snake sex	C 967	10.6	58.9	31	2	AAZ70624	N
58.9	23	2	AAZ88612	Aax88612	Human chr	C 968	10.6	58.9	31	3	AAA06171	C
58.9	23	4	AAZ92236	Aaf92236	Human IGE	C 969	10.6	58.9	31	3	AAA06171	C
58.9	23	6	ABA98579	Ab98579	Human PP9	C 970	10.6	58.9	31	5	AAH45146	F
58.9	24	2	AAZ83543	Aax83543	Sunflower	C 971	10.6	58.9	31	6	ABZ52445	F
58.9	24	2	AAZ07541	Aax07541	Clostridi	C 972	10.6	58.9	31	6	ABA93079	I

58.9 32 2 AAT97443 Human cyt  
 58.9 32 3 AAZ54714 Neisseria  
 58.9 32 6 ABK66218 Human gen  
 58.9 32 6 ABK66220 Human gen  
 58.9 33 2 AAT16703 Forward p  
 58.9 33 2 AAX31827 PCR prime  
 58.9 33 5 AAF63960 Human tan  
 58.9 33 6 ABK13250 Yeast SLF  
 58.9 33 6 ABQ72946 Calman cr  
 58.9 33 6 AAL39946 Human lar  
 58.9 33 6 AAL42595 Human dyn  
 58.9 33 6 ABX14183 Zinc fing  
 58.9 33 6 ABN87605 Human cop  
 58.9 33 9 ACF79280 Phage T5/  
 58.9 34 2 AAX91970 Porphyrom  
 58.9 35 3 AAZ55061 Neisseria  
 58.9 35 6 ABS67336 Chlamydia  
 58.9 36 2 AAG74604 Primer fo  
 58.9 36 2 AAG74513 Primer fo  
 58.9 36 2 AAT61298 Primer A  
 58.9 36 6 ABS76584 Human ind  
 58.9 40 6 ABX10490 Human BRC  
 58.9 41 2 AAG26585 CAEV PCR  
 58.9 41 4 AAH49770 Human gro  
 58.9 41 6 AAL39948 Human lar  
 58.9 41 6 AAL39949 Human lar  
 58.9 41 6 ABQ79276 Probe #2  
 58.9 41 9 ADE25942 GalNAC-tr

## ALIGNMENTS

andard; DNA; 18 BP.

) (first entry)

se PCR primer SEQ ID NO:16.

oma; oesophagus; malignancy; PCR primer; ss.

s.

-Al.

; 2002WO-US006504.

2001US-0273277P.

V PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

32795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 the esophagus comprising conducting a PCR amplification on a DNA sample in  
 a mixture.

age 40; 141pp; English.

The present invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 mixture comprising denaturing, annealing and elongating steps  
 where the elongating step may be conducted at the same temperature as the  
 annealing step. The second amplification stage of (M1) is conducted under

different reaction conditions from that of the first amplification  
 to modulate the relative rate of production of the first amplification  
 first primer set and a second amplification by a second primer set  
 first and second amplification stages. Also described: (1) an  
 oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 PCR diagnostic; (3) rapid detection of a malignancy or of metast  
 adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 automated PCR system. (M1) is useful for detecting malignancies  
 adenocarcinoma of the oesophagus. (M1) eliminates contamination  
 decreases the time it takes to carry out a PCR reaction. The pr  
 sequence represents a glucuronidase (gus) PCR primer, which is  
 example from the present invention

Sequence 18 BP; 3 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTCATTGGGAATTTGGC 18  
 |||||  
 Db 1 CTCATTGGGAATTTGGC 18

## RESULT 2

ABQ82537

ID ABQ82537 standard; DNA; 22 BP.

AC ABQ82537;

DT 18-DEC-2002 (first entry)

DE Beta-glucuronidase PCR primer SEQ ID NO:3.

KW Adenocarcinoma; oesophagus; malignancy; PCR primer; ss.

OS Homo sapiens.

XX WO200270751-Al.

XX 12-SEP-2002.

PF 04-MAR-2002; 2002WO-US006504.

PR 02-MAR-2001; 2001US-0273277P.

PA (UYPI-) UNIV PITTSBURGH.

PI Godfrey TE, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

XX WPI; 2002-732795/79.

Multiplex PCR method for detecting malignancies, e.g. adenocarc  
 the esophagus comprises conducting a PCR amplification on a DNA  
 a PCR reaction mixture.

PS Claim 4; Page 30; 141pp; English.

The present invention describes a multiplex polymerase chain re  
 (PCR) (M1) comprising conducting PCR on a DNA sample in a react  
 mixture conducted in first and second amplification stages, eac  
 or more PCR cycles comprising denaturing, annealing and elongat  
 where the elongating step may be conducted at the same temperat  
 annealing step. The second amplification stage of (M1) is condu  
 different reaction conditions from that of the first amplificat  
 to modulate the relative rate of production of the first amplif  
 first primer set and a second amplicon by a second primer set d  
 first and second amplification stages. Also described: (1) an  
 oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 PCR diagnostic; (3) rapid detection of a malignancy or of metast  
 adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 automated PCR system. (M1) is useful for detecting malignancies  
 adenocarcinoma of the oesophagus. (M1) eliminates contamination

09:38:22 2004

us-10-090-326-16.max.rng

ie time it takes to carry out a PCR reaction. The present  
presents a beta-glucuronidase (beta-gus) PCR primer, which is  
example from the present invention

BP; 4 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

100.0%; Score 18; DB 6; Length 22;

ilarity 100.0%; Pred. No. 43;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGGAATTTGCC 18

|||||

ATTGGGAATTTGCC 18

undard; DNA; 22 BP.

(first entry)

relating to the invention ZC40,574 SEQ ID NO:128.

umer; zcytor17; antiinflammatory; dermatological;  
ssive; antimicrobial; vaccine; inflammatory disease;  
/ bowel disease; ulcerative colitis; Crohn's disease;  
itis; eczema; psoriasis; endotoxaemia; septicemia;  
syndrome; infectious disease.

-A2.

2003WO-US001984.

2002US-0350325P.

2002US-0375323P.

2002US-0435315P.

GENETICS INC.

Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;

Gross JA, Dillon SR;

18179/58.

7 ligand polypeptides, useful for treating inflammatory  
ach as inflammatory bowel disease, ulcerative colitis, Crohn's  
pic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.

SEQ ID NO 128; 372pp; English.

on relates to a novel isolated zcytor17 ligand polypeptide. A  
of the invention has antiinflammatory, dermatological,  
assive, and antimicrobial activity, and may have a use in a  
a polypeptide is useful for treating inflammatory diseases,  
lammatary bowel disease, ulcerative colitis, Crohn's disease,  
atitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
me or infectious diseases. The present sequence is used in  
fication of the invention.

BP; 4 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

100.0%; Score 18; DB 9; Length 22;

ilarity 100.0%; Pred. No. 43;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CATTGGGAATTTGCC 18

|||||

Db 1 CTCATTGGGAATTTGCC 18

RESULT 4

ADD36583/c

ID ADD36583 standard; DNA; 52 BP.

XX

AC ADD36583;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human papillomavirus E6 gene-specific preferred PCR primer/prob

XX

KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervic

XX

KW cervical cell; cervix; PCR; primer; probe; ss.

XX

OS Human papillomavirus.

XX

PN WO2003057914-A2.

XX

PD 17-JUL-2003.

XX

PF 07-JAN-2003; 2003WO-GB0000034.

XX

PR 07-JAN-2002; 2002GB-00000239.

PR

19-JUN-2002; 2002GB-00014124.

XX

PA (NORC-) NORCHIP AS.

PA

(ALLA/) ALLARD S J.

XX

PI Karlsen F;

XX

DR MPI; 2003-587136/55.

XX

PT An in vitro method of screening human subjects to assess their  
PT developing cervical carcinoma, comprises screening the subject  
PT expression of mRNA transcripts from the L1 gene and the E6 gene  
PT papillomavirus.

XX

PS Disclosure; Page 47; 102pp; English.

XX

CC This invention relates to a novel method for the detection of h  
CC papillomavirus mRNA for use in the screening of human female su  
CC assesses their risk of developing cervical carcinoma. The inventi  
CC comprises screening the subject for expression of mRNA transcri  
CC the L1 gene and the E6 gene of human papillomavirus, where subj  
CC positive for expression of L1 and/or E6 mRNA are scored as bein  
CC of developing cervical carcinoma. The presence of the human  
CC papillomavirus (in particular HPV16 and HPV18) has been associa  
CC cervical cancer in numerous epidemiological studies. The method  
CC invention are useful for screening human subjects to assess the  
CC developing cervical carcinoma, or for identifying human subj  
CC abnormal cell changes in the cervix. The present sequence is th  
CC preferred PCR primer (which may also be suitable as a probe) wh  
CC used to amplify the E6 gene of human papillomavirus in the meth  
CC invention.

XX

SQ Sequence 52 BP; 19 A; 12 C; 10 G; 11 T; 0 U; 0 Other;  
Query Match 82.2%; Score 14.8; DB 9; Length 52;  
Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18

|||||

Db 47 CTCATTGGGAATCGTGCC 30

RESULT 5

ADD22161/c

ID ADD22161 standard; DNA; 52 BP.

XX

AC ADD22161;

(first entry)

transcribed mRNA detecting NASBA primer/probe #63.

apillomavirus; HPV; NASBA; primer; probe; PCR; ss.

lomavirus type 31.

7-A2.

; 2003WO-GB000030.

; 2002GB-00000258.

CHIP AS.

ARD S J.

87141/55.

cleotide primer and probe for detecting the presence of mRNA from the E6 gene of a human papillomavirus in clinical

Page 19; 28pp; English.

on relates to a novel oligonucleotide molecule used for RNA transcribed from the E6 gene of a human papillomavirus oligonucleotide comprises any of the 133 fully defined having 17-26 bp given in the specification. The invention provides the detection of HPV mRNA in a test sample suspected of HPV, comprising performing an amplification reaction on a of a nucleic acid isolated from the test sample to amplify a the mRNA transcribed from the E6 gene of HPV, where the on reaction is performed using the primer-pair of tide cited above. The invention also provides: a reagent kit the detection of HPV by NASBA, comprising an oligonucleotide and, optionally, an enzyme mixture comprising an RNA directed ase, a ribonuclease that hydrolyzes the RNA strand of an RNA- without hydrolyzing single or double stranded RNA or DNA, and merase that recognises the promoter sequence present in at ASBA P1 primer oligonucleotide included in the reagent kit. cleotide of the invention is useful in detecting mRNA from the E6 gene of HPV in clinical samples. This ide sequence represents an oligonucleotide used for detecting ribed from the E6 gene of a human papillomavirus (HPV) of the

BP; 19 A; 12 C; 10 G; 11 T; 0 U; 0 Other;

ilarity 82.2%; Score 14.8; DB 9; Length 52;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CAATTGGGAATTTTGC 18

|||||

'CAATTGGGATCGTGC 30

andard; DNA; 20 BP.

(first entry)

ie biallelic marker primer 98.

KW Biallelic marker; human; high density disequilibrium map; disea  
KW identification; Alzheimer's disease; drug response; drug effica  
KW drug toxicity; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9904038-A2.

XX PD 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-IB001193.

XX PR 18-JUL-1997; 97EP-00401740.

XX PR 21-APR-1998; 98US-0082614P.

XX PA (GEST ) GENSET.

XX FI Cohen D, Blumenfeld M, Tchoumakov I;

XX DR WPI; 1999-132278/11.

XX Production of biallelic markers - by obtaining a genomic DNA li  
PT determining the order and sequence of DNA fragments and identif  
PT nucleotides which vary between individuals.

XX Example 7; Page 227; 288pp; English.

XX This invention describes a novel method for obtaining a set of  
CC markers represented in AAX52533-X52632 and AAX52833-X52843 for  
CC constructing a high density equilibrium map of the human genome  
CC method involves (a) obtaining a nucleic acid library comprising  
CC DNA fragments comprising the full genome or a portion (b) deter  
CC order of genomic DNA fragments in the genome, (c) determining t  
CC sequence of selected regions of the genomic DNA fragments and (d  
CC identifying nucleotides in the genomic DNA fragments which vary  
CC individuals, thereby defining a set of biallelic markers. The m  
CC be used for identifying traits such as disease (e.g. Alzheimer  
CC disease), drug response, drug efficacy and drug toxicity. They  
CC used for selecting an individual for inclusion in a clinical tr  
CC method is used to map the position of genes in a genome (prefer  
CC human genome). The sequences described in AAX52633-X52832 and A  
CC X52868 represent primers used in the method of the invention  
XX

SQ Sequence 20 BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 77.8%; Score 14; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0;

Qy 3 CAATTGGGAATTTTG 16

|||||

Db 3 CAATTGGGAATTTTG 16

RESULT 7

AAX76753

ID AAX76753 standard; DNA; 20 BP.

XX AAX76753;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID N

XX Human genome; biallelic marker; high density disequilibrium map  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.

OS Homo sapiens.

99WO-1B000822.

98US-0082614P.

98US-0109732P.

RET.

umenfeld M, Chumakov I;

3267/01.

ilic markers used to construct a high density disequilibrium human genome.

je 2599; 2745pp; English.

AAZ69578 represent human biallelic markers from the present which contain a polymorphic base at position 24 of their sequences. AAZ69579 to AAZ77440 represent amplification the biallelic markers. The biallelic markers of the invention ity of uses: they can be used for high density mapping of the , and in complex association studies and haplotyping studies eful in determining the genetic basis for disease states. ; and methods of the invention can also be useful for the on of the targets for the development of pharmaceutical diagnostic methods, as well as the characterisation of the efficacious responses to and side effects from al agents acting on a disease as well as other treatment. ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and it actually given a sequence in the Sequence Listing from the ntion

BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;

larity 77.8%; Score 14; DB 3; Length 20;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTGGAATTG 16

|||||

TTGGAATTG 16

andard; DNA; 41 BP.

(first entry)

hormone protein family 10 coding sequence probe #1.

h hormone protein family 10; cancer; HIV infection; immunological disease; inflammation; gene therapy; probe; ss.

-A1.

: 2000WO-CN000654.

: 99CN-00127207.

/ FUDAN.

NGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;

XX

DR WPI; 2001-432886/46.

XX

PT Growth hormone protein family 10 and encoded polynucleotide, us  
PT diagnosis and treatment of malignant tumor, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.

XX

PS Example 7; Page 21; 35pp; Chinese.

XX

CC The present invention provides the protein and coding sequences  
CC growth hormone protein family 10. The sequences are useful in th  
CC treatment of cancer, HIV infection, haemopathy, immunological di  
CC and inflammation. The present sequence is a probe for the coding  
CC of the invention

XX

SQ Sequence 41 BP; 14 A; 6 C; 9 G; 12 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 4; Length 41;

Best Local Similarity 88.2%; Pred. NO. 4.5e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCATTGGAAATTTGCC 18

| | | | | | | | | |

Db 8 TGATTGAAATTTGCC 24

RESULT 9

AAV94759

ID AAV94759 standard; RNA; 17 BP.

XX

AC AAV94759;

XX

DT 24-FEB-1999 (first entry)

XX

DE Human IL-2 receptor g-chain substrate position 1238.

XX

KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain  
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; c  
KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
KW graft rejection; ss.

XX

OS Homo sapiens.

XX

PN WO9824913-A2.

XX

PD 11-JUN-1998.

XX

PF 02-DEC-1997; 97WO-US021748.

XX

PR 03-DEC-1996; 96US-00758306.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PI Stinchcomb DT, Mcswiggen JA;

XX

WPI; 1998-333332/29.

XX

PT Ribozymes targetted to interleukin 2 - useful for treating e.g.  
PT autoimmune disease and allergies.

XX

PS Claim 4; Page 36; 6lpp; English.

XX

CC The present sequence describes ribozymes targeted to n  
CC the synthesis and/or expression of interleukin (IL)-2R gamma enc  
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, a  
CC AAV94575 to AAV95260 represent specifically claimed substrate se  
CC from the present invention. The ribozymes can be used for the t  
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,  
CC and other inflammatory conditions. The ribozymes are also used t  
CC tolerance in a recipient to alloantigen from a donor

XX

BP; 3 A; 1 C; 5 G; 0 T; 8 U; 0 Other;

74.4%; Score 13.4; DB 2; Length 17;  
ilarity 40.0%; Pred. No. 6.7e+03;  
Conservative 8; Mismatches 1; Indels 0; Gaps 0;

CATTGGAATTTT 15  
|:|||||:  
GAUUGGAUUU 17

andard; DNA; 21 BP.

(first entry)

zavirus Type 3 detecting biotinylated probe PIV3C.

microorganism; infectious disease pathogen; screening;  
polymerase chain reaction; digoxigenin-labelling; diagnostic;  
tract; antibiotic; detection; ss.

za virus.

Al.

;

; 97DE-01016456.

; 97DE-01016456.

MITT H.

84377/50.

ion of microorganisms, especially respiratory tract pathogens  
lex polymerase chain reaction on sample which been partly  
o reverse transcription and then digoxigenin-labelling the  
h probes corresponding to primers used in PCR.

ge 5; 7pp; German.

.5070 are probes used in a process for the identification of  
sms, especially infectious disease pathogens. The method  
forming a simultaneous amplification of several target  
multiplex polymerase chain reaction) in which a patient sample  
d with a solution containing several primers and where a part  
le has been subjected to a previous reverse transcription for  
a-possessing pathogen. The PCR product is subjected to  
labelling with selected probes corresponding to the primers  
sence of a microorganism (relating to the primer) is detected  
sample-evaluation and/or photometrically measurable colour  
tion of the sample. The method allows the rapid screening of  
fectious diseases especially of the respiratory tract and can  
a diagnostic aid indicating whether antibiotics are required

BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

74.4%; Score 13.4; DB 2; Length 21;  
ilarity 93.3%; Pred. No. 6.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CATTGGAATTTT 15  
|:|||||:  
CTTTTGAATTTT 1

RESULT 11  
AAA14173/c  
ID AAA14173 standard; DNA; 21 BP.  
XX  
AC AAA14173;  
XX  
DT 15-SEP-2003 (revised)  
DT 21-JUL-2000 (first entry)  
XX  
DE PIV-3 fusion protein gene 5' non-coding region probe piv31, SEQ  
XX  
KW Acute respiratory tract infection; multiplex reverse transcript  
paediatric; detection; identification; human respiratory syncyt  
parainfluenza virus type 1; parainfluenza virus type 3;  
KX  
KW Mycoplasma pneumoniae; Chlamydia pneumoniae; human enterovirus;  
KX  
KW influenza virus type A; influenza virus type B; adenovirus;  
KX  
KW Bordetella pertussis; Bordetella parapertussis; hybridisation F  
XX  
OS Human parainfluenza virus 3.  
XX  
PN WO200017391-A1.  
XX  
PD 30-MAR-2000.  
XX  
PF 22-SEP-1999; 99WO-EP007065.  
XX  
PR 24-SEP-1998; 98EP-00870203.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Janes G, Schmitt H;  
XX  
DR WPI; 2000-283612/24.  
XX  
PT Identifying organisms causing acute respiratory tract infection  
PT reverse transcription-polymerase chain reactions.  
XX  
PS Claim 7; Page 23; 45pp; English.  
XX  
CC The invention relates to a novel method for the detection of ac  
respiratory tract infection via multiplex reverse transcriptase  
PCR). The method comprises the simultaneous amplification of se  
target nucleotide sequences of different species origin present  
biological sample, and uses primer sets designed to amplify ger  
of a variety of organisms implicated in causing acute respirat  
infection. The amplified DNA is then detected via the use of a  
and gene-specific probe. The gene regions that are amplified ar  
in the method of the invention are the human respiratory syncyt  
(RSV) fusion glycoprotein F1 subunit gene; the parainfluenza vi  
CC (PIV-1) haemagglutinin neuraminidase gene; the parainfluenza vi  
CC (PIV-3) fusion protein gene 5' non-coding region; the 16S rRNA  
from Mycoplasma pneumoniae and Chlamydia pneumoniae; the human  
enterovirus 5' non-coding region; the non-structural protein ge  
influenza virus type A (InfA) and type B (InfB); and the hexon  
adenoviruses. The spacer region between the 16S and 23S rRNA se  
M. pneumoniae, C. pneumoniae, Bordetella pertussis and Bordetel  
parapertussis may also be amplified and detected. The method of  
invention makes it possible to detect the presence of a range c  
microorganisms which infect the respiratory tract, particularly  
children, using one amplification step. The different microorga  
be detected simultaneously within one day. The precise identifi  
the causative organism(s) of acute respiratory tract infection  
CC patient should result in more tailored antibiotic therapies, an  
usage of antibiotics. This would in turn help to delay the emer  
antibiotic resistant bacteria, and would reduce side-effects an  
healthcare costs. Sequences AAA14161-A14176, AAA14184-A14194 an  
CC - AAA14217 represent gene-specific hybridisation probes used in  
practice and exemplifications of the invention. (Updated on 15-  
CC to standardise OS field)  
XX  
SQ Sequence 21 BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

74.4%; Score 13.4; DB 3; Length 21;  
 Query Match 74.4%; Score 13.4; DB 3; Length 21;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;  
 Query 1 CTCATTGGGAATTTT 15  
 |||||  
 Db 15 CTCATTGGGAATTTT 1

standard; DNA; 21 BP.

(revised)  
 (first entry)

1 protein gene 5' non-coding region probe, SEQ ID NO:3.  
 detection; multiplex reverse transcriptase-PCR;  
 detection; identification; human respiratory syncytial virus;  
 za virus type 1; parainfluenza virus type 3;  
 pneumoniae; Chlamydia pneumoniae; human enterovirus;  
 irus type A; influenza virus type B; adenovirus;  
 pertussis; Bordetella parapertussis; hybridisation probe; ss.  
 influenza virus 3.  
 -Al.

; 99WO-EP007065.

; 98EP-00870203.

GENETICS NV.

Schmitt H;

33612/24.

organisms causing acute respiratory tract infections via a  
 ascription-polymerase chain reactions.

Page 15; 45pp; English.

on relates to a novel method for the detection of acute  
 tract infection via multiplex reverse transcriptase-PCR (RT-  
 method comprises the simultaneous amplification of several  
 actide sequences of different species origin present in a  
 sample, and uses primer sets designed to amplify gene regions  
 of organisms implicated in causing acute respiratory tract  
 the amplified DNA is then detected via the use of a species-  
 specific probe. The gene regions that are amplified and detected  
 of the invention are the human respiratory syncytial virus  
 1 glycoprotein F1 subunit gene; the parainfluenza virus type 1  
 haemagglutinin neuraminidase gene; the parainfluenza virus type 3  
 ion protein gene 5' non-coding region; the 16S rRNA sequences  
 pneumoniae and Chlamydia pneumoniae; the human  
 5' non-coding region; the non-structural protein genes from  
 irus type A (InfA) and type B (InfB); and the hexon gene from  
 s. The spacer region between the 16S and 23S rRNA sequences of  
 ae, C. pneumoniae, Bordetella pertussis and Bordetella  
 is may also be amplified and detected. The method of the  
 makes it possible to detect the presence of a range of  
 sms which infect the respiratory tract, particularly in  
 sing one amplification step. The different microorganisms can  
 simultaneously within one day. The precise identification of  
 ve organism(s) of acute respiratory tract infection in a  
 uid result in more tailored antibiotic therapies, and reduced

CC usage of antibiotics. This would in turn help to delay the emer  
 CC antibiotic resistant bacteria, and would reduce side-effects an  
 CC healthcare costs. Sequences AAA14161-Al4176, AAA14184-Al4194 an  
 CC - AAA14217 represent gene-specific hybridisation probes used in  
 CC practice and exemplifications of the invention. (Updated on 15-  
 CC to standardise OS field)

XX SQ Sequence 21 BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 74.4%; Score 13.4; DB 3; Length 21;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;  
 Query 1 CTCATTGGGAATTTT 15  
 |||||  
 Db 15 CTCATTGGGAATTTT 1

# RESULT 13

AAH27357  
 ID AAH27357 standard; DNA; 23 BP.  
 XX AC AAH27357;  
 XX DT 08-AUG-2001 (first entry)  
 XX DE PCR primer #26.  
 XX KW Tumour suppressor gene 16; TSG16; immune response modulator;  
 KW inflammatory response modulator; signal transduction activator;  
 KW cytokine inhibitor; gene therapy; anticancer; anti-inflammatory  
 KW autoimmune disorder; infection; chromosome 16q24.3; human;  
 KW cellular proliferation suppressor; PCR primer; ss.  
 XX OS Homo sapiens.  
 XX DN WO200132861-Al.  
 XX PD 10-MAY-2001.  
 XX PF 30-OCT-2000; 2000WO-AUG01329.  
 XX PR 29-OCT-1999; 99AU-00003771.  
 XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
 XX Callen DF, Whitmore SA, Kremmidiotis G, Kochetkova M, Crawf  
 WPI; 2001-316439/33.

XX New nucleic acid representing the human tumor suppressor gene T  
 PT useful e.g. for diagnosis and treatment of tumors, inflammatory  
 PT immunological disorders.

PS Disclosure; Page 192; 215pp; English.

XX The present invention relates to human tumour suppressor gene 1  
 CC see AAH23688). TSG16 was isolated from chromosome 16q24.3. TSG1  
 CC suppresses cellular proliferation. TSG16 is useful for treating  
 CC associated with decreased expression or activity of TSG16, e.g.  
 CC (auto)immune disorders, inflammation, complications of wound he  
 CC infections (by viruses, bacteria, fungi, parasites, protozoa or  
 CC helminths). The present sequence is a PCR primer, which was use  
 CC present invention

XX SQ Sequence 23 BP; 3 A; 5 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 8.5e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 Query 1 CTCATTGGGAATTTGCC 18  
 |||||



TTTTCGAATTTGTC 20

andard; DNA; 30 BP.

(first entry)

agment PCR primer MPSYN787.

e therapy; vaccine; ALVAC; translation factor; K3L; E3L; HIV;  
; ss.

odeficiency virus 1.

1.

; 98WO-US003710.

; 97US-00815809.

OGENETICS CORP.  
V ARIZONA STATE.

, Jacobs BL, Goebel SJ, Cox WI, Gettig RR, Pincus SE;

20819/44.

xpression of nucleic acids in cells - by using modified  
ch comprise the nucleic acid and also nucleic acid encoding a  
factor.

Page 50; 90pp; English.

YN787 and MPSYN788 (see AAV58255) were used in the PCR  
on of a 210 bp fragment (C) containing HIV Pol2, using PHXBD2,  
ins the entire proviral DNA sequence of HIV IIB, as template.  
, a 270 bp fragment (D) containing Nef1 was obtained using  
YN789 and MPSYN790 (see AAV58256-57), and a 170 bp fragment  
ing Poll was prepared using primers MPSYN791 and MPSYN92 (see  
). Fragments C and D were combined using MPSYN787/MPSYN790,  
, and E using MPSYN789/MPSYN792, and fragments C+D and D+E  
is MPSYN787/MPSYN792 to produce a Pol2/Nef central  
) fragment. This was utilised in the 'string of beads'  
pMPC5H6PN and hence in recombinants vCP1433 (see AAV58243)  
(see AAV58244). The invention relates to novel vectors that  
ed expression of nucleic acids in cells through the actions of  
rus K3L and E3L sequences (see AAW71644 and AAW30564) that  
nslation. Immunological, vaccine and therapeutic compositions  
such vectors are claimed

; BP; 10 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 2; Length 30;

Conservative 83.3%; Pred. No. 8.6e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTGTC 18

|||||

TACTTTGGAATATTGCC 12

andard; DNA; 30 BP.

AAV60282;  
XX 15-FEB-1999 (first entry)  
XX HIV-1 Pol2 fragment PCR primer MPSYN787.  
XX Vector; gene therapy; vaccine; ALVAC; translation factor; K3L;  
KW HIV-1; PCR; primer; ss.  
XX Synthetic.  
OS Human immunodeficiency virus 1.  
XX WO98040501-A1.  
FN 17-SEP-1998.  
XX 13-FEB-1998; 98WO-US002669.  
XX 12-MAR-1997; 97US-00816155.  
XX (VIRO-) VIROGENETICS CORP.  
XX Tartaglia J, Cox WI, Gettig RR, Martinez H, Paoletti E;  
PI Pincus SE;  
XX MPI; 1998-520820/44.  
XX Enhancing expression of nucleic acids in cells - by using modif  
vectors which comprise nucleic acid and also nucleic acid encod  
transcription factor and optionally translation factor.  
XX Example 2; Page 60; 102pp; English.  
XX Primers MPSYN787 and MPSYN788 (see AAV60283) were used in the P  
amplification of a 210 bp fragment (C) containing HIV Pol2, usi  
which contains the entire proviral DNA sequence of HIV IIB, as  
In addition, a 270 bp fragment (D) containing Nef1 was obtained  
primers MPSYN789 and MPSYN790 (see AAV60284-85), and a 170 bp f  
(E) containing Poll was prepared using primers MPSYN791 and MPS  
AAV60286-87). Fragments C and D were combined using MPSYN787/M  
fragments D and E using MPSYN789/MPSYN792, and fragments C+D an  
using primers MPSYN787/MPSYN792 to produce a Pol2/Nef central  
CC (Nef1)/Poll) fragment. This was utilised in the 'string of bea  
cassette of pMPC5H6PN and hence in recombinants vCP1433 (see AA  
CC and vCP1452 (see AAV60250). The invention relates to novel vect  
show enhanced expression of nucleic acids in cells through the  
CC vaccinia virus K3L and E3L sequences (see AAW71365 and AAW30571  
CC enhance translation. Immunological, vaccine and therapeutic com  
CC comprising such vectors are claimed  
XX Sequence 30 BP; 10 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
SQ Query Match 73.3%; Score 13.2; DB 2; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 1 CTCATTGGAATTTGTC 18  
||| ||||| |||||  
Db 29 CTACTTTGGAATATTGCC 12  
RESULT 16  
ABT44474/c  
ID ABT44474 standard; DNA; 30 BP.  
XX  
AC ABT44474;  
XX  
XT 06-NOV-2003 (first entry)  
XX PCR primer Seq ID31 related to nucleic acid delivery and expres  
DE Nucleic acid delivery; nucleic acid expression; bacterium;  
KW bacteriophage P1; bacteriophage mediated transformation;  
KW

promoter; Pac; Bof; Doc; Coi; host cell transformation; psid; prokaryotic cell; eukaryotic cell; PCR; primer; ss.

-A2.

2002WO-US035891.

2001US-0347839P.

2002US-0410398P.

: FOUND RES DEV.

Schofield DA, Westwater C, Dolan JW, Hoel BD; Norris JS;

18513/56.

A nucleic acid comprising a C1-regulated promoter sequence linked to a nucleic acid sequence, and a promoter sequence linked to a second nucleic acid sequence, useful for host cells.

Page 44; 126pp; English.

on relates to a novel methods and materials involved in delivery and expression. In particular, the invention methods and materials involved in bacteriophage mediated on of bacteria. The isolated nucleic acid of the invention bacteriophage P1 C1-regulated promoter sequence operably nucleic acid sequence, and a promoter sequence operably second nucleic acid sequence, wherein the C1-regulated nence, the nucleic acid sequence, and second nucleic acid e heterologous. Bacteriophage P1 proteins Pac, Bof, Doc and g the nucleic acid sequences used for the exemplification of n. The nucleic acids of the invention may be useful for a wide range of host cells. Nucleic acid vectors such as capsids may be used to deliver the nucleic acids of the or the transformation of prokaryotic and eukaryotic cells. The nence is that of a PCR primer which was used in the ion of the invention

BP; 8 A; 6 C; 8 G; 8 T; 0 U; 0 Other;

larity 73.3%; Score 13.2; DB 8; Length 30;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATTGGGAATTTTGGC 18

|||||

ATTAGGATTCGGC 3

undard; DNA; 30 BP.

(first entry)

[ PCR primer #2.

non-lytic; bacteriophage; pathogenic; antimicrobial; PCR;

coli.

-A2.

PD 18-SEP-2003.  
XX  
XX 06-MAR-2003; 2003WO-US006941.  
XX  
PR 06-MAR-2002; 2002US-0362409P.  
PR 15-APR-2002; 2002US-0372892P.  
PR 13-DEC-2002; 2002US-0433178P.  
XX  
XX (MUSC-) MUSC FOUND RES DEV.  
XX  
XX Kasman IM, Kasman A, Westwater C, Dolan JW, Schmidt MG;  
PI Norris JS, Schofield DA,  
XX  
XX WPI; 2003-748394/70.  
XX  
XX New non-lytic bacteriophage comprising a nucleic acid encoding a  
PT agent, useful for treating an infection by a pathogenic organism  
PT delivering nucleic acids encoding antigens or antimicrobial agen  
PT bacteria.

Example 1; Page 22; 94pp; English.

XX The invention relates to a novel non-lytic bacteriophage compris  
CC nucleic acid encoding a lethal agent for treating an infection b  
CC pathogenic organism. A bacteriophage of the invention has antim  
CC activity. The non-lytic bacteriophage is useful for treating an  
CC by a pathogenic organism, or for delivering nucleic acids encod  
CC more polypeptides (e.g. antigens or antimicrobial agents) to bac  
CC The present sequence represents a PCR primer used in the exampl  
CC of the invention.

XX SQ Sequence 30 BP; 8 A; 6 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTTGGC 18

|||||

Db 20 CTCATTAGGATTCGGC 3

RESULT 18

ABV76515/c

ID ABV76515 standard; DNA; 33 BP.

XX AC ABV76515;

XX DT 20-FEB-2003 (first entry)

XX DE Human cytochrome constitutive protein 9.02 PCR primer, SEQ ID N  
XX Human; cytochrome constitutive protein 9.02; recombinant product  
KW gene therapy; malignant tumour; cancer; blood disease; HIV infec  
KW human immunodeficiency virus; immune disorder; inflammatory con  
XX cytostatic; antiinflammatory; immunomodulator; PCR; primer; ss.

XX OS Homo sapiens.

XX PN CN1358756-A.

XX PD 17-JUL-2002.

XX PF 13-DEC-2000; 2000CN-00127871.

XX PR 13-DEC-2000; 2000CN-00127871.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX PI Mao Y, Xie Y;

XX WPI; 2002-733545/80.

XX

epitide-human cytochrome constitutive protein 9.02 and ide for encoding the polypeptide.

Page 18 (Disclosure); 32pp; Chinese.

on relates to human cytochrome constitutive protein 9.02 and nucleic acids encoding it (ABV76512). The protein has a length of 9.02 kb. The invention also relates to a method for the production of the protein, an antagonist of the protein, of the protein, gene and antagonist in therapeutic use. Cytochrome constitutive protein 9.02 can be used in the treatment of a variety of diseases such as malignant tumours, blood disorders (human immunodeficiency virus) infection, immune disorders (AIDS). Sequences ABV76515-ABV76516 represent PCR products in an exemplification of the invention to amplify human constitutive protein 9.02 cDNA for cloning.

BP; 11 A; 8 C; 7 G; 7 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 6; Length 33;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTGTC 18  
| | | | | | | | | |  
CCTTGGGAATTTGTC 16

andard; DNA; 41 BP.

(first entry)

hrome constitutive protein 9.02 probe, SEQ ID NO:8.

chrome constitutive protein 9.02; recombinant production; Y; malignant tumour; cancer; blood disease; HIV infection; deficiency virus; immune disorder; inflammatory condition; antiinflammatory; immunomodulator; probe; ss.

s.

; 2000CN-00127871.

; 2000CN-00127871.

NGHAI BIOWINDOW GENE DEV INC.

Y;

33545/80.

epitide-human cytochrome constitutive protein 9.02 and ide for encoding the polypeptide.

Page 20 (Disclosure); 32pp; Chinese.

on relates to human cytochrome constitutive protein 9.02 and nucleic acids encoding it (ABV76512). The protein has a length of 9.02 kb. The invention also relates to a method for the production of the protein, an antagonist of the protein, of the protein, gene and antagonist in therapeutic use. Cytochrome constitutive protein 9.02 can be used in the treatment of a variety of diseases such as malignant tumours, blood disorders (human immunodeficiency virus) infection, immune disorders (AIDS). Sequences ABV76517-ABV76518 represent human

CC cytochrome constitutive protein 9.02 probes used in an exemplification of the invention

XX Sequence 41 BP; 11 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 41;  
Best Local Similarity 83.3%; Pred. No. 8.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCTTTGGGAATTTGTC 18  
| | | | | | | | | |  
Db 23 CACCTTGGGAATTTGTC 6

RESULT 20

ABS70690/c

ID ABS70690 standard; DNA; 43 BP.

XX AC ABS70690;

XX DT 26-NOV-2002 (first entry)

XX DE Mouse immunoglobulin heavy chain PCR primer #50.

XX KW Chimeric antibody library; display screening method; mouse; immunoglobulin heavy chain; PCR; primer; ss.

XX OS Mus sp.

XX PN US6420113-B1.

XX PD 16-JUL-2002.

XX PF 02-OCT-1999; 99US-00410903.

XX PR 04-APR-1997; 97US-00832985.

XX PR 04-APR-1997; 97US-00835159.

XX PR 03-APR-1998; 98WO-US006704.

XX PA (BIOS-) BIOSITE DIAGNOSTICS INC.

XX PI Buechler J, Valkirs G, Gray J;

XX DR WPI; 2002-626079/67.

XX PT Producing polyclonal libraries of chimeric antibodies for use, diagnostic or therapeutic reagents, using display screening method

XX PS Example 3; Fig 1; 54pp; English.

XX The present invention relates to a new method of producing a chimeric antibody library having affinity for a target, using display screening methods. The method enriches conventional display libraries for displaying more than one copy of the polypeptide. The method also subclones nucleic acids from a display vector to an expression vector where the nucleic acids encode the displayed polypeptides. The invention can be used to produce polyclonal libraries of chimeric antibodies for use, e.g., as diagnostic or therapeutic reagents. The method is based in part on two related but self-sufficient improvement in conventional display methods. The first improvement provides for enriching conventional display libraries for members displaying a single copy of a polypeptide prior to affinity screening of the libraries with a target of interest. These methods can achieve high enrichment in which the vast majority of members retaining full coding sequences encode polypeptides having specific affinity for a target. Additionally, the invention provides methods of subcloning nucleic acids encoding displayed polypeptides of enriched libraries into a display vector to an expression vector without the need for isolation of individual members. The present nucleic acid sequence represents a PCR primer that was used in the methods of the invention to amplify the mouse immunoglobulin heavy chain

XX Sequence 43 BP; 12 A; 9 C; 13 G; 9 T; 0 U; 0 Other;

73.3%; Score 13.2; DB 6; Length 43;  
 ilarity 83.3%; Pred. No. 8.8e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTGGAAATTTGCC 18  
 |||||  
 TATTGGCGTTTGGC 11  
 andard; DNA; 43 BP.

(first entry)  
 yglobulin heavy (H) chain gene amplifying primer# 50.  
 library; diagnostic kit; antibody library; immunoglobulin;  
 / chain; H chain; PCR; primer; ss.

1.  
 ; 97US-00835159.  
 ; 97US-00835159.  
 SITE DIAGNOSTICS INC.  
 schler J, Valkirs G;  
 36289/74.  
 polypeptide library having affinity for a target for use in  
 and therapeutic purposes, comprises producing modified forms  
 asion vector before expression and screening of polypeptides.  
 Fig 1; 50pp; English.  
 on relates to a method for producing a polypeptide library  
 nity for a target. The method involves subcloning DNA encoding  
 : polypeptides of a library of viral particles into multiple  
 i expression vector to produce modified forms of the  
 vector, introducing the modified forms into a host and  
 a library of 10 different polypeptides. The method is used for  
 polypeptide library or an antibody library having affinity  
 :. It is also used to prepare a diagnostic kit or reagent or a  
 composition containing the library of polypeptides. The  
 nence is a PCR primer used for amplifying mouse immunoglobulin  
 main gene. This sequence is used to illustrate the method of  
 on

BP; 12 A; 9 C; 13 G; 9 T; 0 U; 0 Other;  
 73.3%; Score 13.2; DB 9; Length 43;  
 ilarity 83.3%; Pred. No. 8.8e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTGGAAATTTGCC 18  
 |||||  
 TATTGGCGTTTGGC 11  
 andard; DNA; 51 BP.

AC AAL27046;  
 XX 24-JAN-2002 (first entry)  
 XX Human SNP oligonucleotide #254.  
 DE  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytosta  
 neuroprotective; antimicrobial; gene therapy; vaccine; amylase;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadhe  
 cyclin; polymerase; oncogene; histone; kinase; colony stimulat  
 KW complement related protein; cytochrome; kinesin; cytokine; inte  
 KW interleukin; G-protein coupled receptor; thioesterase; inflamma  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, poly  
 oncogenes and histones, useful for diagnosing and treating, e.g  
 autoimmune diseases and infections.  
 PT  
 PT  
 XX  
 PS Claim 1; Page 1467; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding poly  
 variants of proteins related to amylases, amyloid proteins, ang  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncoq  
 CC histones, kinases, colony stimulating factors, complement relat  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interl  
 CC protein coupled receptors and thioesterases. The present sequen  
 CC such oligonucleotide. The oligonucleotides and the peptides enc  
 CC them may be used in the prevention, diagnosis and treatment of  
 CC associated with inappropriate expression of the proteins listed  
 CC Disorders that may be prevented, diagnosed and/or treated inclu  
 CC multifactorial diseases with a genetic component, such as autoi  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabet  
 CC systemic lupus erythematosus and Grave's disease), inflammatio  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of ;  
 CC organisms  
 XX  
 SQ Sequence 51 BP; 18 A; 15 C; 10 G; 8 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 13.2; DB 4; Length 51;  
 Best Local Similarity 83.3%; Pred. No. 8.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGAAATTTGCC 18  
 |||||  
 Db 35 CCATTGGAAATTTGAC 18  
 RESULT 23  
 AAT04743/C  
 ID AAT04743 standard; DNA; 53 BP.  
 XX  
 AC AAT04743;  
 XX  
 DT 10-JUN-1996 (first entry)

P2A, used in the construction of pCSPOL75A.

CPV; ALVAC; attenuated; therapy; prevention; rabies; vector;  
ribbody; CTL1; CTL2; PCR; primer; HIV; ss.

1.

; 95WO-US003989.

; 94US-00223842.

; 95US-00417210.

OGENETICS CORP.

Tartaglia J, Cox WI;

66231/47.

attenuated virus encoding an immunodeficiency virus epitope -  
penhagen strain of vaccinia virus, used in the prevention and  
of diseases, e.g. vaccination against HIV.

Page 127; 208pp; English.

4752 are PCR primers used in the construction of pCSPOL75A, a  
tg. attenuated virus ALVAC recombinant expressing 3 CTL pol  
IVI gag (+pro), gp120 and transmembrane region. ALVAC-based  
viruses expressing extrinsic immunogens are efficacious as  
tators. Attenuated recombinant viruses such as ALVAC or NVAC  
needed to comprise exogenous DNA in a non-essential region of  
e, the exogenous DNA encodes at least one immunodeficiency  
pe. Such attenuated viruses (as above) and derived antigens  
ies are used in the prevention, therapy and diagnosis of  
NA from the recombinant viruses can be used as probes or for  
primers or for immunisation. Attenuated recombinant viruses  
ed safety making them safer for use in vaccines

BP; 21 A; 8 C; 8 G; 16 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 2; Length 53;

Conservative 83.3%; Pred. No. 8.9e+03;  
3; Mismatches 3; Indels 0; Gaps 0;

'CATTGGAAATTTGGC 18

|||||

'ACTTTGGAAATTTGGC 30

andard; DNA; 60 BP.

; (first entry)

red transcript detection oligonucleotide SEQ ID NO:22707.

ie; rat; splice transcript; detection; RNA transcript;  
.ant; transcriptome; oligonucleotide library; ss.

19.

1-A2.

2.

1; 2001WO-IB001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR

XX MPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcription  
genome, useful for detecting tissue-, pathology-, and developme  
specific genes.

PT

XX

PS Example 1; SEQ ID NO 22707; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for d  
messenger RNAs that populate a (sub-)transcriptome, where the ( )  
transcriptome comprises messenger RNAs transcribed from multip  
transcription units that populate a genome. The library compris  
oligonucleotides, each capable of hybridising selectively to a  
messenger RNAs transcribed from a given transcription unit of t  
which encodes one or more messenger RNA splice variants. The  
oligonucleotide libraries are useful for detecting mRNAs from a  
biological sample, in expression profiling studies, in qualitat  
quantitatively characterising the corresponding transcriptome,  
detecting RNA transcripts and splice variants of human or anima  
transcriptomes. The libraries may also be used as specialised m  
libraries to detect transcripts of a sub-transcriptome under a  
biological or pathological state, and so allowing the detection  
- and pathology-specific genes such as those genes only express  
specific tissue under a specific pathological condition; to det  
developmental specific genes; and to detect RNA transcripts and  
variants of a transcriptome of a patient suffering from a parti  
disorder. ABN27253 to ABN59589 represent oligonucleotide sequen  
rats, humans and mice, which are used in the exemplification of  
present invention. N.B. The sequence data for this patent did n  
part of the printed specification, but was obtained in electron  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

Sequence 60 BP; 12 A; 24 C; 11 G; 13 T; 0 U; 0 Other;

Query March

73.3%; Score 13.2; DB 6; Length 60;

Best Local Similarity 83.3%; Pred. No. 9e+03; 3; Indels 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGGC 18

|||||

Db 38 CTCATTGGAAATTTGGC 55

RESULT 25

ABF80741/c

ID ABF80741 standard; DNA; 13 BP.

XX

AC ABF80741;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 180738 for detecting SNP TSC0044732.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; car  
peptide nucleic acid; cytosine methylation; cardiovascular; pri  
central nervous system; gastrointestinal; respiratory; immune;

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

2000DE-01019173.

GENOMICS AG.

penbrock C, Berlin K;

37177/75.

nucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine status.

ID NO 180738; 29pp + Sequence Listing; German.

on describes novel oligonucleotide primers or peptide nucleic oligomers for detecting single nucleotide polymorphisms (SNP) methylation status in chemically pretreated genomic DNA. The oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-BF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH182073 are oligomers described in the invention. NOTE: The sequence is patent did not form part of the printed specification, but is in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0; Mismatches 0; Conservative 0; Mismatches 0; Indels 0;

TGGGAATTTG 16

|||||

TGGGAATTTG 1

undard; DNA; 13 BP.

(first entry)

side SEQ ID NO 180737 for detecting SNP TSC0044732.

nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; eic acid; cytosine methylation; cardiovascular; primer; ss; ous system; gastrointestinal; respiratory; immune; metabolic.

.

A2.

2001WO-1B000713.

2000DE-01019173.

GENOMICS AG.

penbrock C, Berlin K;

37177/75.

nucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine status.

PS Claim 1; SEQ ID NO 180737; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide acid (PNA) oligomers for detecting single nucleotide polymorphisms and cytosine methylation status in chemically pretreated genomic oligonucleotides are used for diagnosis and/or prognosis of cancer range of diseases including immune system, gastrointestinal, respiratory, nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99989, ABH00010-ABH99989, ABH00010-ABH99989 and ABH00010-ABH182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Mismatches 13; Conservative 0; Mismatches 0; Indels 0;

QY 4 ATTGGGAATTTG 16

|||||

Db 1 ATTGGGAATTTG 13

RESULT 27

ABZ30652/c

ID ABZ30652 standard; DNA; 24 BP.

XX AC ABZ30652;

XX DT 30-JAN-2003 (first entry)

XX DE Candida albicans GRACE strain PCR primer SEQ ID NO 4803.

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;

XX signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; PCR; pr;

XX Candida albicans.

XX WO200253728-A2.

XX 11-JUL-2002.

XX 26-DEC-2001; 2001WO-US049486.

XX 29-DEC-2000; 2000US-0259128P.

XX 20-FEB-2001; 2001US-00792024.

XX 22-AUG-2001; 2001US-0314050P.

XX (ELIT-) ELITRA PHARM INC.

XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX WPI; 2002-566694/60.

XX Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one a gene and placing other allele of the gene under conditional expression.

XX Claim 36; SEQ ID NO 4803; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid cells in which both alleles of a gene are modified, comprising one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a hetero-

XX promoter, so that expression of the second allele is regulated by a promoter. (M1) is useful for constructing a strain of diploid cells in which both alleles of a gene are modified. The diploid cells having both alleles modified are useful for identifying a

1 to the survival or growth of a fungus, a gene that to the virulence and/or pathogenicity of a fungus, a gene butes to the resistance of a diploid fungus to an antifungal antifungal agent that inhibits the growth of a diploid fungus ntifying a therapeutic agent for treatment of a mammalian 1) is useful for identifying a compound which modulates the a gene product, preferably enzymatic activity, carbon tabolism, biosynthetic, transporter, transcriptional, al, signal transduction, DNA replication and cell division he method is useful for identifying a compound having the inhibit growth or proliferation of C. albicans cells and for ffection by C. albicans. The present sequence is that of a PCR in the method of the invention. Note: The sequence data for is not represented in the printed specification but is based information supplied to Derwent by the European Patent Office

BP; 11 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

72.2%; Score 13; DB 6; Length 24;  
ilarity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TGGAATTTC 17  
|||||  
TGGAATTTC 2

andard; DNA; 25 BP.

(first entry)

c SNPE primer SEQ ID 863.

eoride polymorphism; SNP; single nucleotide primer extension;  
yping; agammaglobulinaemia; diabetes insipidus; cancer;  
' syndrome; muscular dystrophy; familial hypercholesterolaemia;  
kidney disease; osteogenesis imperfecta; autoimmune disease;  
mittent porphyria; rheumatoid arthritis; multiple sclerosis;  
n; forensic investigation; paternity analysis; primer; ss.

is.

-A2.

; 2000WO-US028436.

; 99US-0160096P.

HID BIOSCIENCES INC.

burg L, Pohl M;

90930/30.

ing oligonucleotide, useful for detecting the presence,  
identity of single polynucleotide polymorphism in a nucleic

ge 54; 83pp; English.

AH37205 - AAH40944 represent PCR primers, single nucleotide  
single (SNPE) primers, and the sequences of regions flanking  
ngle nucleotide polymorphisms SNPs. The present invention  
ts for determining the presence or absence of a SNP, using the  
tides of the invention. The PCR primers are used to amplify a  
g sequence, the SNPE primer is used as a genotyping primer.  
cleotides are useful for genotyping a nucleic acid sample by

performing a single-nucleotide primer extension reaction. The  
oligonucleotides are useful for determining the presence, abser  
identity of a SNP and for genotyping nucleic acid samples, for  
asses by association analysis the genotype of an individual or  
CC individuals, having a pathological phenotypic trait suspected c  
CC caused by one or more SNPs. Phenotypic traits include diseases  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome,  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney di  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenoc  
CC traits also include symptoms of or susceptibility to multifact  
CC disease of which a component is or may be genetic such as autoi  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by  
CC microorganism. The method is also useful in forensic investigat  
CC paternity analysis. The present sequence represents a single nu  
CC primer extension (SNPE) primer specific for a human SNP contain  
CC sequence

Sequence 25 BP; 7 A; 4 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;

Qy 3 CATTGGAAATTT 15  
|||||  
Db 3 CATTGGAAATTT 15

RESULT 29

ABX03639/C

ID ABX03639 standard; DNA; 30 BP.

AC ABX03639;

DT 07-JAN-2003 (first entry)

DE Human aurora 2 protein phosphorylating enzyme related primer #2  
XX Aurora 2 protein phosphorylating enzyme; Aurora 2 protein phosf  
KW primer; ss.

OS Synthetic.

FN JP2002236125-A.

XX 23-AUG-2002.

XX 06-FEB-2001; 2001JP-00029774.

XX 06-FEB-2001; 2001JP-00029774.

PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2002-744730/81.

DR Determination of protein phosphorylation enzyme activity with a  
PT which specifically recognizes a phosphorylated substrate with h  
PT Aurora2 protein phosphorylating enzyme.

XX Example 5; Page 16; 29pp; Japanese.

XX The invention describes a method of determination of human Auro  
CC protein phosphorylating enzyme activity comprising (a) contact  
CC Aurora 2 protein phosphorylating enzyme and a substrate to be  
CC phosphorylated to give phosphorylated substrate, (b) antibody b  
CC step composed of binding of an antibody that solely recognises  
CC phosphorylated substrate and the phosphorylated substrate; and  
CC determination of the bound product. The method, antibody and ki  
CC useful for the determination of phosphorylating activity of hum  
CC 2 protein phosphorylase. This sequence represents a human auro  
CC protein phosphorylating enzyme associated primer

09:38:22 2004

us-10-090-326-16.max.rng

BP; 10 A; 6 C; 7 G; 7 T; 0 U; 0 Other;  
72.2%; Score 13; DB 6; Length 30;  
Identity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ATTGGAATT 13  
|||||  
ATTGGAATT 5

undard; DNA; 50 BP.

(first entry)

: noncoding SNP oligonucleotide SEQ ID NO:213.

le nucleotide polymorphism; SNP; polymorphism; cytostatic;  
ssive; antiinflammatory; neuroprotective; antimicrobial;  
disease; inflammation; cancer; nervous system disease;  
polymorphic protein; ds.

3.

-A2.

: 2000WO-US032311.

: 99US-0167383P.

AGEN CORP.

Leach M;

5949/37.

an nucleic acids comprising one or more single nucleotide  
as, useful for treating a subject suffering from a pathology,  
ane diseases, ascribed to the presence of a sequence  
n.

je 311; 674pp; English.

ABL01104 represent human nucleic acid oligonucleotides  
one or more single nucleotide polymorphisms (SNPs). ABB56531  
represent human peptides encoded by some of the SNP  
ides. The sequences from the present invention can have  
ssive, cytostatic, antiinflammatory, neuroprotective and  
al activities. Nucleic acids, polypeptides, oligonucleotides  
es from the present invention can be used for treating a  
-ering from, at risk for, or suspected of, suffering from a  
cribed to the presence of a sequence polymorphism. The  
y be autoimmune diseases, inflammation, cancer, diseases of  
system, and infection by pathogenic microorganisms. The SNPs  
aful for determining which forms of a characterised  
n are present in individuals. The antibodies may be used in  
on, quantitation and/or cellular or tissue localisation of a  
protein (e.g., for use in measuring levels of the polymorphic  
ain appropriate physiological samples)

BP; 11 A; 9 C; 6 G; 24 T; 0 U; 0 Other;

72.2%; Score 13; DB 5; Length 50;  
Identity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TTTGAATT 15

Db 2 CATTGGAATTT 14

RESULT 31  
AAH38068  
ID AAH38068 standard; DNA; 51 BP.

XX AC AAH38068;

XX DT 14-AUG-2001 (first entry)

XX DE Human SNP flanking oligonucleotide SEQ ID 864.

XX Single nucleotide polymorphism; SNP; single nucleotide primer es;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cance  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholest  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sc  
KW inflammation; forensic investigation; paternity analysis; ds.

XX Homo sapiens.

XX WO200129262-A2.

XX PD 26-APR-2001.

XX PF 13-OCT-2000; 2000WO-US028436.

XX PR 15-OCT-1999; 99US-0160096P.

XX PA (ORCH-) ORCHID BIOSCIENCES INC.

XX PI Picoult-Newburg L, Pohl M;

XX DR WPI; 2001-290930/30.

XX PT New genotyping oligonucleotide, useful for detecting the presen  
PT absence or identity of single polynucleotide polymorphism in a  
PT acid sample.

XX PS Claim 1; Page 54; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nuc  
CC primer extension (SNPE) primers, and the sequences of regions f  
CC sites of single nucleotide polymorphisms SNPs. The present inve  
CC includes kits for determining the presence or absence of a SNP,  
CC oligonucleotides of the invention. The PCR primers are used to  
CC SNP flanking sequence, the SNPE primer is used as a genotyping  
CC The oligonucleotides are useful for genotyping a nucleic acid s  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absen  
CC identity of a SNP and for genotyping nucleic acid samples, for  
CC assess by association analysis the genotype of an individual or  
CC individuals, having a pathological phenotypic trait suspected o  
CC caused by one or more SNPs. Phenotypic traits include diseases  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome,  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney di  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenol  
CC traits also include symptoms of or susceptibility to multifacto  
CC disease of which a component is or may be genetic such as autoi  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by  
CC microorganism. The method is also useful in forensic investigat  
CC paternity analysis. The present sequence represents a fragment  
CC DNA flanking the site of a single nucleotide polymorphism

SQ Sequence 51 BP; 14 A; 12 C; 7 G; 18 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;



72.2%; Score 13; DB 4; Length 51;  
100.0%; Pred. No. 1.1e+04;

RESULT 34  
AAZ94930  
ID AAZ94930 standard: DNA: 17 BP.

.omavirus.

```

PN WC2003057914-A2.
XX
XX PD 17-JUL-2003.
XX PF
XX PF 07-JAN-2003; 2003WO-GB0000034.
XX PR
XX PR 07-JAN-2002; 2002GB-00000239.
XX PR 19-JUN-2002; 2002GB-00014124.
XX PA
XX PA (NORC-) NORCHIP AS.
XX PA (ALLA/) ALLARD S J.
XX PI
XX PI Karlisen F;
XX DR WPI; 2003-587136/55.
XX PT
XX PT An in vitro method of screening human subjects to assess their
XX PT developing cervical carcinoma, comprises screening the subject's
XX PT expression of mRNA transcripts from the L1 gene and the E6 gene
XX PT papillomavirus.
XX PS Disclosure; Page 54; 102pp; English.
XX CC
XX CC This invention relates to a novel method for the detection of hm
XX CC papillomavirus mRNA for use in the screening of human female su
XX CC assesses their risk of developing cervical carcinoma. The inventio
XX CC comprises screening the subject for expression of mRNA transcri
XX CC the L1 gene and the E6 gene of human papillomavirus, where subje
XX CC positive for expression of L1 and/or E6 mRNA are scored as being
XX CC of developing cervical carcinoma. The presence of the human
XX CC papillomavirus (in particular HPV16 and HPV18) has been associat
XX CC cervical cancer in numerous epidemiological studies. The method
XX CC invention are useful for screening human subjects to assess thei
XX CC developing cervical carcinoma, or for identifying human subject
XX CC abnormal cell changes in the cervix. The present sequence is th
XX CC preferred PCR primer which may be used to amplify the E6 gene of
XX CC papillomavirus in the method of the invention.
XX SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 71.1%; Score 12.8; DB 9; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 1 CTCATTGGCAATTTG 16
DB 16 CTCATTGGCAATCGTG 1
|||||||
RESULT 36
ADD36940/c
ID ID ADD36940 standard; DNA; 21 BP.
AC AC
XX AC ADD36940;
XX DT 15-JAN-2004 (first entry)
XX XX
XX DE Human papillomavirus E6 gene-specific PCR primer/probe Seq ID53.
XX KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervic
XX KW cervical cell; cervix; PCR; primer; probe; ss.
XX OS Human papillomavirus.
XX XX
XX PN WO2003057914-A2.
XX PD 17-JUL-2003.
XX PF
XX PF 07-JAN-2003; 2003WO-GB0000034.
XX PR
XX PR 07-JAN-2002; 2002GB-00000239.
XX PR 19-JUN-2002; 2002GB-00014124.

```

CHIP AS.  
ARD S J.

97136/55.

method of screening human subjects to assess their risk of cervical carcinoma, comprises screening the subject for mRNA transcripts from the L1 gene and the E6 gene of human papillomavirus.

SEQ ID NO 53; 102pp; English.

The invention relates to a novel method for the detection of human papillomavirus (HPV) mRNA for use in the screening of human female subjects to assess their risk of developing cervical carcinoma. The invention relates to a method of screening human subjects for expression of mRNA transcripts from the L1 gene and the E6 gene of human papillomavirus, where subjects are scored as being at risk of developing cervical carcinoma. The presence of the human papillomavirus (HPV) mRNA in numerous epidemiological studies. The methods of the invention are useful for screening human subjects to assess their risk of developing cervical carcinoma, or for identifying human subjects having HPV mRNA in the cervix. The present invention is that of a method of screening human subjects for expression of mRNA transcripts from the L1 gene and the E6 gene of human papillomavirus in the method of the invention.

BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 9; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.3e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CATTGGGAATTTTG 16  
|||||||  
CATTGGGAATCGTG 1

standard; DNA; 21 BP.

(first entry)

transcribed mRNA detecting RT-PCR primer #26.  
papillomavirus; HPV; NASBA; primer; RT-PCR; ss.  
papillomavirus type 31.

7-A2.

; 2003WO-GB0000030.  
; 2002GB-00000258.

CHIP AS.  
ARD S J.

87141/55.

oligonucleotide primer and probe for detecting the presence of mRNA from the E6 gene of a human papillomavirus in clinical

XX Disclosure; Page 24; 28pp; English.

XX The invention relates to a novel oligonucleotide molecule used for detecting mRNA transcribed from the E6 gene of a human papillomavirus (HPV). The oligonucleotide comprises any of the 133 fully defined sequences having 17-26 bp given in the specification. The invention further provides the detection of HPV mRNA in a test sample suspected of containing HPV, comprising performing an amplification reaction of a nucleic acid isolated from the test sample to a portion of the mRNA transcribed from the E6 gene of HPV, where amplification reaction is performed using the primer-pair of oligonucleotide cited above. The invention also provides a reaction for use in the detection of HPV by NASBA, comprising an oligonucleotide primer-pair and, optionally, an enzyme mixture comprising an RNA polymerase, a ribonuclease that hydrolyzes the RNA strand of a DNA hybrid without hydrolyzing single or double stranded RNA or an RNA polymerase that recognises the promoter sequence present in at least one NASBA P1 primer oligonucleotide included in the reaction. The oligonucleotide of the invention is useful in detecting mRNA transcripts from the E6 gene of HPV in clinical samples. This polynucleotide sequence represents an oligonucleotide used for mRNA transcribed from the E6 gene of a human papillomavirus (HPV) invention.

XX Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 9; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CTCATTGGGAATTTTG 16  
Db 16 CTCATTGGGAATCGTG 1

RESULT 38

ADD21998/c  
ID ADD21998 standard; DNA; 21 BP.

XX AC ADD21998;

XX 15-JAN-2004 (first entry)

XX HPV E6 gene transcribed mRNA detecting oligonucleotide, SEQ ID  
XX E6; human papillomavirus; HPV; NASBA; primer; PCR; ss.

XX Human papillomavirus type 31.

XX WO2003057927-A2.

XX 17-JUL-2003.

XX 07-JAN-2003; 2003WO-GB0000030.

XX 07-JAN-2002; 2002GB-00000258.

XX (NORC-) NORCHIP AS.  
XX (ALLA/) ALLARD S J.

XX Karlsten F;

XX WPI; 2003-587141/55.

XX New oligonucleotide primer and probe for detecting the presence  
XX transcripts from the E6 gene of a human papillomavirus in clinical  
XX samples.

XX Claim 1; SEQ ID NO 37; 28pp; English.

XX The invention relates to a novel oligonucleotide molecule used  
XX detecting mRNA transcribed from the E6 gene of a human papillomavirus

ligonucleotide comprises any of the 133 fully defined  
 wing 17-26 bp given in the specification. The invention  
 provides the detection of HPV mRNA in a test sample suspected of  
 HPV, comprising performing an amplification reaction on a  
 of a nucleic acid isolated from the test sample to amplify a  
 he mRNA transcribed from the E6 gene of HPV, where the  
 n reaction is performed using the primer-pair of  
 he detection of HPV by NASBA, comprising an oligonucleotide  
 and, optionally, an enzyme mixture comprising an RNA directed  
 se, a ribonuclease that hydrolyzes the RNA strand of an RNA-  
 without hydrolyzing single or double stranded RNA or DNA, and  
 erase that recognises the promoter sequence present in at  
 SEA P1 primer oligonucleotide included in the reagent kit.  
 leotide of the invention is useful in detecting mRNA  
 from the E6 gene of HPV in clinical samples. This  
 de sequence represents one of the 133 oligonucleotides used  
 g mRNA transcribed from the E6 gene of a human papillomavirus  
 invention.

BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 9; Length 21;

larity 87.5%; Pred. No. 1.3e+04; Mismatches 0; Indels 0; Gaps 0;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTG 16

|||||

ATTGGAATG 1

indard; DNA; 22 BP.

(first entry)

igonucleotide primer AFMc021xg5m (Rev).

utant; target nucleotide; hybridization; lung cancer; ss;  
 head cancer; saliva test; chemotherapy; early detection;  
 amplification.

99WO-US005220.

98US-00038637.

7 JOHNS HOPKINS SCHOOL MEDICINE.

il428/46.

ancers comprises assaying for a genetic mutation associated

Page 23; 99pp; English.

exemplary oligonucleotide primer, for use in the detection of  
 related gene mutations of the D13S1286 region. There are over  
 oto-oncogenes and suppressor genes to date, which control  
 ploiment, and cell differentiation. Regulation of these genes  
 certain circumstances, be altered and normal cells can assume  
 growth characteristics. The invention provides a method for

CC detecting a neoplastic disorder of the head and neck or lung in  
 CC subject. The detection of a target mutant nucleotide sequence in  
 CC saliva is indicative of a neoplastic disorder of the head, neck  
 CC This allows early detection and therefore treatment of the prene  
 CC or cancer, and can also be used to monitor high risk patients ur  
 CC chemoprevention or chemotherapy

XX Sequence 22 BP; 5 A; 4 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 2; Length 22;

Best Local Similarity 87.5%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGAAATTTGCC 18

|||||

Db 6 CATCTGAATTTGCC 21

RESULT 40

AAS12638

ID AAS12638 standard; DNA; 22 BP.

XX AC AAS12638;

XX DT 04-DEC-2001 (first entry)

XX DE Mouse PS-1 probe #3 PCR primer PS1-1.

XX Mouse; PS1-1; presenilin-1; PS-1; familial Alzheimer's disease;

KW PCR primer; ss; gene targeting; P264L.

XX OS Mus sp.

XX PN US6284944-B1.

XX PD 04-SEP-2001.

XX PF 10-MAR-1998; 98US-00041185.

XX PR 29-AUG-1997; 97US-0057069P.

XX (CEPH-) CEPHALON INC.

XX PI Scott RW, Reaume AG, Dorfman K;

XX WPI; 2001-540726/60.

XX Gene-targeted mouse heterozygous or homozygous for human presenilin-1 mutation (P264L); useful as a tool or model to elucidate the role of presenilin-1 mutation in the pathology and symptomatology of Alzheimer's disease.

XX Example 1; Col 11; 34pp; English.

XX The invention relates to a new gene-targeted mouse heterozygous genome, a DNA sequence encoding a functionally active PS-1 protein comprising the human P264L mutation, where the PS-1 protein is co-expressed with the Abeta42 protein level is elevated relative to the protein level in a wild-type mouse. The gene-targeted mouse may be used as a model to elucidate the role of PS-1 comprising the human P264L mutation in the pathology and symptomatology of Alzheimer's disease (especially FAD, familial Alzheimer's disease). The gene-targeted mouse and its generation offspring also may be used as assay systems for screening for in vivo inhibitors and for discovering and testing compounds for their ability to inhibit the formation, presence, or deposition of excessive amounts of Abeta42 in the brain tissues, tissues and body fluids. As the non-human mammal is generated by targeting, as opposed to transgenic techniques, the mammal produced is a non-transgenic mammal. The gene-targeted mouse may be used to study the role of PS-1 in the normal processing of Abeta42 and the role of PS-1 in the control of the endoplasmic reticulum. The present sequence is a

09:38:22 2004

us-10-090-326-16.max.rng

to construct a probe which is in turn used to isolate mouse spanning exon 7 of PS-1

BP; 4 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 5; Length 22;

ilarity 87.5%; Pred. No. 1.3e+04;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CATTGGGAATTTG 16

|||||

GATCTGGAATTTG 22

andard; DNA; 22 BP.

(first entry)

exon 7 specific probe generating primer PS1-1.

disease; presenilin-1; PS-1 gene; FAD Swedish mutation; de; transgenic; nontropic; neuroprotective; mouse; PCR primer;

-A2.

; 2001WO-US022693.

; 2000US-00621897.

HALON INC.

Reaume AG, Dorfman K;

27049/28.

ed, non-human mammal for human familial Alzheimer's disease ng compounds that decrease levels of A-beta peptide, has senilin-1, FAD Swedish mutation, and humanized A-beta

Page 22; 71pp; English.

on relates to a gene-targeted, non-human mammal (I) s or homozygous for a human familial Alzheimer's disease (AD) mprising a gene encoding a mutant protein product, of a senilin-1 (PS-1 gene), a human FAD Swedish mutation, and a beta mutation; or of PS-1 gene and a human Swedish APP695 I) or a generational offspring of (I), where mutant PS-1 gene d is useful for screening chemical compounds having ability to vivo levels of Abeta peptide, or for identifying a compound g AD. The method comprises administering the chemical compound measuring the amount of Abeta peptide in a tissue sample from where a decrease in the amount of the peptide in the tissue ndicative of a chemical compound that has the ability to vivo levels of the peptide, where tissue sample is from brain n tissue or body fluids. The chemical compounds identified are treating an individual suspected of having AD. The present presents a primer used for generating a probe specific for the gene exon 7

; BP; 4 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 6; Length 22;

ilarity 87.5%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CTCATTGGGAATTTG 16

|||||

Db 7 CTGATCTGGAATTTG 22

RESULT 42

ACC72192/c

ID ACC72192 standard; DNA; 27 BP.

XX ACC72192;

XX 07-JUL-2003 (first entry)

XX Ag4300 probe.

XX Human; NOV; antidiabetic; anorectic; antibacterial; virucide;

XX immunomodulator; cytostatic; nontropic; neuroprotective;

XX antiparkinsonian; antilipemic; gene therapy; metabolic disorder

XX diabetes; obesity; infection; cachexia; cancer; probe;

XX neurodegenerative disorder; Alzheimer's disease; Parkinson's di

XX immune disorder; haematopoietic disorder; dyslipidaemia; ss.

XX Homo sapiens.

XX WO2003029423-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031358.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327342P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328044P.

XX 09-OCT-2001; 2001US-0328056P.

XX 12-OCT-2001; 2001US-0328849P.

XX 15-OCT-2001; 2001US-0329414P.

XX 17-OCT-2001; 2001US-0330142P.

XX 22-OCT-2001; 2001US-0341058P.

XX 24-OCT-2001; 2001US-0339286P.

XX 24-OCT-2001; 2001US-0343629P.

XX 29-OCT-2001; 2001US-0349575P.

XX 01-NOV-2001; 2001US-0346357P.

XX 12-APR-2002; 2002US-0371972P.

XX 12-APR-2002; 2002US-0371980P.

XX 17-APR-2002; 2002US-0373261P.

XX 19-APR-2002; 2002US-0373805P.

XX 23-APR-2002; 2002US-0374738P.

XX 16-MAY-2002; 2002US-0381101P.

XX 17-MAY-2002; 2002US-0381635P.

XX 29-MAY-2002; 2002US-0383830P.

XX 01-OCT-2002; 2002US-00262839.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton

XX Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W;

XX Ketuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger

XX Rothenberg MB, Shmukles RA, Smithson G, Spytek KA, Taupier

XX Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;

XX WPI; 2003-381625/36.

XX NOVX polypeptides and nucleic acids useful for diagnosing, prev

XX treating NOVX-associated disorders, e.g. diabetes, obesity, can

XX dyslipidemia, and in chromosome mapping, tissue typing or

XX pharmacogenomics.

XX Example C; Page 303; 487pp; English.

XX

invention relates to novel human NOV proteins and their uses (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV is useful in manufacturing a medicament for treating a syndrome with a human disease. The NOV proteins and coding sequences to diagnose, treat or prevent metabolic disorders such as obesity, infections, cachexia, cancer, neurodegenerative diseases such as Alzheimer's disease or Parkinson's disease, immune haematopoietic disorders and various dyslipidaemias. The invention is a probe, used in an example from the invention

BP; 11 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 7; Length 27;

ilarity 87.5%; Pred. No. 1.3e+04; Indels 0; Gaps 0;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGGAATTTGTC 17

TTTTTTTTTTTTTTT

TTTGGGAATTTGTC 12

indard; DNA; 29 BP.

(first entry)

actor construction related PCR primer SEQ ID NO:4.

aa 1-3 galactosyltransferase; immunosuppressive;

; host disease; PCR primer; ss.

-A.

2000JP-00202748.

2000JP-00202748.

OKU NOGYO KYODO KUMIAI RENGOKAI.

TOKYO JOSHI IKA.

3242/31.

actosyltransferase gene knocked down somatic cells.

pe 4; 9pp; Japanese.

invention describes mammal somatic cells with alpha 1-3 galactase (alpha 1-3 GT) gene knocked down gene other than mouse, particularly bovine, especially fibroblast cells. The gene is prepared by homologous recombination of a DNA domain containing part of an exon domain in genomic alpha 1-3 GT gene of mammals human and mouse, a selection marker and a promoter at the 5' and 3' ends, and restricting the expression of the selective marker, screening the cells with aimed recombination. The cells have selective activity. The cells can be used in the preparation of transgenic animals. The invention is useful for inhibition of graft versus host disease. The invention represents a PCR primer used in the construction of a vector, which is used in an example from the present invention

BP; 5 A; 7 C; 8 G; 9 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 6; Length 29;

ilarity 87.5%; Pred. No. 1.3e+04; Indels 0; Gaps 0;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGGAATTTGTC 18

Db 9 CATTGGGAATTTTGAC 24

RESULT 44

AAC63949

ID AAC63949 standard; DNA; 30 BP.

XX AAC63949;

XX 09-FEB-2001 (first entry)

DT Acinetobacter calcoaceticus PQQGDH S231K mutagenic oligo, SEQ II

DE Pyroloquinoline quinone glucose dehydrogenase; PQQGDH;

XX PQQ glucose dehydrogenase; thermal stability; glucose assay;

KW diagnostic reagent; blood glucose monitoring; diabetes; mutant;

KW mutagenic oligonucleotide; ss.

XX Acinetobacter calcoaceticus.

OS Synthetic.

XX WO200061730-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-JP002322.

XX 08-APR-1999; 99JP-00101143.

PR 18-JAN-2000; 2000JP-00009152.

XX (SODE/) SODE K.

PA Sode K;

XX WPI; 2000-665126/64.

XX Modified pyroloquinolinequinone glucose dehydrogenase with imp;

PT stability for use in assay kits and sensors.

XX Example 2; Page 13; 43pp; Japanese.

CC The invention relates to novel modified forms of the water-soluble pyroloquinoline quinone glucose dehydrogenase (PQGDH) of Acinetobacter calcoaceticus having an amino acid substitution which confers improved thermal stability. The invention also relates to a gene sequence encoding the modified enzyme, expression vectors and host cells comprising the modified gene, and glucose assay kits and sensors containing the modified enzyme. The modified enzyme may be used in glucose assays and sensors for research and diagnostic purposes, such as monitoring blood glucose levels (e.g., in a diabetic patient). The present invention represents a mutagenic oligonucleotide used to generate DNA encoding mutant Acinetobacter calcoaceticus pyroloquinoline quinone (PQ) dehydrogenase in an exemplification of the invention

XX Sequence 30 BP; 8 A; 6 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 3; Length 30;

Best Local Similarity 87.5%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTTGCC 18

Db 1 CCTTTGGGAATTTTCC 16

RESULT 45

ABV73543

ID ABV73543 standard; DNA; 30 BP.

XX ABV73543;

XX 07-JAN-2003 (first entry)

er calcoaceticus PQGSDH mutagenic PCR primer SEQ ID NO 8.  
er calcoaceticus; pyroquinoline-quinone glucose dehydrogenase;  
ucose sensor; diabetes; PCR; primer; ss.  
er calcoaceticus.

-Al.

..

.; 2002WO-JP002124.

.; 2001JP-00070413.

DE K.

arashi S;

23360/78.

er calcoaceticus-originated water-soluble pyroquinoline-  
cose dehydrogenase with two subunits combined through  
ond, applicable in glucose sensors for determining serum

Page 10; 36pp; Japanese.

on relates to water-soluble pyroquinoline-quinone glucose  
se (PQGDH) (I) comprising two subunits combined with each  
disulfide bond. (I) is applicable in glucose sensors in  
serum glucose e.g. in diagnosis and management of diabetes.  
sequence is that of a mutagenic PCR primer used in examples  
ntion

BP; 8 A; 6 C; 4 G; 12 T; 0 U; 0 Other;

ilarity 71.1%; Score 12.8; DB 6; Length 30;

Conservative 87.5%; Pred. No. 1.3e+04;

Mismatches 0; Indels 2; Gaps 0;

TTTGGAAATTTGCC 18

|||||

TTTGGAAATTTGCC 16

: February 29, 2004, 09:03:34  
84 secs

09:38:22 2004

us-10-090-326-16.max.rni

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

eic search, using sw model

February 29, 2004, 08:44:24 ; Search time 33.8961 seconds  
(without alignments)  
294.698 Million cell updates/sec

S-10-090-326-16

8 ctcatttggaatttggc 18

DENITY NUC

apop 10.0 , Gapext 1.0

82709 seqs, 277475446 residues

its satisfying chosen parameters: 874574

length: 0  
length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA: \*  
: /cgn2\_6/prodata/2/ina/5A COMB.seq: \*  
: /cgn2\_6/prodata/2/ina/5B COMB.seq: \*  
: /cgn2\_6/prodata/2/ina/6A COMB.seq: \*  
: /cgn2\_6/prodata/2/ina/6B COMB.seq: \*  
: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq: \*  
: /cgn2\_6/prodata/2/ina/backfiles1.seq: \*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

#### SUMMARIES

Query	Length	DB	ID	Description
77.8	20	4	US-09-422-978-11109	Sequence 11109, A
74.4	17	1	US-08-758-306-377	Sequence 377, App
73.3	30	2	US-08-816-155B-33	Sequence 33, Appl
73.3	30	3	US-08-815-809-18	Sequence 18, Appl
73.3	30	3	US-09-079-587-33	Sequence 33, Appl
73.3	43	3	US-08-832-985-28	Sequence 28, Appl
73.3	43	4	US-09-410-903-9	Sequence 9, Appli
73.3	43	4	US-08-835-159-28	Sequence 28, Appl
73.3	53	2	US-08-417-210A-101	Sequence 101, App
73.3	53	4	US-09-136-159A-101	Sequence 101, App
71.1	17	3	US-09-411-578-35	Sequence 35, Appl
71.1	17	3	US-09-411-578-37	Sequence 37, Appl
71.1	17	4	US-09-749-233-35	Sequence 35, Appl
71.1	17	4	US-09-749-233-37	Sequence 37, Appl
71.1	19	4	US-09-442-143A-46	Sequence 46, Appl
71.1	22	3	US-09-038-637-66	Sequence 66, Appl
71.1	22	3	US-09-041-185-6	Sequence 6, Appli
68.9	17	1	US-08-758-306-375	Sequence 375, App
68.9	27	3	US-08-192-271-5	Sequence 5, Appli
68.9	27	5	PCT-US94-01572-5	Sequence 379, App
67.8	20	3	US-09-021-701-379	Sequence 380, App
67.8	20	3	US-09-021-701-380	Sequence 381, App
67.8	20	3	US-09-021-701-381	Sequence 382, App
67.8	22	4	US-09-446-301A-28	Sequence 28, Appl
67.8	22	4	US-09-099-932-26	Sequence 26, Appl
67.8	34	1	US-07-753-738B-3	Sequence 3, Appli

28	12.2	67.8	34	2	US-08-924-695A-17	Sequence
29	12.2	67.8	36	1	US-08-479-852-16	Sequence
30	12.2	67.8	36	1	US-08-479-852-96	Sequence
31	12.2	67.8	36	1	US-08-479-852-133	Sequence
32	12.2	67.8	36	1	US-08-479-852-137	Sequence
33	12.2	67.8	36	2	US-08-462-646-16	Sequence
34	12.2	67.8	36	2	US-08-462-646-96	Sequence
35	12.2	67.8	36	2	US-08-462-646-133	Sequence
36	12.2	67.8	36	2	US-08-462-646-137	Sequence
37	12.2	67.8	36	3	US-08-792-832A-11	Sequence
38	12.2	67.8	36	3	US-09-013-406-16	Sequence
39	12.2	67.8	36	3	US-09-013-406-96	Sequence
40	12.2	67.8	36	3	US-09-013-406-133	Sequence
41	12.2	67.8	36	3	US-09-013-406-137	Sequence
42	12.2	67.8	36	4	US-09-766-095-16	Sequence
43	12.2	67.8	36	4	US-09-766-095-96	Sequence
44	12.2	67.8	36	4	US-09-766-095-133	Sequence
45	12.2	67.8	36	4	US-09-766-095-137	Sequence
46	12.2	67.8	40	4	US-08-703-477E-80	Sequence
47	12.2	67.8	50	1	US-07-630-288A-19	Sequence
48	12.2	67.8	50	1	US-08-468-049-19	Sequence
49	12.2	67.8	59	4	US-09-331-793-63	Sequence
50	12.2	67.8	60	4	US-09-331-793-64	Sequence
51	12	66.7	17	1	US-08-758-306-379	Sequence
52	12	66.7	22	4	US-09-380-836-92	Sequence
53	12	66.7	53	4	US-08-956-171E-2738	Sequence
54	11.8	65.6	20	3	US-09-104-068-6	Sequence
55	11.8	65.6	27	4	US-08-980-241-1	Sequence
56	11.8	65.6	38	4	US-09-371-772B-10088	Sequence
57	11.8	65.6	55	1	US-08-243-870-15	Sequence
58	11.8	65.6	55	1	US-08-409-439A-15	Sequence
59	11.6	64.4	27	3	US-09-052-778-5	Sequence
60	11.6	64.4	30	2	US-09-038-227-48	Sequence
61	11.6	64.4	36	1	US-08-391-000-40	Sequence
62	11.6	64.4	36	2	US-08-741-931-40	Sequence
63	11.6	64.4	48	1	US-08-105-483-91	Sequence
64	11.6	64.4	48	1	US-08-709-209-91	Sequence
65	11.6	64.4	48	1	US-08-458-101-91	Sequence
66	11.6	64.4	50	3	US-08-660-645A-30	Sequence
67	11.6	64.4	50	3	US-09-298-718-30	Sequence
68	11.6	64.4	50	3	US-09-546-969-30	Sequence
69	11.6	64.4	50	3	US-08-980-832-9	Sequence
70	11.6	64.4	50	4	US-09-547-267-30	Sequence
71	11.6	64.4	50	4	US-09-920-923B-9	Sequence
72	11.6	64.4	52	2	US-08-417-210A-105	Sequence
73	11.6	64.4	52	2	US-09-136-159A-105	Sequence
74	11.4	63.3	18	1	US-08-758-306-553	Sequence
75	11.4	63.3	20	3	US-09-021-701-383	Sequence
76	11.4	63.3	20	3	US-09-021-701-384	Sequence
77	11.4	63.3	20	3	US-09-021-701-385	Sequence
78	11.4	63.3	20	3	US-09-021-701-386	Sequence
79	11.4	63.3	20	4	US-09-861-159-16	Sequence
80	11.4	63.3	20	4	US-09-198-452A-4356	Sequence
81	11.4	63.3	21	2	US-08-776-944-14	Sequence
82	11.4	63.3	21	4	US-09-422-978-9774	Sequence
83	11.4	63.3	23	1	US-08-465-590-98	Sequence
84	11.4	63.3	23	1	US-08-711-417C-98	Sequence
85	11.4	63.3	23	4	US-09-723-909-98	Sequence
86	11.4	63.3	23	5	PCT-US93-08743-98	Sequence
87	11.4	63.3	25	4	US-09-580-497B-23	Sequence
88	11.4	63.3	30	3	US-08-952-089A-24	Sequence
89	11.4	63.3	35	2	US-08-867-941-53	Sequence
90	11.4	63.3	35	3	US-09-074-658-53	Sequence
91	11.4	63.3	36	3	US-08-951-130-7	Sequence
92	11.4	63.3	36	3	US-09-591-694-48	Sequence
93	11.4	63.3	38	3	US-08-444-818-237	Sequence
94	11.4	63.3	41	2	US-08-369-829A-6	Sequence
95	11.4	63.3	41	2	US-08-586-676E-10	Sequence
96	11.4	63.3	42	3	US-09-150-213-5	Sequence
97	11.4	63.3	47	4	US-09-422-978-1439	Sequence
98	11.4	63.3	47	4	US-09-422-978-2214	Sequence
99	11.2	62.2	17	3	US-09-411-578-19	Sequence
100	11.2	62.2	17	3	US-09-411-578-21	Sequence



62.2	17	3	US-09-411-578-31	Sequence 31, Appl	c 174	11	61.1	20	2	US-08-967-104-11	Sequence
62.2	17	3	US-09-411-578-33	Sequence 33, Appl	175	11	61.1	23	1	US-09-031-485-42	Sequence
62.2	17	3	US-09-411-578-36	Sequence 36, Appl	176	11	61.1	23	1	US-08-847-429A-42	Sequence
62.2	17	3	US-09-411-578-38	Sequence 38, Appl	177	11	61.1	23	3	US-09-065-474-42	Sequence
62.2	17	4	US-08-584-040-3777	Sequence 3777, Ap	c 178	11	61.1	23	3	US-09-268-140-25	Sequence
62.2	17	4	US-08-584-040-3777	Sequence 1544, Ap	179	11	61.1	23	4	US-09-557-034-42	Sequence
62.2	17	4	US-09-371-772B-1544	Sequence 6170, Ap	180	11	61.1	27	4	US-09-263-892A-12	Sequence
62.2	17	4	US-09-749-233-19	Sequence 19, Appl	c 181	11	61.1	34	1	US-08-463-090B-22	Sequence
62.2	17	4	US-09-749-233-21	Sequence 21, Appl	c 182	11	61.1	40	4	US-09-241-888-4	Sequence
62.2	17	4	US-09-749-233-31	Sequence 31, Appl	c 183	11	61.1	47	4	US-09-422-978-454	Sequence
62.2	17	4	US-09-749-233-33	Sequence 33, Appl	c 184	11	61.1	47	4	US-09-422-978-1724	Sequence
62.2	17	4	US-09-749-233-36	Sequence 36, Appl	c 185	11	61.1	54	4	US-08-956-171E-1707	Sequence
62.2	17	4	US-09-749-233-38	Sequence 38, Appl	c 186	10.8	60.0	17	4	US-08-584-040-3776	Sequence
62.2	18	3	US-09-143-212-75	Sequence 75, Appl	187	10.8	60.0	17	4	US-08-584-040-6115	Sequence
62.2	20	2	US-08-756-806A-41	Sequence 41, Appl	c 188	10.8	60.0	17	4	US-08-584-040-6116	Sequence
62.2	20	3	US-09-143-214-41	Sequence 41, Appl	c 189	10.8	60.0	17	4	US-09-371-772B-1543	Sequence
62.2	20	3	US-08-867-230A-5	Sequence 5, Appli	190	10.8	60.0	17	4	US-09-371-772B-2952	Sequence
62.2	20	3	US-09-021-701-378	Sequence 378, App	191	10.8	60.0	17	4	US-09-371-772B-2953	Sequence
62.2	20	4	US-09-489-765A-66	Sequence 66, Appl	c 192	10.8	60.0	18	1	US-08-290-448A-36	Sequence
62.2	20	4	US-09-506-073-43	Sequence 43, Appl	c 193	10.8	60.0	18	1	US-08-290-448A-36	Sequence
62.2	20	4	US-09-446-301A-25	Sequence 25, Appl	c 194	10.8	60.0	18	1	US-08-175-069A-36	Sequence
62.2	20	4	US-09-198-452A-6723	Sequence 6723, Ap	c 195	10.8	60.0	18	4	US-08-461-939B-36	Sequence
62.2	20	4	US-09-099-932-23	Sequence 23, Appl	c 196	10.8	60.0	18	4	US-08-464-000-36	Sequence
62.2	20	5	PCT-US95-0711A-41	Sequence 41, Appl	197	10.8	60.0	20	2	US-08-117-952-291	Sequence
62.2	24	4	US-09-657-346A-4	Sequence 4, Appli	c 198	10.8	60.0	20	3	US-09-249-730-165	Sequence
62.2	28	1	US-08-220-606B-37	Sequence 37, Appl	199	10.8	60.0	20	3	US-09-021-701-718	Sequence
62.2	31	3	US-09-235-246-18	Sequence 18, Appl	200	10.8	60.0	20	3	US-09-021-701-719	Sequence
62.2	31	3	US-09-446-504-20	Sequence 20, Appl	201	10.8	60.0	20	3	US-09-021-701-720	Sequence
62.2	31	4	US-09-712-266-20	Sequence 20, Appl	202	10.8	60.0	20	3	US-09-021-701-721	Sequence
62.2	34	2	US-08-846-762-40	Sequence 40, Appl	203	10.8	60.0	20	3	US-09-021-701-722	Sequence
62.2	37	4	US-09-530-157B-8	Sequence 8, Appli	204	10.8	60.0	20	3	US-09-021-701-723	Sequence
62.2	38	1	US-08-373-124A-833	Sequence 833, App	205	10.8	60.0	20	3	US-09-021-701-724	Sequence
62.2	38	1	US-08-373-124A-991	Sequence 991, App	206	10.8	60.0	20	4	US-09-689-255C-29	Sequence
62.2	38	1	US-08-373-124A-2072	Sequence 2072, Ap	c 207	10.8	60.0	20	4	US-09-060-299-331	Sequence
62.2	38	1	US-08-435-628-833	Sequence 833, App	c 208	10.8	60.0	20	4	US-09-060-299-331	Sequence
62.2	38	1	US-08-435-628-991	Sequence 991, App	c 209	10.8	60.0	20	4	US-09-060-299-331	Sequence
62.2	38	1	US-08-435-628-991	Sequence 2072, Ap	c 210	10.8	60.0	20	4	US-09-198-452A-4004	Sequence
62.2	40	1	US-08-207-226A-5	Sequence 5, Appli	c 211	10.8	60.0	20	4	US-09-249-247-165	Sequence
62.2	41	3	US-08-332-420-53	Sequence 53, Appl	212	10.8	60.0	21	1	US-08-753-147-45	Sequence
62.2	41	3	US-08-813-507-78	Sequence 78, Appl	c 213	10.8	60.0	21	1	US-09-422-978-9573	Sequence
62.2	41	4	US-08-464-453-78	Sequence 78, Appl	214	10.8	60.0	22	1	US-07-722-798A-38	Sequence
62.2	42	1	US-08-224-657-119	Sequence 119, App	c 215	10.8	60.0	24	1	US-07-722-798A-37	Sequence
62.2	42	1	US-08-303-275-201	Sequence 201, App	216	10.8	60.0	24	2	US-08-360-606B-18	Sequence
62.2	42	2	US-08-184-009-170	Sequence 170, App	217	10.8	60.0	25	1	US-08-465-590-81	Sequence
62.2	42	2	US-08-566-398-60	Sequence 60, Appl	c 218	10.8	60.0	25	3	US-09-217-101-5	Sequence
62.2	42	2	US-08-716-284-3	Sequence 3, Appli	219	10.8	60.0	25	3	US-08-711-417C-81	Sequence
62.2	42	2	US-08-458-356-170	Sequence 170, App	220	10.8	60.0	25	4	US-09-514-302-13	Sequence
62.2	42	2	US-08-658-665-159	Sequence 159, App	221	10.8	60.0	25	4	US-09-723-909-81	Sequence
62.2	42	3	US-08-675-566-73	Sequence 73, Appl	222	10.8	60.0	25	5	PCT-US93-08743-81	Sequence
62.2	42	3	US-08-796-101-135	Sequence 135, App	c 223	10.8	60.0	26	2	US-08-766-439-71	Sequence
62.2	42	3	US-08-460-736-170	Sequence 170, App	c 224	10.8	60.0	27	1	US-08-624-545-70	Sequence
62.2	42	3	US-09-085-273-159	Sequence 159, App	c 225	10.8	60.0	27	2	US-08-995-927-6	Sequence
62.2	42	4	US-09-354-138-119	Sequence 119, App	c 226	10.8	60.0	27	4	US-09-582-096-6	Sequence
62.2	42	4	US-09-583-545-3	Sequence 3, Appli	c 227	10.8	60.0	27	4	US-08-584-040-5305	Sequence
62.2	42	4	US-09-535-370-170	Sequence 370, App	c 228	10.8	60.0	27	5	PCT-US94-03744-10	Sequence
62.2	42	4	US-09-617-594A-16	Sequence 16, Appl	c 229	10.8	60.0	29	1	US-07-681-703B-40	Sequence
62.2	42	4	US-09-916-963-159	Sequence 159, App	c 230	10.8	60.0	29	3	US-09-201-075-5	Sequence
62.2	45	1	US-08-332-420-52	Sequence 52, Appl	231	10.8	60.0	29	3	US-09-275-850-172	Sequence
62.2	47	4	US-09-671-317-661	Sequence 661, App	c 232	10.8	60.0	29	4	US-09-462-843A-17	Sequence
62.2	47	4	US-09-671-317-800	Sequence 800, App	233	10.8	60.0	29	4	US-09-304-232-877	Sequence
62.2	47	4	US-09-422-978-337	Sequence 337, App	234	10.8	60.0	30	4	US-09-322-409-146	Sequence
62.2	47	4	US-09-422-978-907	Sequence 907, App	235	10.8	60.0	30	4	US-09-451-527-146	Sequence
62.2	47	4	US-09-422-978-1064	Sequence 1064, Ap	c 236	10.8	60.0	31	4	US-09-621-625A-5	Sequence
62.2	47	4	US-09-422-978-1500	Sequence 1500, Ap	237	10.8	60.0	33	3	US-09-461-697-102	Sequence
62.2	47	4	US-09-422-978-2295	Sequence 2295, Ap	238	10.8	60.0	33	4	US-08-169-715-48	Sequence
62.2	47	4	US-09-422-978-2743	Sequence 2743, Ap	239	10.8	60.0	35	1	US-08-437-815-13	Sequence
62.2	47	4	US-09-422-978-2845	Sequence 2845, Ap	240	10.8	60.0	35	1	US-08-897-040-13	Sequence
62.2	47	4	US-09-422-978-2870	Sequence 2870, Ap	c 241	10.8	60.0	36	2	US-08-897-340-16	Sequence
62.2	60	3	US-08-896-449A-3	Sequence 3, Appli	c 242	10.8	60.0	36	3	US-09-252-329-16	Sequence
62.2	60	3	US-09-132-652-3	Sequence 3, Appli	c 243	10.8	60.0	37	4	US-09-479-479-17	Sequence
61.1	15	4	US-09-138-958-3	Sequence 381, App	c 244	10.8	60.0	37	4	US-09-297-851-17	Sequence
61.1	17	1	US-08-758-306-381	Sequence 11, Appl	c 245	10.8	60.0	38	1	US-08-373-124A-441	Sequence
61.1	20	2	US-08-596-366-11		c 246	10.8	60.0	38	1	US-08-373-124A-1488	Sequence

60.0	38	1	US-08-435-628-441	Sequence 441, App	c 320	10.6	58.9	28	2	US-08-859-998-289	Sequence
60.0	38	1	US-08-435-628-1488	Sequence 1488, App	c 321	10.6	58.9	28	4	US-09-225-928-289	Sequence
60.0	38	1	US-09-371-772B-7432	Sequence 7432, Ap	c 322	10.6	58.9	28	4	US-09-225-201B-289	Sequence
60.0	38	4	US-09-371-772B-9045	Sequence 9045, Ap	c 323	10.6	58.9	30	1	US-08-392-818-18	Sequence
60.0	38	4	US-09-371-772B-13280	Sequence 13280, A	c 324	10.6	58.9	30	3	US-08-952-089A-25	Sequence
60.0	40	1	US-09-313-221A-40	Sequence 40, Appl	c 325	10.6	58.9	30	3	US-09-203-939-16	Sequence
60.0	45	1	US-08-145-681-9	Sequence 9, Appl	c 326	10.6	58.9	30	3	US-09-251-835-16	Sequence
60.0	45	1	US-08-453-703-9	Sequence 9, Appl	c 327	10.6	58.9	30	3	US-09-318-503-17	Sequence
60.0	45	2	US-08-456-106-9	Sequence 9, Appl	c 328	10.6	58.9	30	3	US-09-038-261A-15	Sequence
60.0	45	3	US-08-456-108-9	Sequence 9, Appl	c 329	10.6	58.9	30	4	US-09-564-329A-23	Sequence
60.0	45	3	US-09-265-577-9	Sequence 9, Appl	c 330	10.6	58.9	31	3	US-08-544-381B-181	Sequence
60.0	45	4	US-09-164-714-16	Sequence 16, Appl	c 331	10.6	58.9	32	2	US-08-859-998-306	Sequence
60.0	45	4	US-09-633-739-9	Sequence 9, Appl	c 332	10.6	58.9	32	2	US-08-859-998-308	Sequence
60.0	47	4	US-09-552-322-43	Sequence 43, Appl	c 333	10.6	58.9	32	4	US-09-189-129-8	Sequence
60.0	47	4	US-09-671-317-673	Sequence 673, App	c 334	10.6	58.9	32	4	US-09-225-928-306	Sequence
60.0	47	4	US-09-422-978-271	Sequence 271, App	c 335	10.6	58.9	32	4	US-09-225-928-308	Sequence
60.0	47	4	US-09-422-978-517	Sequence 517, App	c 336	10.6	58.9	32	4	US-09-225-201B-306	Sequence
60.0	47	4	US-09-422-978-1657	Sequence 1657, Ap	c 337	10.6	58.9	32	4	US-09-225-201B-308	Sequence
60.0	47	4	US-09-422-978-3212	Sequence 3212, Ap	c 338	10.6	58.9	32	1	US-08-285-936-19	Sequence
60.0	50	4	US-09-554-929-45	Sequence 45, Appl	c 339	10.6	58.9	33	1	US-08-487-860-19	Sequence
60.0	50	4	US-09-554-929-149	Sequence 149, App	c 340	10.6	58.9	33	3	US-09-138-024-11	Sequence
60.0	50	4	US-08-956-171B-2475	Sequence 2475, Ap	c 341	10.6	58.9	33	4	US-09-404-066-11	Sequence
60.0	51	4	US-09-443-199C-797	Sequence 797, App	c 342	10.6	58.9	33	4	US-09-573-322-11	Sequence
60.0	51	4	US-09-443-199C-798	Sequence 798, App	c 343	10.6	58.9	34	4	US-09-085-720-5	Sequence
60.0	57	4	US-08-956-171B-1668	Sequence 1668, App	c 344	10.6	58.9	35	1	US-08-473-852-32	Sequence
60.0	58	1	US-08-169-303-3	Sequence 3, Appl	c 345	10.6	58.9	35	1	US-08-479-852-112	Sequence
60.0	58	1	US-08-327-525A-10	Sequence 10, Appl	c 346	10.6	58.9	35	2	US-08-462-646-32	Sequence
60.0	59	1	US-08-327-525A-11	Sequence 11, Appl	c 347	10.6	58.9	35	2	US-08-462-646-112	Sequence
60.0	59	2	US-08-531-137B-10	Sequence 10, Appl	c 348	10.6	58.9	35	3	US-09-013-406-32	Sequence
60.0	59	2	US-08-531-137B-11	Sequence 11, Appl	c 349	10.6	58.9	35	3	US-09-013-406-112	Sequence
60.0	59	3	US-09-158-765-10	Sequence 10, Appl	c 350	10.6	58.9	35	4	US-09-766-095-32	Sequence
60.0	59	3	US-09-158-765-11	Sequence 11, Appl	c 351	10.6	58.9	35	4	US-09-766-095-112	Sequence
60.0	59	4	US-09-796-071-10	Sequence 10, Appl	c 352	10.6	58.9	36	3</		

58.9	58	4	US-09-790-317-3	Sequence 3, Appli	C 466	10.4	57.8	30	4	US-09-266-965-94	Sequence
58.9	60	2	US-08-663-566A-43	Sequence 43, Appl	C 467	10.4	57.8	31	1	US-08-766-014-12	Sequence
58.9	60	2	US-08-023-610-43	Sequence 43, Appl	C 468	10.4	57.8	31	3	US-09-260-283-5	Sequence
58.9	60	2	US-08-288-065A-43	Sequence 43, Appl	C 469	10.4	57.8	31	3	US-08-886-886-25	Sequence
58.9	60	2	US-08-362-240A-43	Sequence 43, Appl	C 470	10.4	57.8	31	3	US-08-886-886-27	Sequence
58.9	60	5	PCT-US95-10245-43	Sequence 43, Appl	C 471	10.4	57.8	31	3	US-09-183-217-3	Sequence
57.8	15	1	US-08-440-787A-115	Sequence 115, App	C 472	10.4	57.8	31	4	US-09-651-656-47	Sequence
57.8	17	1	US-08-758-306-391	Sequence 391, App	C 473	10.4	57.8	31	4	US-09-650-855-47	Sequence
57.8	17	1	US-08-758-306-393	Sequence 393, App	C 474	10.4	57.8	31	4	US-09-510-925A-1	Sequence
57.8	17	4	US-09-509-565-17	Sequence 17, Appl	C 475	10.4	57.8	31	4	US-09-848-464-1	Sequence
57.8	17	4	US-09-371-772B-6169	Sequence 6169, Ap	C 476	10.4	57.8	32	2	US-08-687-916-4	Sequence
57.8	18	4	US-09-651-656-61	Sequence 61, Appl	C 477	10.4	57.8	32	3	US-09-138-614-4	Sequence
57.8	18	4	US-09-650-855-61	Sequence 61, Appl	C 478	10.4	57.8	32	4	US-09-549-831-18	Sequence
57.8	20	1	US-07-910-288-6	Sequence 6, Appli	C 479	10.4	57.8	34	3	US-09-133-914-1	Sequence
57.8	20	2	US-08-928-419-17	Sequence 17, Appl	C 480	10.4	57.8	34	3	US-08-886-886-23	Sequence
57.8	20	3	US-09-106-216-29	Sequence 29, Appl	C 481	10.4	57.8	34	3	US-09-469-197-1	Sequence
57.8	20	3	US-09-034-205-65	Sequence 65, Appl	C 482	10.4	57.8	34	4	US-09-949-109-1	Sequence
57.8	20	3	US-09-021-701-387	Sequence 387, App	C 483	10.4	57.8	35	1	US-08-418-032-12	Sequence
57.8	20	3	US-09-291-283-17	Sequence 17, Appl	C 484	10.4	57.8	36	4	US-09-625-225-16	Sequence
57.8	20	4	US-09-484-617-154	Sequence 154, App	C 485	10.4	57.8	36	4	US-09-625-225-17	Sequence
57.8	20	4	US-09-677-218B-65	Sequence 65, Appl	C 486	10.4	57.8	36	4	US-09-625-225-18	Sequence
57.8	20	4	US-09-677-192-65	Sequence 65, Appl	C 487	10.4	57.8	36	4	US-09-625-225-19	Sequence
57.8	20	4	US-09-844-521-46	Sequence 46, Appl	C 488	10.4	57.8	36	4	US-09-403-422-7	Sequence
57.8	20	4	US-09-422-978-6395	Sequence 6395, Ap	C 489	10.4	57.8	37	6	5185431-27	Patent No
57.8	20	4	US-09-522-761-1	Sequence 1, Appli	C 490	10.4	57.8	38	2	US-08-316-439A-25	Sequence
57.8	21	1	US-07-952-442-1	Sequence 1, Appli	C 491	10.4	57.8	38	2	US-08-809-267-25	Sequence
57.8	21	1	US-08-263-766-1	Sequence 1, Appli	C 492	10.4	57.8	38	3	US-08-444-818-238	Sequence
57.8	21	1	US-08-319-545A-1	Sequence 1, Appli	C 493	10.4	57.8	38	3	US-09-110-517-15	Sequence
57.8	21	2	US-08-928-419-12	Sequence 12, Appl	C 494	10.4	57.8	38	3	US-09-284-832-41	Sequence
57.8	21	2	US-09-092-988-1	Sequence 1, Appli	C 495	10.4	57.8	38	4	US-09-371-772B-9731	Sequence
57.8	21	3	US-09-106-216-1	Sequence 1, Appli	C 496	10.4	57.8	38	4	US-09-371-772B-13684	Sequence
57.8	21	3	US-09-429-034-1	Sequence 12, Appl	C 497	10.4	57.8	38	5	PCT-US95-13662A-25	Sequence
57.8	21	3	US-09-291-283-12	Sequence 12, Appl	C 498	10.4	57.8	40	4	US-09-332-902-7	Sequence
57.8	21	4	US-09-422-978-5641	Sequence 5641, Ap	C 499	10.4	57.8	42	3	US-08-155-005A-14	Sequence
57.8	22	2	US-08-611-880-6	Sequence 6, Appli	C 500	10.4	57.8	42	3	US-09-363-783-14	Sequence
57.8	23	1	US-07-722-788A-55	Sequence 55, Appl	C 501	10.4	57.8	42	4	US-09-661-758A-14	Sequence
57.8	23	1	US-08-224-616-2	Sequence 2, Appli	C 502	10.4	57.8	45	1	US-08-766-014-15	Sequence
57.8	23	3	US-08-433-522A-52	Sequence 52, Appl	C 503	10.4	57.8	47	4	US-09-422-978-221	Sequence
57.8	23	3	US-09-135-166-52	Sequence 52, Appl	C 504	10.4	57.8	47	4	US-09-422-978-559	Sequence
57.8	23	3	US-08-942-046-52	Sequence 52, Appl	C 505	10.4	57.8	47	4	US-09-422-978-732	Sequence
57.8	23	4	US-08-446-648-2	Sequence 2, Appli	C 506	10.4	57.8	47	4	US-09-422-978-842	Sequence
57.8	23	4	US-09-982-610-2	Sequence 2, Appli	C 507	10.4	57.8	47	4	US-09-422-978-3080	Sequence
57.8	23	5	PCT-US95-04228-2	Sequence 2, Appli	C 508	10.4	57.8	47	4	US-09-422-978-3364	Sequence
57.8	24	1	US-08-374-770-4	Sequence 4, Appli	C 509	10.4	57.8	47	4	US-09-422-978-3399	Sequence
57.8	24	1	US-08-461-593B-4	Sequence 4, Appli	C 510	10.4	57.8	47	4	US-09-422-978-3528	Sequence
57.8	24	1	US-08-651-323A-4	Sequence 4, Appli	C 511	10.4	57.8	47	4	US-09-422-978-3571	Sequence
57.8	24	2	US-08-553-304-2	Sequence 2, Appli	C 512	10.4	57.8	48	4	US-09-583-447A-44	Sequence
57.8	24	3	US-08-444-818-239	Sequence 239, App	C 513	10.4	57.8	48	4	US-09-583-447A-45	Sequence
57.8	24	3	US-09-011-600-1	Sequence 1, Appli	C 514	10.4	57.8	50	1	US-08-207-901-55	Sequence
57.8	24	4	US-09-722-348-1	Sequence 1, Appli	C 515	10.4	57.8	50	4	US-09-371-489-4	Sequence
57.8	24	4	US-09-600-031-12	Sequence 12, Appl	C 516	10.4	57.8	50	4	US-09-621-976-12165	Sequence
57.8	25	1	US-08-445-640-16	Sequence 16, Appl	C 517	10.4	57.8	50	4	US-09-621-976-13498	Sequence
57.8	25	3	US-08-170-558-16	Sequence 16, Appl	C 518	10.4	57.8	53	1	US-08-766-014-13	Sequence
57.8	25	3	US-08-447-314-16	Sequence 16, Appl	C 519	10.4	57.8	53	3	US-09-275-850-282	Sequence
57.8	25	3	US-08-445-461-16	Sequence 16, Appl	C 520	10.4	57.8	56	4	US-08-956-171E-3389	Sequence
57.8	27	2	US-08-809-267-16	Sequence 16, Appl	C 521	10.4	57.8	57	2	US-08-935-927-1	Sequence
57.8	27	3	US-09-311-042-4	Sequence 4, Appli	C 522	10.4	57.8	57	4	US-09-582-096-1	Sequence
57.8	27	4	US-08-584-040-4897	Sequence 4897, Ap	C 523	10.4	57.8	57	4	US-09-371-489-6	Sequence
57.8	27	4	US-09-454-204A-29	Sequence 29, Appl	C 524	10.2	56.7	15	2	US-08-292-620A-224	Sequence
57.8	27	5	PCT-US95-13662A-16	Sequence 16, Appl	C 525	10.2	56.7	15	2	US-08-292-620A-225	Sequence
57.8	28	2	US-08-811-492-58	Sequence 58, Appl	C 526	10.2	56.7	15	3	US-09-071-845-224	Sequence
57.8	28	5	PCT-US96-10545A-58	Sequence 58, Appl	C 527	10.2	56.7	15	3	US-09-071-845-225	Sequence
57.8	29	1	US-07-910-288-14	Sequence 14, Appl	C 528	10.2	56.7	17	1	US-08-308-196A-5	Sequence
57.8	29	1	US-07-910-288-16	Sequence 16, Appl	C 529	10.2	56.7	17	1	US-09-371-772B-6171	Sequence
57.8	29	1	US-09-304-232-478	Sequence 478, App	C 530	10.2	56.7	17	5	PCT-US91-06452-5	Sequence
57.8	29	4	US-09-304-232-876	Sequence 876, App	C 531	10.2	56.7	18	1	US-08-132-168A-18	Sequence
57.8	30	1	US-08-766-014-14	Sequence 14, Appl	C 532	10.2	56.7	18	3	US-09-630-706-81	Sequence
57.8	30	2	US-08-629-001A-92	Sequence 92, Appl	C 533	10.2	56.7	20	1	US-08-185-301-1	Sequence
57.8	30	2	US-08-867-941-51	Sequence 51, Appl	C 534	10.2	56.7	20	1	US-08-588-821-49	Sequence
57.8	30	3	US-09-074-658-51	Sequence 51, Appl	C 535	10.2	56.7	20	1	US-08-915-214-49	Sequence
57.8	30	3	US-08-642-274D-171	Sequence 171, App	C 536	10.2	56.7	20	2	US-09-005-532-49	Sequence
57.8	30	4	US-09-059-584-44	Sequence 44, Appl	C 537	10.2	56.7	20	2	US-08-888-982A-16	Sequence
57.8	30	4			C 538	10.2	56.7	20	3	US-09-344-519-46	Sequence

56.7	20	3	US-09-021-701-377	Sequence 377, Appl	612	10.2	56.7	36	1	US-08-273-362-6	Sequence
56.7	20	3	US-09-488-744A-64	Sequence 64, Appl	c 613	10.2	56.7	36	1	US-08-311-486C-387	Sequence
56.7	20	4	US-09-462-261-16	Sequence 16, Appl	c 614	10.2	56.7	36	2	US-08-292-620A-1114	Sequence
56.7	20	4	US-09-506-073-105	Sequence 105, Appl	c 615	10.2	56.7	36	2	US-08-292-620A-1494	Sequence
56.7	20	4	US-09-657-346A-55	Sequence 55, Appl	c 616	10.2	56.7	36	2	US-08-585-684B-585	Sequence
56.7	20	4	US-09-422-978-8723	Sequence 8723, Appl	c 617	10.2	56.7	36	2	US-08-585-684B-1450	Sequence
56.7	20	4	US-09-138-452A-2664	Sequence 2664, Appl	c 618	10.2	56.7	36	2	US-08-585-684B-1885	Sequence
56.7	20	4	US-09-198-452A-2671	Sequence 2671, Appl	c 619	10.2	56.7	36	2	US-08-585-684B-1886	Sequence
56.7	20	4	US-09-198-452A-4621	Sequence 4621, Appl	c 620	10.2	56.7	36	2	US-08-350-260A-127	Sequence
56.7	20	4	US-09-198-452A-4730	Sequence 4730, Appl	c 621	10.2	56.7	36	3	US-09-071-845-1114	Sequence
56.7	21	4	US-09-081-149-14	Sequence 14, Appl	c 622	10.2	56.7	36	3	US-09-071-845-1494	Sequence
56.7	21	4	US-09-422-978-4378	Sequence 4378, Appl	c 623	10.2	56.7	36	3	US-09-038-073-585	Sequence
56.7	21	4	US-09-422-978-6173	Sequence 6173, Appl	c 624	10.2	56.7	36	3	US-09-038-073-1450	Sequence
56.7	22	2	US-08-807-200-9	Sequence 6574, Appl	c 625	10.2	56.7	36	3	US-09-038-073-1885	Sequence
56.7	22	2	US-08-836-134-11	Sequence 9, Appl	c 626	10.2	56.7	36	3	US-09-038-073-1886	Sequence
56.7	22	3	US-09-001-777-9	Sequence 11, Appl	c 627	10.2	56.7	36	3	US-09-367-953B-16	Sequence
56.7	22	3	US-09-493-784-11	Sequence 9, Appl	c 628	10.2	56.7	36	4	US-09-104-337A-127	Sequence
56.7	23	1	US-08-321-356-26	Sequence 11, Appl	c 629	10.2	56.7	37	1	US-08-468-700-5	Sequence
56.7	23	3	US-09-487-445-4	Sequence 26, Appl	c 630	10.2	56.7	37	1	US-08-468-700-7	Sequence
56.7	24	1	US-08-229-781-25	Sequence 4, Appl	c 631	10.2	56.7	37	1	US-08-468-700-11	Sequence
56.7	24	1	US-08-630-918-25	Sequence 25, Appl	c 632	10.2	56.7	37	1	US-08-468-700-12	Sequence
56.7	24	1	US-08-465-590-27	Sequence 27, Appl	c 633	10.2	56.7	37	2	US-08-450-905B-13	Sequence
56.7	24	2	US-08-702-105A-36	Sequence 36, Appl	c 634	10.2	56.7	37	2	US-08-704-706A-5	Sequence
56.7	24	3	US-08-702-110A-36	Sequence 36, Appl	c 635	10.2	56.7	37	2	US-08-704-706A-7	Sequence
56.7	24	3	US-08-711-417C-27	Sequence 27, Appl	c 636	10.2	56.7	37	2	US-08-704-706A-11	Sequence
56.7	24	3	US-09-325-571-36	Sequence 27, Appl	c 637	10.2	56.7	37	2	US-08-704-706A-12	Sequence
56.7	24	3	US-09-344-700-19	Sequence 36, Appl	c 638	10.2	56.7	37	3	US-07-982-759B-13	Sequence
56.7	24	4	US-09-004-422-25	Sequence 19, Appl	c 639	10.2	56.7	37	3	US-08-985-659-5	Sequence
56.7	24	4	US-09-514-907A-3	Sequence 25, Appl	c 640	10.2	56.7	37	3	US-08-985-659-7	Sequence
56.7	24	4	US-09-723-909-27	Sequence 3, Appl	c 641	10.2	56.7	37	3	US-08-985-659-12	Sequence
56.7	24	4	US-09-848-585-36	Sequence 27, Appl	c 642	10.2	56.7	38	1	US-08-373-124A-1043	Sequence
56.7	24	4	US-09-896-994-3	Sequence 36, Appl	c 643	10.2	56.7	38	1	US-08-373-124A-1876	Sequence
56.7	24	4	US-09-563-997A-19	Sequence 3, Appl	c 644	10.2	56.7	38	1	US-08-373-124A-1954	Sequence
56.7	24	5	PCT-US93-08743-27	Sequence 19, Appl	c 645	10.2	56.7	38	1	US-08-435-628-1043	Sequence
56.7	25	3	US-08-971-782-5	Sequence 27, Appl	c 646	10.2	56.7	38	1	US-08-435-628-1046	Sequence
56.7	25	3	US-09-309-026-5	Sequence 5, Appl	c 647	10.2	56.7	38	1	US-08-435-628-1876	Sequence
56.7	26	3	US-09-049-569-5	Sequence 5, Appl	c 648	10.2	56.7	38	4	US-09-371-772B-8260	Sequence
56.7	26	3	US-09-402-515A-13	Sequence 13, Appl	c 649	10.2	56.7	38	4	US-09-371-772B-10397	Sequence
56.7	27	4	US-08-995-162-1637	Sequence 1637, Appl	c 650	10.2	56.7	38	4	US-09-371-772B-11991	Sequence
56.7	27	4	US-09-401-063-1637	Sequence 12, Appl	c 651	10.2	56.7	38	4	US-09-371-772B-13962	Sequence
56.7	27	4	US-08-716-374-3	Sequence 1637, Appl	c 652	10.2	56.7	38	4	US-09-461-697-132	Sequence
56.7	28	1	US-09-345-814-34	Sequence 3, Appl	c 653	10.2	56.7	39	3	US-09-270-957-34	Sequence
56.7	28	4	US-09-386-962C-36	Sequence 36, Appl	c 654	10.2	56.7	39	4	US-07-811-052A-2	Sequence
56.7	28	4	US-09-661-596A-1	Sequence 36, Appl	c 655	10.2	56.7	40	1	US-07-741-940-17	Sequence
56.7	29	4	US-09-661-596A-3	Sequence 1, Appl	c 656	10.2	56.7	40	1	US-08-178-014A-2	Sequence
56.7	29	4	US-09-661-596A-3	Sequence 1, Appl	c 657	10.2	56.7	40	1	US-08-308-196A-4	Sequence
56.7	30	1	US-08-602-010A-45	Sequence 45, Appl	c 658	10.2	56.7	40	1	US-08-289-548A-17	Sequence
56.7	30	1	US-08-680-726A-45	Sequence 45, Appl	c 659	10.2	56.7	40	1	US-08-452-654-17	Sequence
56.7	30	3	US-09-092-409-45	Sequence 45, Appl	c 660	10.2	56.7	40	1	US-08-271-880A-1	Sequence
56.7	31	4	US-09-085-720-11	Sequence 11, Appl	c 661	10.2	56.7	40	1	US-08-399-696-49	Sequence
56.7	31	4	US-08-138-608-14	Sequence 14, Appl	c 662	10.2	56.7	40	1	US-08-452-655B-17	Sequence
56.7	33	1	US-08-583-318-9	Sequence 9, Appl	c 663	10.2	56.7	40	1	US-08-385-590A-22	Sequence
56.7	33	1	US-08-386-198A-13	Sequence 13, Appl	c 664	10.2	56.7	40	2	US-08-450-905B-12	Sequence
56.7	33	2	US-08-377-309-11	Sequence 11, Appl	c 665	10.2	56.7	40	2	US-08-910-408-1	Sequence
56.7	33	2	US-09-186-723-11	Sequence 11, Appl	c 666	10.2	56.7	40	2	US-09-982-759F-12	Sequence
56.7	33	4	US-08-505-012-16	Sequence 16, Appl	c 667	10.2	56.7	40	3	US-09-021-520-22	Sequence
56.7	33	4	US-09-186-949A-12	Sequence 12, Appl	c 668	10.2	56.7	40	3	US-08-450-582-17	Sequence
56.7	33	4	US-08-758-757-11	Sequence 11, Appl	c 669	10.2	56.7	40	3	US-09-249-215-1	Sequence
56.7	33	4	US-09-187-978-11	Sequence 11, Appl	c 670	10.2	56.7	40	3	US-09-113-750A-52	Sequence
56.7	33	4	US-10-115-701A-11	Sequence 11, Appl	c 671	10.2	56.7	40	4	US-09-052-521C-17	Sequence
56.7	33	4	US-09-340-308A-11	Sequence 11, Appl	c 672	10.2	56.7	40	4	US-08-449-731-17	Sequence
56.7	33	5	PCT-US96-00996-16	Sequence 16, Appl	c 673	10.2	56.7	40	5	PCT-US91-06452-4	Sequence
56.7	34	1	US-08-670-901-3	Sequence 3, Appl	c 674	10.2	56.7	40	5	US-08-480-510-11	Sequence
56.7	34	2	US-08-794-795-8	Sequence 8, Appl	c 675	10.2	56.7	42	2	US-08-185-949B-98	Sequence
56.7	34	2	US-08-793-410-17	Sequence 17, Appl	c 676	10.2	56.7	42	2	US-08-956-047-18	Sequence
56.7	34	3	US-09-182-859-18	Sequence 18, Appl	c 677	10.2	56.7	42	4	US-09-097-319A-18	Sequence
56.7	34	3	US-09-249-200-8	Sequence 8, Appl	c 678	10.2	56.7	42	4	US-09-204-858-1	Sequence
56.7	34	4	US-09-537-168-17	Sequence 17, Appl	c 679	10.2	56.7	42	5	PCT-US94-01780-11	Sequence
56.7	34	4	US-09-672-459-18	Sequence 18, Appl	c 680	10.2	56.7	42	5	US-08-832-985-47	Sequence
56.7	34	4	US-10-186-042-18	Sequence 18, Appl	c 681	10.2	56.7	43	3	US-09-410-903-28	Sequence
56.7	35	3	US-08-491-954-91	Sequence 91, Appl	c 682	10.2	56.7	43	4	US-08-835-159-47	Sequence
56.7	36	1	US-08-273-362-3	Sequence 3, Appl	c 683	10.2	56.7	44	2	US-08-350-260A-562	Sequence

56.7	44	4	US-09-104-337A-562	Sequence 562, App	758	10	55.6	22	3	US-08-943-731-574	Sequence
56.7	45	3	US-08-792-295-3	Sequence 3, Appli	759	10	55.6	22	4	US-09-246-963A-20	Sequence
56.7	45	3	US-09-076-432-3	Sequence 3, Appli	760	10	55.6	22	4	US-09-618-166-88	Sequence
56.7	45	4	US-09-254-352B-58	Sequence 58, Appl	761	10	55.6	23	1	US-08-390-850-367	Sequence
56.7	45	4	US-09-254-352B-61	Sequence 61, Appl	762	10	55.6	23	1	US-08-435-634-367	Sequence
56.7	45	4	US-09-254-352B-63	Sequence 63, Appl	763	10	55.6	23	4	US-09-457-708B-3	Sequence
56.7	46	1	US-07-598-873-3	Sequence 3, Appli	764	10	55.6	23	4	US-09-950-046A-3	Sequence
56.7	46	1	US-08-073-425-3	Sequence 3, Appli	765	10	55.6	24	4	US-10-072-094-104	Sequence
56.7	46	1	US-08-396-531-3	Sequence 3, Appli	766	10	55.6	25	1	US-08-468-557-19	Sequence
56.7	47	4	US-09-641-638-819	Sequence 819, App	767	10	55.6	27	1	US-08-238-163-10	Sequence
56.7	47	4	US-09-671-317-526	Sequence 526, App	768	10	55.6	27	1	US-08-413-118-99	Sequence
56.7	47	4	US-09-671-317-551	Sequence 551, App	769	10	55.6	27	1	US-08-716-374-4	Sequence
56.7	47	4	US-09-422-978-258	Sequence 258, App	770	10	55.6	27	1	US-08-758-306-378	Sequence
56.7	47	4	US-09-422-978-422	Sequence 422, App	771	10	55.6	27	1	US-08-758-306-380	Sequence
56.7	47	4	US-09-422-978-477	Sequence 477, App	772	10	55.6	27	3	US-08-473-446-99	Sequence
56.7	47	4	US-09-422-978-855	Sequence 855, App	773	10	55.6	27	4	US-08-584-040-3476	Sequence
56.7	47	4	US-09-422-978-899	Sequence 899, App	774	10	55.6	27	4	US-08-584-040-4900	Sequence
56.7	47	4	US-09-422-978-2498	Sequence 2498, Ap	775	10	55.6	28	1	US-08-413-118-98	Sequence
56.7	47	4	US-09-422-978-2621	Sequence 2621, Ap	776	10	55.6	28	2	US-08-598-998-584	Sequence
56.7	47	4	US-09-422-978-2927	Sequence 2927, Ap	777	10	55.6	28	3	US-08-473-446-98	Sequence
56.7	47	4	US-09-422-978-3406	Sequence 3406, Ap	778	10	55.6	28	4	US-09-225-928-584	Sequence
56.7	48	1	US-09-422-978-3744	Sequence 3744, Ap	779	10	55.6	28	4	US-03-225-201B-584	Sequence
56.7	48	1	US-07-854-603-21	Sequence 21, Appl	780	10	55.6	30	1	US-08-160-317-9	Sequence
56.7	48	1	US-07-854-603-23	Sequence 23, Appl	781	10	55.6	30	1	US-08-351-147-9	Sequence
56.7	48	1	US-07-854-603-37	Sequence 37, Appl	782	10	55.6	30	1	US-08-471-154-9	Sequence
56.7	48	1	US-07-854-603-39	Sequence 39, Appl	783	10	55.6	30	1	US-08-440-787A-61	Sequence
56.7	50	1	US-08-105-483-135	Sequence 135, App	784	10	55.6	30	1	US-08-629-600-7	Sequence
56.7	50	1	US-08-105-483-136	Sequence 136, App	785	10	55.6	30	2	US-08-331-081B-15	Sequence
56.7	50	1	US-08-709-209-135	Sequence 135, App	786	10	55.6	30	3	US-08-513-968-69	Sequence
56.7	50	1	US-08-709-209-136	Sequence 136, App	787	10	55.6	30	3	US-08-367-685-61	Sequence
56.7	50	1	US-08-458-101-135	Sequence 135, App	788	10	55.6	30	5	PCT-US91-07141-61	Sequence
56.7	50	1	US-08-458-101-136	Sequence 136, App	789	10	55.6	31	1	US-07-906-930E-26	Sequence
56.7	53	1	US-08-105-483-67	Sequence 67, Appl	790	10	55.6	31	1	US-08-390-850-281	Sequence
56.7	53	1	US-08-709-209-67	Sequence 67, Appl	791	10	55.6	31	1	US-08-390-850-282	Sequence
56.7	53	1	US-08-458-101-67	Sequence 67, Appl	792	10	55.6	31	1	US-08-390-850-283	Sequence
56.7	53	4	US-09-622-540A-5	Sequence 5, Appli	793	10	55.6	31	1	US-08-435-634-281	Sequence
56.7	53	4	US-09-622-540A-5	Sequence 5, Appli	794	10	55.6	31	1	US-08-435-634-282	Sequence
56.7	54	3	US-09-307-621-29	Sequence 29, Appl	795	10	55.6	31	1	US-08-435-634-283	Sequence
56.7	55	2	US-08-715-941-11	Sequence 11, Appl	796	10	55.6	31	4	US-09-206-942-83	Sequence
56.7	55	2	US-08-715-941-14	Sequence 14, Appl	797	10	55.6	32	1	US-08-510-215A-14	Sequence
56.7	56	4	US-09-220-557-12	Sequence 12, Appl	798	10	55.6	33	2	US-08-709-874A-27	Sequence
56.7	56	4	US-08-956-171E-2085	Sequence 2085, Ap	799	10	55.6	33	3	US-09-104-382-27	Sequence
56.7	59	4	US-09-532-656-10	Sequence 10, Appl	800	10	55.6	33	4	US-08-169-715-12	Sequence
56.7	60	3	US-08-613-009A-25	Sequence 25, Appl	801	10	55.6	33	4	US-09-833-555-27	Sequence
56.7	60	3	US-08-613-009A-25	Sequence 25, Appl	802	10	55.6	34	3	US-09-026-958-10	Sequence
56.7	60	4	US-08-778-570B-19	Sequence 19, Appl	803	10	55.6	34	3	US-09-063-667-8	Sequence
56.7	60	4	US-09-053-584-19	Sequence 19, Appl	804	10	55.6	34	4	US-09-390-207-38	Sequence
55.6	17	1	US-08-758-306-383	Sequence 383, App	805	10	55.6	34	4	US-09-594-127-12	Sequence
55.6	18	2	US-08-970-269A-18	Sequence 18, App	806	10	55.6	35	2	US-08-727-449-3	Sequence
55.6	18	3	US-09-407-562-18	Sequence 18, App	807	10	55.6	35	3	US-08-776-265-15	Sequence
55.6	19	4	US-09-422-978-4876	Sequence 4876, Ap	808	10	55.6	35	3	US-09-232-479-43	Sequence
55.6	19	4	US-09-422-978-6312	Sequence 6312, Ap	809	10	55.6	35	3	US-09-784-990-43	Sequence
55.6	20	3	US-09-249-730-186	Sequence 186, App	810	10	55.6	35	4	US-09-398-184-15	Sequence
55.6	20	3	US-08-860-635A-4	Sequence 4, Appli	811	10	55.6	36	1	US-08-325-224-27	Sequence
55.6	20	3	US-09-253-025-6	Sequence 6, Appli	812	10	55.6	36	3	US-08-722-258-27	Sequence
55.6	20	3	US-09-073-377A-5	Sequence 5, Appli	813	10	55.6	36	4	US-09-479-005A-739	Sequence
55.6	20	3	US-09-428-583-71	Sequence 71, Appl	814	10	55.6	36	5	PCT-US95-04468-27	Sequence
55.6	20	3	US-09-330-330-4	Sequence 4, Appli	815	10	55.6	37	1	US-08-297-299B-12	Sequence
55.6	20	4	US-03-281-476-4	Sequence 4, Appli	816	10	55.6	37	1	US-08-297-299B-54	Sequence
55.6	20	4	US-09-668-313A-137	Sequence 137, App	817	10	55.6	37	1	US-08-297-299B-55	Sequence
55.6	20	4	US-09-422-978-6720	Sequence 6720, Ap	818	10	55.6	37	1	US-08-297-299B-56	Sequence
55.6	20	4	US-09-679-239A-114	Sequence 114, App	819	10	55.6	37	1	US-08-403-762A-66	Sequence
55.6	20	4	US-09-249-247-186	Sequence 186, App	820	10	55.6	37	2	US-08-858-083-12	Sequence
55.6	20	4	US-07-734-188-6	Sequence 6, Appli	821	10	55.6	37	2	US-08-858-083-54	Sequence
55.6	20	4	US-09-762-195-12	Sequence 12, Appl	822	10	55.6	37	2	US-08-858-083-55	Sequence
55.6	20	4	US-09-762-195-20	Sequence 20, Appl	823	10	55.6	37	2	US-08-858-083-56	Sequence
55.6	21	3	US-08-388-353-623	Sequence 623, App	824	10	55.6	37	5	PCT-US95-11029-12	Sequence
55.6	21	3	US-08-488-551B-623	Sequence 623, App	825	10	55.6	37	5	PCT-US95-11029-54	Sequence
55.6	21	3	US-09-109-663-64	Sequence 64, Appl	826	10	55.6	37	5	PCT-US95-11029-56	Sequence
55.6	21	4	US-09-312-748-12	Sequence 12, Appl	827	10	55.6	37	5	PCT-US95-11029-56	Sequence
55.6	21	4	US-09-422-978-11600	Sequence 11600, A	828	10	55.6	40	4	US-08-628-422-54	Sequence
55.6	21	4	US-09-526-193A-178	Sequence 178, App	829	10	55.6	40	4	US-09-643-596B-156	Sequence
55.6	22	3	US-08-781-891-88	Sequence 88, Appl	830	10	55.6	42	1	US-08-439-585-1	Sequence

55.6	44	1	US-08-258-026A-22	Sequence 22, Appl	904	9.8	54.4	17	4	US-09-401-063-40	Sequence
55.6	44	5	PCT-US95-07541-22	Sequence 22, Appl	C 905	9.8	54.4	18	1	US-08-753-147-14	Sequence
55.6	45	2	US-08-495-695B-19	Sequence 19, Appl	906	9.8	54.4	18	3	US-09-235-246-8	Sequence
55.6	45	5	PCT-US94-14436-19	Sequence 19, Appl	C 907	9.8	54.4	18	4	US-09-907-794A-241	Sequence
55.6	46	4	US-09-593-580B-42	Sequence 42, Appl	C 908	9.8	54.4	18	4	US-09-905-125A-241	Sequence
55.6	47	4	US-09-671-317-717	Sequence 717, Appl	C 909	9.8	54.4	18	4	US-09-902-775A-241	Sequence
55.6	47	4	US-09-422-978-365	Sequence 365, Appl	C 910	9.8	54.4	19	1	US-08-480-604A-11	Sequence
55.6	47	4	US-09-422-978-1280	Sequence 1280, Appl	C 911	9.8	54.4	19	2	US-08-405-496A-11	Sequence
55.6	47	4	US-09-422-978-1842	Sequence 1842, Appl	912	9.8	54.4	19	3	US-09-338-907-485	Sequence
55.6	47	4	US-09-422-978-1876	Sequence 1876, Appl	913	9.8	54.4	19	3	US-09-338-907-486	Sequence
55.6	47	4	US-09-422-978-2317	Sequence 2317, Appl	C 914	9.8	54.4	19	3	US-08-915-136-11	Sequence
55.6	47	4	US-09-422-978-2531	Sequence 2531, Appl	915	9.8	54.4	19	4	US-09-218-207-485	Sequence
55.6	47	4	US-09-422-978-2725	Sequence 2725, Appl	916	9.8	54.4	19	4	US-09-218-207-486	Sequence
55.6	47	4	US-09-422-978-2735	Sequence 2735, Appl	C 917	9.8	54.4	19	4	US-08-957-310-11	Sequence
55.6	50	4	US-09-390-867A-30	Sequence 30, Appl	918	9.8	54.4	19	4	US-09-360-416-64	Sequence
55.6	50	4	US-09-548-260-30	Sequence 30, Appl	919	9.8	54.4	19	4	US-09-422-978-4636	Sequence
55.6	52	3	US-09-135-639-5	Sequence 5, Appl	C 920	9.8	54.4	19	4	US-10-011-366-11	Sequence
55.6	53	2	US-08-687-559-26	Sequence 26, Appl	C 921	9.8	54.4	19	4	US-09-084-517-11	Sequence
55.6	53	4	US-09-401-415-26	Sequence 26, Appl	C 922	9.8	54.4	20	1	US-08-273-776-7	Sequence
55.6	54	1	US-08-564-955-60	Sequence 60, Appl	923	9.8	54.4	20	1	US-08-530-492-86	Sequence
55.6	54	3	US-08-621-859-60	Sequence 60, Appl	C 924	9.8	54.4	20	1	US-08-255-892-49	Sequence
55.6	54	3	US-09-075-511-60	Sequence 60, Appl	C 925	9.8	54.4	20	1	US-08-802-547-3	Sequence
55.6	54	3	US-09-099-015-60	Sequence 60, Appl	C 926	9.8	54.4	20	1	US-08-802-547-3	Sequence
55.6	54	3	US-09-165-060-60	Sequence 60, Appl	C 927	9.8	54.4	20	1	US-08-712-357-3	Sequence
55.6	54	4	US-09-240-310-60	Sequence 60, Appl	C 928	9.8	54.4	20	1	US-08-712-357-3	Sequence
55.6	54	4	US-09-590-778-60	Sequence 60, Appl	C 929	9.8	54.4	20	3	US-09-357-071-16	Sequence
55.6	54	4	US-09-590-774-60	Sequence 60, Appl	930	9.8	54.4	20	3	US-08-906-517-86	Sequence
55.6	54	4	US-09-619-550-60	Sequence 60, Appl	C 931	9.8	54.4	20	3	US-09-488-671-140	Sequence
55.6	54	4	US-09-240-734-60	Sequence 60, Appl	932	9.8	54.4	20	3	US-09-021-701-717	Sequence
55.6	54	4	US-09-636-322-60	Sequence 60, Appl	C 933	9.8	54.4	20	3	US-09-021-701-725	Sequence
55.6	54	4	US-09-717-391-60	Sequence 60, Appl	C 934	9.8	54.4	20	4	US-09-676-610B-119	Sequence
55.6	54	4	US-09-636-313-60	Sequence 60, Appl	935	9.8	54.4	20	4	US-09-198-452A-1293	Sequence
55.6	54	4	US-09-240-307-60	Sequence 60, Appl	C 936	9.8	54.4	20	4	US-09-198-452A-1793	Sequence
55.6	56	4	US-08-778-570B-28	Sequence 28, Appl	937	9.8	54.4	20	4	US-09-198-452A-4738	Sequence
55.6	56	4	US-09-599-584-36	Sequence 36, Appl	C 938	9.8	54.4	20	4	US-09-198-452A-6576	Sequence
55.6	56	4	US-08-956-171E-2303	Sequence 36, Appl	C 939	9.8	54.4	20	4	US-09-780-045-56	Sequence
55.6	58	4	US-08-956-171E-3368	Sequence 3368, Appl	C 940	9.8	54.4	21	1	US-08-105-483-350	Sequence
55.6	58	4	US-09-738-274-8	Sequence 8, Appl	C 941	9.8	54.4	21	1	US-08-324-001-9	Sequence
55.6	60	2	US-08-379-057-20	Sequence 20, Appl	C 942	9.8	54.4	21	1	US-08-709-209-350	Sequence
55.6	60	3	US-09-023-228B-28	Sequence 28, Appl	C 943	9.8	54.4	21	1	US-08-303-275-99	Sequence
55.6	60	3	US-09-163-025B-28	Sequence 28, Appl	C 944	9.8	54.4	21	1	US-08-458-101-350	Sequence
55.6	60	4	US-10-037-282-28	Sequence 28, Appl	C 945	9.8	54.4	21	3	US-09-057-740-3	Sequence
54.4	14	1	US-08-068-945A-28	Sequence 28, Appl	C 946	9.8	54.4	21	3	US-08-640-906-22	Sequence
54.4	14	1	US-08-442-806-28	Sequence 28, Appl	C 947	9.8	54.4	21	3	US-08-611-587-13	Sequence
54.4	14	3	US-08-442-806-28	Sequence 28, Appl	C 948	9.8	54.4	21	3	US-09-461-697-442	Sequence
54.4	15	2	US-08-287-844A-97	Sequence 97, Appl	C 949	9.8	54.4	21	4	US-09-395-936-22	Sequence
54.4	15	2	US-08-209-521-4	Sequence 223, Appl	C 950	9.8	54.4	21	4	US-09-422-978-5239	Sequence
54.4	15	3	US-09-071-845-223	Sequence 223, Appl	951	9.8	54.4	21	4	US-09-422-978-5513	Sequence
54.4	15	3	US-08-352-902D-138	Sequence 138, Appl	C 952	9.8	54.4	21	4	US-09-422-978-5981	Sequence
54.4	15	4	US-09-265-503B-142	Sequence 142, Appl	C 953	9.8	54.4	21	4	US-09-422-978-7102	Sequence
54.4	17	1	US-08-390-850-629	Sequence 629, Appl	C 954	9.8	54.4	21	4	US-09-422-978-8119	Sequence
54.4	17	1	US-08-435-634-629	Sequence 629, Appl	955	9.8	54.4	21	4	US-09-422-978-9630	Sequence
54.4	17	3	US-08-985-162-40	Sequence 40, Appl	C 956	9.8	54.4	21	4	US-09-422-978-10722	Sequence
54.4	17	4	US-08-584-040-2638	Sequence 2638, Appl	C 957	9.8	54.4	22	3	US-08-851-350-7	Sequence
54.4	17	4	US-08-584-040-2639	Sequence 2639, Appl	C 958	9.8	54.4	22	3	US-09-050-159-118	Sequence
54.4	17	4	US-08-584-040-4162	Sequence 4162, Appl	C 959	9.8	54.4	22	3	US-09-050-159-119	Sequence
54.4	17	4	US-08-584-040-4247	Sequence 4247, Appl	C 960	9.8	54.4	22	3	US-09-182-117-19	Sequence
54.4	17	4	US-08-584-040-5708	Sequence 5708, Appl	C 961	9.8	54.4	22	3	US-09-263-904-11	Sequence
54.4	17	4	US-08-584-040-5709	Sequence 5709, Appl	C 962	9.8	54.4	22	3	US-09-434-039A-19	Sequence
54.4	17	4	US-08-584-040-5710	Sequence 5710, Appl	C 963	9.8	54.4	22	4	US-09-296-477-12	Sequence
54.4	17	4	US-08-584-040-5732	Sequence 5732, Appl	C 964	9.8	54.4	22	4	US-07-932-379A-44	Sequence
54.4	17	4	US-08-584-040-6114	Sequence 6114, Appl	965	9.8	54.4	23	1	US-08-379-295-44	Sequence
54.4	17	4	US-09-371-772B-1162	Sequence 1162, Appl	966	9.8	54.4	23	1	US-08-379-296-44	Sequence
54.4	17	4	US-09-371-772B-1163	Sequence 1163, Appl	967	9.8	54.4	23	1	US-08-588-821-50	Sequence
54.4	17	4	US-09-371-772B-1929	Sequence 1929, Appl	968	9.8	54.4	23	1	US-08-915-214-50	Sequence
54.4	17	4	US-09-371-772B-2014	Sequence 2014, Appl	969	9.8	54.4	23	2	US-08-478-386A-67	Sequence
54.4	17	4	US-09-371-772B-2592	Sequence 2592, Appl	C 970	9.8	54.4	23	2	US-08-292-597-67	Sequence
54.4	17	4	US-09-371-772B-2593	Sequence 2593, Appl	C 971	9.8	54.4	23	2	US-08-388-653-67	Sequence
54.4	17	4	US-09-371-772B-2594	Sequence 2594, Appl	C 972	9.8	54.4	23	2	US-08-005-532-50	Sequence
54.4	17	4	US-09-371-772B-2611	Sequence 2611, Appl	973	9.8	54.4	23	2	US-08-483-898-67	Sequence
54.4	17	4	US-09-371-772B-2951	Sequence 2951, Appl	C 974	9.8	54.4	23	3	US-09-087-716-67	Sequence
54.4	17	4	US-09-371-772B-5493	Sequence 5493, Appl	C 975	9.8	54.4	23	3	US-09-157-753-67	Sequence

us-10-090-326-16.max.rni

APPLICANT: McSwiggen, James A.  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITRATION OF ANTIBODIES TO ANTIGENS  
 TITLE OF INVENTION: TREATMENT OF DISEASES  
 ASSOCIATED WITH  
 TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
 NUMBER OF SEQUENCES: 1379  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/758,306  
 FILING DATE: December 3, 1996  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:

FILING DATE: 3/27/83  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 213  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 377:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 -758-306-377

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 377:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
-758-306-377

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 377:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
-758-306-377

LELEX: 67-3510 377:  
 INFORMATION FOR SEQ ID NO:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 758-306-377

```

ry Match      74.4%; Score 13.4; DB 1; Length 17;
t Local Similarity 40.0%; Pred. No. 8.8e+02;
ches 6; Conservative 8; Mismatches 1; Indels 0;

```

```

1 CTCATTGGAAATTT 15
   | : : : | : : :
3 CUGAATTGGAAATTT 17

```

T 3  
-816

Sequence 33, Application US/08816155B  
ent No. 5990091

GENERAL INFORMATION:  
 APPLICANT: TARTAGLIA, JAMES  
 APPLICANT: COX, WILLIAM I.  
 APPLICANT: GETTIG, RUSSELL R.  
 APPLICANT: MARTINEZ, HECTOR  
 APPLICANT: PAOLETTI, ENZO  
 APPLICANT: PINCUS, STEVEN E.  
 TITLE OF INVENTION: VECTORS HAVING  
 TITLE OF INVENTION: METHODS OF  
 NUMBER OF SEQUENCES: 48

TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF MAKING AND USES THEREOF

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: FROMMER LAWRENCE & HAUG LLP

STREET: 745 FIFTH AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

```

51 ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
LICATON DATA: US/08/816,155B
ON NUMBER: US/08/816,155B
TE: 12-MAR-1997
ATION: 514
ENT INFORMATION:
WALSKE, THOMAS J.
ION NUMBER: 32,147
/DOCKET NUMBER: 454310-2990
CATION INFORMATION:
: 212-588-0800
212-588-0500
DR SEQ ID NO: 33:
ARACTERISTICS:
30 base pairs
cleic acid
ESS: single
linear
PE: DNA (genomic)
3

73.3%; Score 13.2; DB 2; Length 30;
ilarity 83.3%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTGGC 18
|||||
ACTTTGGAATATTGCC 12

/c
pplication US/08815809
1777
ATION:
TAGLIA, James
BEL, Scott J.
William I.
TTIG, Russell R.
ACUS, Steven E.
LETTI, Enzo
COBS, Bertram L.
TION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
TION: MAKING AND USES THEREOF
3: 454310-3010
CATION NUMBER: US/08/815,809
3 DATE: 1997-03-12
ID NOS: 23
antIn Ver. 2.0

scinia virus

73.3%; Score 13.2; DB 3; Length 30;
ilarity 83.3%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTGGC 18
|||||
ACTTTGGAATATTGCC 12

/c
pplication US/09079587
066

GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
METHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-079-587-33

Query Match 73.3%; Score 13.2; DB 3; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTGGC 18
|||
Db 29 CTACTTTGGAATATTGCC 12

RESULT 6
US-08-832-985-28/c
Sequence 28, Application US/08832985
Patent No. 6057098
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
TITLE OF INVENTION: POLYVALENT DISPLAY LIBRARIES
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

```



1 09:38:22 2004

us-10-090-326-16.max.rni

IBM Compatible  
SYSTEM: DOS  
FastSEQ for Windows Version 2.0  
PLICATION DATA:  
ION NUMBER: US/08/832,985  
ATE: 04-APR-1997  
TATION: 435  
ICATION DATA:  
ION NUMBER:  
ATE:  
ENT INFORMATION:  
ebeschuetz, Joseph O.  
TION NUMBER: 37,505  
/DOCKET NUMBER: 014907-001000US  
ICATION INFORMATION:  
3: 415-576-0200  
415-576-0300

OR SEQ ID NO: 28:

ARACTERISTICS:  
43 base pairs  
cleic acid  
ESS: single  
linear  
PE: CDNA

73.3%; Score 13.2; DB 3; Length 43;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTGCC 18  
|||||  
CTATTCGGCTTTGCC 11

C  
plication US/09410903  
0113  
ATION:  
uechler, Joe  
alkirs, Gunars  
ray, Jeff  
osite Diagnostics Inc.  
NTION: Chimeric Polyclonal Antibodies  
E: 014907-002700US  
CATION NUMBER: US/09/410,903  
G DATE: 1999-10-02  
TION NUMBER: US 08/832,985  
DATE: 1997-04-04  
TION NUMBER: US 08/835,159  
DATE: 1997-04-04  
TION NUMBER: WO PCT/US98/06704  
DATE: 1998-04-03  
ID NOS: 100  
stSEQ for Windows Version 3.0

tificial Sequence

ATION: oligo 50

73.3%; Score 13.2; DB 4; Length 43;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTGCC 18  
|||||  
CTATTCGGCTTTGCC 11

RESULT 8

US-08-835-159-28/c  
Sequence 28, Application US/08835159  
Patent No. 6555310  
GENERAL INFORMATION:  
APPLICANT: Gray, Jeff  
APPLICANT: Buechler, Joe  
APPLICANT: Valkirs, Gunars  
TITLE OF INVENTION: POLYCLONAL LIBRARIES  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/835,159  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joseph O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 014907-001100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-835-159-28

Query Match 73.3%; Score 13.2; DB 4; Length 43;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Oy 1 CTCATTGGAAATTTGCC 18  
|||||  
Db 28 CTCATTGGCTTTGCC 11

RESULT 9

US-08-417-210A-101/c  
Sequence 101, Application US/08417210A  
Patent No. 5863542  
GENERAL INFORMATION:  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
STREET: 530 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

09:38:22 2004

us-10-090-326-16.max.rni

SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
LOCATION DATA:  
ON NUMBER: US/08/417,210A  
TE: 05-APR-1995  
ATION: 435  
ENT INFORMATION:  
WALSKI, THOMAS J.  
ION NUMBER: 32,147  
/DOCKET NUMBER: 454310-2690  
CATION INFORMATION:  
: 212-840-3333  
OR SEQ ID NO: 101:  
ARACTERISTICS:  
53 base pairs  
cleic acid  
ESS: single  
linear  
PE: DNA (genomic)  
01

73.3%; Score 13.2; DB 2; Length 53;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTTGCG 18  
|||||  
ACTTTGGAATATTGCG 30

1/c  
Application US/09136159A  
3279  
ATION:  
ogenetics Corporation  
ioletti, Enzo  
rtaglia, James  
xx, William I  
ATION: Immunodeficiency recombinant poxvirus  
3: 454310-2690.1  
ATION NUMBER: US/09/136,159A  
; DATE: 1998-08-14  
ION NUMBER: US 08/417,210  
ATE: 1995-04-05  
ION NUMBER: US 08/223,842  
ATE: 1994-04-06  
ION NUMBER: US 07/897,382  
ATE: 1992-06-11  
ION NUMBER: US 07/715,921  
ATE: 1991-06-14  
ION NUMBER: US 08/105,483  
ATE: 1993-08-12  
ION NUMBER: US 07/847,951  
ATE: 1992-03-06  
ION NUMBER: US 07/713,967  
ATE: 1991-06-11  
ION NUMBER: US 07/666,056  
ATE: 1991-03-07  
ID NOS: 149  
ntIn version 3.1

ificial Sequence

ATION: Oligonucleotide primer referred to as P2A  
1

73.3%; Score 13.2; DB 4; Length 53;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTCATTGGGAATTTGCG 18  
|||  
Db 47 CTACTTTGGGATATTGCG 30  
RESULT 11  
US-09-411-578-35  
; Sequence 35, Application US/09411578  
; Patent No. 6203801  
; GENERAL INFORMATION:  
; APPLICANT: Schaap, Theodorus C  
; APPLICANT: Kuiper, Catharina M  
; APPLICANT: Vermeulen, Arnoldus N  
; TITLE OF INVENTION: Coccidiosis Vaccines  
; FILE REFERENCE: schaap  
; CURRENT APPLICATION NUMBER: US/09/411,578  
; CURRENT FILING DATE: 1999-10-04  
; EARLIER APPLICATION NUMBER: 98203384.7  
; EARLIER FILING DATE: 1998-10-07  
; EARLIER APPLICATION NUMBER: 98203457.1  
; EARLIER FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Eimeria tenella  
US-09-411-578-35

Query Match 71.1%; Score 12.8; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTGCG 17  
|||||  
Db 2 TCAATTGGGATTTGCG 17

RESULT 12  
US-09-411-578-37  
; Sequence 37, Application US/09411578  
; Patent No. 6203801  
; GENERAL INFORMATION:  
; APPLICANT: Schaap, Theodorus C  
; APPLICANT: Kuiper, Catharina M  
; APPLICANT: Vermeulen, Arnoldus N  
; TITLE OF INVENTION: Coccidiosis Vaccines  
; FILE REFERENCE: schaap  
; CURRENT APPLICATION NUMBER: US/09/411,578  
; CURRENT FILING DATE: 1999-10-04  
; EARLIER APPLICATION NUMBER: 98203384.7  
; EARLIER FILING DATE: 1998-10-07  
; EARLIER APPLICATION NUMBER: 98203457.1  
; EARLIER FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Eimeria tenella  
US-09-411-578-37

Query Match 71.1%; Score 12.8; DB 3; Length 17;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTGCG 17  
|||||  
Db 2 TCAATTGGGATTTGCG 17

RESULT 13  
US-09-749-233-35

L 09:38:22 2004

us-10-090-326-16.max.rni

application US/09749233  
10061  
ATION:  
haap, Theodor C  
uiper, Catharina M  
ermeulen, Arnoldus N  
NTION: Coccidiosis Vaccines  
E: schaa  
CATION NUMBER: US/09749,233  
G DATE: 2000-12-27  
TION NUMBER: 09/411,578  
DATE: 1999-10-04  
TION NUMBER: 98203457.1  
DATE: 1998-10-16  
ID NOS: 41  
entIn Ver. 2.1

meria tenella

71.1%; Score 12.8; DB 4; Length 17;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATTGGGAATTTGC 17  
|||||  
AATTGGGAATTTGC 17

application US/09749233  
10061  
ATION:  
haap, Theodor C  
uiper, Catharina M  
ermeulen, Arnoldus N  
NTION: Coccidiosis Vaccines  
E: schaa  
CATION NUMBER: US/09749,233  
G DATE: 2000-12-27  
TION NUMBER: 09/411,578  
DATE: 1999-10-04  
TION NUMBER: 98203457.1  
DATE: 1998-10-16  
ID NOS: 41  
entIn Ver. 2.1

meria tenella

71.1%; Score 12.8; DB 4; Length 17;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATTGGGAATTTGC 17  
|||||  
AATTGGGAATTTGC 17

6/c  
plication US/09442143A  
3089  
ATION:

Vy, Gary  
ark, David A.  
NTION: Methods of Modulating Immune Coagulation  
E: 9579-14

CURRENT APPLICATION NUMBER: US/09/442,143A  
CURRENT FILING DATE: 1999-11-15  
PRIOR APPLICATION NUMBER: US 60/046,537  
PRIOR FILING DATE: 1997-05-17  
PRIOR APPLICATION NUMBER: US 60/061,684  
PRIOR FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-442-143A-46

Query Match 71.1%; Score 12.8; DB 4; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTGCC 18  
|||||  
Db 19 CATTAGATTTTGCC 4

RESULT 16

US-09-038-637-66  
Sequence 66, Application US/09038637  
Patent No. 6235470  
GENERAL INFORMATION:  
APPLICANT: Sidransky, David  
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALI  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,637  
FILING DATE: 10-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/579,233  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/152,313  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/146001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-038-637-66

Query Match 71.1%; Score 12.8; DB 3; Length 22;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

TTTGAATTTGCC 18  
|||||||  
TCTGAATTTGCC 21

plication US/09041185  
4944

MARION:  
Scott, Richard W.  
Reaume, Andrew G.  
Dorfman, Karen  
VENTION: Gene-Targeted No. 6284944-Human Mammal With A Human Fad Presen  
SEQUENCES: 16  
NCE ADDRESS:  
: William J. McNichol, Jr.  
: Reed Smith Shaw & McClay  
2500 One Liberty Place  
Philadelphia  
Pennsylvania  
USA  
03

ADABLE FORM:  
PE: Diskette, 3.5 inch, 1.44 Mb storage  
IBM PC or compatibles  
SYSTEM: Windows 95  
Microsoft Word Version 6.0C  
JICATION DATA:  
ON NUMBER: US/09/041,185  
PE: 10-MAR-1998  
ATION: 800  
ATION DATA:  
ON NUMBER: 60/057,069  
PE: 29-AUG-1997  
ENT INFORMATION:  
Nichol, Jr., William J.  
ON NUMBER: 31,179  
DOCKET NUMBER: 98-353  
ATION INFORMATION:  
(215) 241-7950  
(215) 851-1420  
R SEQ ID NO: 6:  
RACTERISTICS:  
2 base pairs  
leic acid  
SS: single  
linear  
E: Genomic DNA

71.1%; Score 12.8; DB 3; Length 22;  
larity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTTG 16  
|||||||  
ATCTGGAATTTG 22

application US/08758306  
743

ATION:  
Stinchcomb, Dan T.  
McSwiggen, James A.  
ENTION: METHOD AND REAGENT FOR THE  
ENTION: TREATMENT OF DISEASES  
ENTION: ASSOCIATED WITH  
ENTION: INTERLEUKIN-2 RECEPTOR  
ENTION: GAMMA-CHAIN EXPRESSION  
SEQUENCES: 1379

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306  
FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
Prior APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 375:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-306-375

Query Match 68.9%; Score 12.4; DB 1; Length 17;  
Best Local Similarity 42.9%; Pred. No. 2.6e+03;  
Matches 6; Conservative 7; Mismatches 1; Indels 0;

QY 1 CTCATTTGGAATTT 14  
|: |||||  
Db 4 CUGAUUGGAUUU 17

RESULT 19  
US-08-192-271-5/c  
Sequence 5, Application US/08192271  
Patent No. 6294376  
GENERAL INFORMATION:  
APPLICANT: OVERTURF, MERRILL L.  
APPLICANT: LOOSE-MITCHELL, DAVID S.  
TITLE OF INVENTION: CHOLESTEROL 7-ALPHA HYDROXYLASE  
TITLE OF INVENTION: EXPRESSION REGULATION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MARTIN L. MCGREGOR  
STREET: 910 LOUISIANA STREET  
CITY: HOUSTON  
STATE: TX  
COUNTRY: USA  
ZIP: 77002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/192,271  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:

1 09:38:22 2004

us-10-090-326-16.max.rni

GREGOR,, MARTIN L.  
ION NUMBER: 29,329  
/DOCKET NUMBER: 02638-0106  
ICATION INFORMATION:  
3: (713)229-1874  
FOR SEQ ID NO: 5:  
HARACTERISTICS:  
27 base pairs  
nucleic acid  
NESS: single  
linear  
PE: DNA (genomic)

68.9%; Score 12.4; DB 3; Length 27;  
ilarity 92.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGGAAATTTGCC 18  
|||||  
GGGAATTTGCC 11

/c  
Application PC/TUS9401572  
INATION:  
OVERTURF,, MERRILL L.  
LOOSE-MITCHELL,, DAVID S.  
VENTION: CHOLESTEROL 7-ALPHA HYDROXYLASE  
VENTION: EXPRESSION REGULATION  
SEQUENCES: 8  
NCE ADDRESS:  
?: MARTIN L. GREGOR  
910 LOUISIANA STREET  
USTON  
X. USA

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
ICATION DATA:  
ION NUMBER: PCT/US94/01572  
ATE:  
ATION:  
ENT INFORMATION:  
GREGOR,, MARTIN L.  
ION NUMBER: 29,329  
/DOCKET NUMBER: 02638-0106  
ICATION INFORMATION:  
3: (713)229-1874  
OR SEQ ID NO: 5:  
HARACTERISTICS:  
27 base pairs  
nucleic acid  
NESS: single  
linear  
PE: DNA (genomic)

68.9%; Score 12.4; DB 5; Length 27;  
ilarity 92.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGGAAATTTGCC 18  
|||||  
GGGAATTTGCC 11

RESULT 21  
US-09-021-701-379  
Sequence 379, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Records Manager, Legal Department, Hewlett-Packar  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 379:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-379

Query Match 67.8%; Score 12.2; DB 3; Length 20;  
Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGTC 17  
Db 4 CTACTTTGGGAATATGTC 20

RESULT 22  
US-09-021-701-380  
Sequence 380, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Records Manager, Legal Department, Hewlett-Packar  
STREET: 3000 Hanover Street

lo Alto

A. USA

04

ADABLE FORM:  
PE: Floppy disk

SYSTEM: PC-DOS/MS-DOS  
Patentin Release #1.0, Version #1.30

LOCATION DATA:  
ON NUMBER: US/09/021,701

TE: 10-FEB-1998

ATION:

ENT INFORMATION:

oi, Wendy A.

ION NUMBER: 36,697

/DOCKET NUMBER: 10971464-1

CATION INFORMATION:

: 650-236-2386

650-852-8063

DR SEQ ID NO: 380:

ARACTERISTICS:

20 base pairs

cleic acid

ESS: single

linear

PE: CDNA

G: NO

NO

0

67.8%; Score 12.2; DB 3; Length 20;

ilarity 82.4%; Pred. No. 3.3e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTTTGGAATTTCG 17

ACTTTGGAATTTCG 19

Application US/09021701

588

ATION:

Shannon, Karen W.

Wolber, Paul K.

Delenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

ENTION: Methods for evaluating oligonucleotide

ENTION: probe sequences

QUENCES: 1165

ICE ADDRESS:

Records Manager, Legal Department, Hewlett-Packard Company M/S 20

000 Hanover Street

o Alto

USA

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

LOCATION DATA:

ON NUMBER: US/09/021,701

TE: 10-FEB-1998

ATION:

NT INFORMATION:

oi, Wendy A.

ON NUMBER: 36,697

DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 381:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-021-701-381

Query Match 67.8%; Score 12.2; DB 3; Length 20;

Best Local Similarity 82.4%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCAATTGGAATTTCG 17

Db 2 CTCAATTGGAATTTCG 18

RESULT 24

US-09-021-701-382

Sequence 382, Application US/09021701

Patent No. 6251588

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

APPLICANT: Wolber, Paul K.

APPLICANT: Delenstarr, Glenda C.

APPLICANT: Webb, Peter G.

APPLICANT: Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701

FILING DATE: 10-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 382:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-021-701-382

Query Match 67.8%; Score 12.2; DB 3; Length 20;

Best Local Similarity 82.4%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

TCATTGGAATTTGCC 17  
 ||||| |||||  
 TACTTGGAAATATGTC 17

28 Application US/09446301A  
 26893  
 MATION:  
 J. SOLH, NEVINE  
 ALIGNET, JEANINE  
 ENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE  
 ENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED  
 ENTION: COMPOUNDS  
 E: 03715-0059  
 CATION NUMBER: US/09/446,301A  
 G DATE: 1999-12-20  
 ID NOS: 51  
 entIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer  
 18

ilarity 67.8%; Score 12.2; DB 4; Length 22;  
 Conservativity 82.4%; Pred. No. 3.3e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGAAATTTGCC 18  
 ||||| |||||  
 GTTTGTAATTTCTGCC 18

Application US/09099932

0001

ATION:

Solh, Nevine  
 lignet, Jeanine  
 NTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE  
 NTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED  
 NTION: COMPOUNDS  
 E: 03495.0173-00000  
 CATION NUMBER: US/09/099,932  
 G DATE: 1998-06-19  
 CATION NUMBER: 60/050,380  
 G DATE: 1997-06-20  
 ID NOS: 50  
 entIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: primer

ilarity 67.8%; Score 12.2; DB 4; Length 22;  
 Conservativity 82.4%; Pred. No. 3.3e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATTGGAATTTGCC 18  
 ||||| |||||  
 GTTTGTAATTTGCC 18

US-07-753-738B-3/c  
 ; Sequence 3, Application US/07753738B  
 ; Patent No. 5304730  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lawson, Edgar C.  
 ; APPLICANT: Weiss, James D.  
 ; APPLICANT: Hemenway, Cynthia L.  
 ; APPLICANT: Turner, Nilgun E.  
 ; TITLE OF INVENTION: Virus Resistant Plants and Method  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
 ; STREET: 700 Chesterfield Village Parkway  
 ; CITY: St. Louis  
 ; STATE: Missouri  
 ; COUNTRY: USA  
 ; ZIP: 63198  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/753,738B  
 ; FILING DATE: 19910903  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hoerner Jr., Dennis R.  
 ; REGISTRATION NUMBER: 30,914  
 ; REFERENCE/DOCKET NUMBER: 38-21(10536)A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314)537-6099  
 ; TELEFAX: (314)537-6047  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 34 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (synthetic)  
 ; US-07-753-738B-3

Query Match 67.8%; Score 12.2; DB 1; Length 34;  
 Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

OY 1 CTCATTGGAAATTTGCC 17  
 ||||| |||||  
 DB 17 CTTATTTGGGGTTTTC 1

RESULT 28

US-08-924-695A-17  
 ; Sequence 17, Application US/08924695A  
 ; Patent No. 5998583  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KORSMEYER, STANLEY J.  
 ; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MISSOURI  
 ; COUNTRY: USA  
 ; ZIP: 63105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:

09:38:22 2004

us-10-090-326-16.max.rni

ION NUMBER: US/08/324,695A  
 RE: 08-SEP-1997  
 ATION: 514  
 ENT INFORMATION:  
 ELAND, DONALD R.  
 ION NUMBER: 35,197  
 /DOCKET NUMBER: 971798  
 ATION INFORMATION:  
 : (314) 727-5388  
 DR SEQ ID NO: 17:  
 ARACTERISTICS:  
 14 base pairs  
 eic acid  
 35S: single  
 linear  
 PE: CDNA  
 7

```

67.8%; Score 12.2; DB 2; Length 34;
ilarity 82.4%; Pred.No.3.4e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATTGGAATTTTGGC 18
|||||
ATCCGGAATATTGCC 28

```

plication US/08479852

1385  
ATION:  
Sherrol H. McDonough, Thomas B. Ryder,  
Yeasling Yang  
'ENTION: NUCLEIC ACID AMPLIFICATION  
'ENTION: OLIGONUCLEOTIDES AND PROBES  
'ENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
SEQUENCES: 139  
ICE ADDRESS:

Lyon & Lyon  
11 West Sixth Street  
Los Angeles  
California  
USA

FILE FORM:  
 PE: 3.5" Diskette, 1.44 Mb storage  
 IBM PS/2 Model 50Z or 55SX  
 SYSTEM: IBM P.C. DOS (Version 3.30)  
 WordPerfect (Version 5.0)

LOCATION DATA:  
IN NUMBER: US/08/479,852



ATION: 435

ATTENTION DATA: IIS/09/040 745

DATE: 05/05/04 11:30  
E:

N NUMBER: U.S. Serial No. 5712385 07/550,837

E: 7/10/90

IN NUMBER: U.S. Serial No. 5712385 07/379,501  
F. 7/11/88

NT INFORMATION:

burg, Richard J.

ON NUMBER: 32,327

DOCKET NUMBER: 196/189

ATION INFORMATION:  
(273) 489-7600

(213) 955-0440

·-3510

R SEQ ID NO: 16:

### CHARACTERISTICS:

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-479-852-16

```

Query Match	67.8%;	Score 12.2;	DB 1;	Length 36;
Best Local Similarity	82.4%;	Pred. No. 3.4e+03;		
Matches 14;	Conservative	0;	Mismatches 3;	Indels 0;

QY  
1 CTCAATTGGAATTTGC 17

Dd  
1 CTAATTGGAATTTGC 17

RESULT 30  
US-08-479-852-96/c  
; Sequence 96, Application US/08479852  
; Patent No. 5712385

GENERAL INFORMATION:  
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
APPLICANT: Yeasing Yang  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
NUMBER OF SEQUENCES: 139  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,745  
FILING DATE:

; APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837  
 ; FILING DATE: 7/10/90  
 ; APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501  
 ; FILING DATE: 7/11/89

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 196/189

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

```

; INFORMATION FOR SEQ ID NO:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 36
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
US-08-479-852-96

```

Query Match 67.8%; Score 12.2; DB 1; Length 36;  
Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTC 17  
db 36 CTACTTTGGGAATATTC 20

Dbb 36 C T A C T T T G G A A T A T T G C 20



1 09:38:22 2004

us-10-090-326-16.max.rni

```
33 Application US/08479852
12385
3MATION:
  Sherrol H. McDonough, Thomas B. Ryder,
  Yeasing Yang
VENTION: NUCLEIC ACID AMPLIFICATION
VENTION: OLIGONUCLEOTIDES AND PROBES
VENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
SEQUENCES: 139
ENCE ADDRESS:
  3: Lyon & Lyon
  611 West Sixth Street
  28 Angeles
  California
  USA
317
ADABLE FORM:
(P: 3.5" Diskette, 1.44 Mb storage
  IBM PS/2 Model 50Z or 55SX
  SYSTEM: IBM P.C. DOS (Version 3.30)
  WordPerfect (Version 5.0)
PLICATION DATA:
  ON NUMBER: US/08/479,852
TE:
ATION: 435
ATION DATA:
  ON NUMBER: US/08/040,745
TE:
  ON NUMBER: U.S. Serial No. 5712385 07/550,837
  ON NUMBER: U.S. Serial No. 5712385 07/379,501
TE: 7/10/90
  ON NUMBER: 32,327
  ON NUMBER: 196/189
  ON INFORMATION:
  : (213) 489-1600
  : (213) 955-0440
  7-3510
  OR SEQ ID NO: 133:
  36
  leic acid
  ESS: single
  linear
  3
  67.8%; Score 12.2; DB 1; Length 36;
  ilarity 41.2%; Pred. No. 3.4e+03;
  Conservative 7; Mismatches 3; Indels 0; Gaps 0;
  CATTTGGAATTTTGC 17
  : : : : :
  ACUUGGAUAUUGC 17
7/c
Application US/08479852
2385
MATION:
  Sherrol H. McDonough, Thomas B. Ryder,
  Yeasing Yang
VENTION: NUCLEIC ACID AMPLIFICATION
VENTION: OLIGONUCLEOTIDES AND PROBES
VENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
SEQUENCES: 139
ENCE ADDRESS:
  : Lyon & Lyon
  611 West Sixth Street
```

```

/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90017
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
/ COMPUTER: IBM PS/2 Model 50Z or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,852
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/040,745
/ FILING DATE:
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
/ FILING DATE: 7/10/90
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
/ FILING DATE: 7/11/89
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 196/189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 137:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-479-852-137
Query Match 67.8%; Score 12.2; DB 1; Length 36;
Best Local Similarity 82.4%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;
QY 1 CTCATTGGAAATTTGC 17
DB 36 CTACTTTGGAATATTC 20
RESULT 33
US-08-462-646-16
; Sequence 16, Application US/08462646
; Patent No. 5856088
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
; APPLICANT: Yeasing Yang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,646
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```

; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-462-646-96

Query Match          67.8%; Score 12.2; DB 2; Length 36;
Best Local Similarity 82.4%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY      1 CTCATTGGAAATTTGTC 17
DB      36 CTACTTGGAAATTTGC 20

RESULT 35
US-08-462-646-133
; Sequence 133, Application US/08462646
; Patent No. 5856088
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
; APPLICANT: Yeasing Yang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,646
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,745
; FILING DATE: 26-MAR-1993
; APPLICATION NUMBER: U.S. Serial No. 5856088 07/550,837
; FILING DATE: 7/10/90
; APPLICATION NUMBER: U.S. Serial No. 5856088 07/379,501
; FILING DATE: 7/11/89
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 196/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-462-646-133

Query Match          67.8%; Score 12.2; DB 2; Length 36;
Best Local Similarity 41.2%; Pred. No. 3.4e+03;
Matches 7; Conservative 7; Mismatches 3; Indels 0;

QY      1 CTCATTGGAAATTTGTC 17
; : ::|||:::|

```

UACUUGGAUAUUGC 17

37/c  
Application US/08462646  
56088

## INVENTION:

Sherrol H. McDonough, Thomas B. Ryder,  
Yeasing Yang

INVENTION: NUCLEIC ACID AMPLIFICATION

INVENTION: OLIGONUCLEOTIDES AND PROBES

INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

SEQUENCES: 139

ENCE ADDRESS:

S: Lyon &amp; Lyon

611 West Sixth Street

Los Angeles

California

USA

317

## READABLE FORM:

VPE: 3.5" Diskette, 1.44 Mb storage

S: IBM PS/2 Model 50Z or 55SX

S: SYSTEM: IBM P.C. DOS (Version 3.30)

S: WordPerfect (Version 5.0)

PLICATION DATA:

ION NUMBER: US/08/462,646

ATE: 05-JUN-1995

ATION: 435

ICATION DATA:

ION NUMBER: US 08/040,745

ATE: 26-MAR-1993

ION NUMBER: U.S. Serial No. 5856088 07/550,837

ATE: 7/10/90

ION NUMBER: U.S. Serial No. 5856088 07/379,501

ATE: 7/11/89

SENT INFORMATION:

urzburg, Richard J.

ION NUMBER: 32,327

S/DOCKET NUMBER: 196/189

ICATION INFORMATION:

S: (213) 489-1600

S: (213) 955-0440

S: 7-3510

FOR SEQ ID NO: 137:

CHARACTERISTICS:

36

cleic acid

ESS: single

linear

.7

67.8%; Score 12.2; DB 2; Length 36;

ilarity 82.4%; Pred. No. 3.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTC 17

ACTTTGGAATTTC 20

1/c

Application US/08792832A

7734

## INVENTION:

Summers Dr., Max D.

Braunagel Dr., Sharon C.

Hong Dr., Tao

INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID

INVENTION: SEQUENCE AND USES THEREOF

SEQUENCES: 56

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White &amp; Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77210

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/792,832A

FILING DATE: 30-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,955

FILING DATE: 07-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/678,435

FILING DATE: 03-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hibler, David W.

REGISTRATION NUMBER: 41,071

REFERENCE/DOCKET NUMBER: TAMK:190

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-792-832A-11

## Query Match

Best Local Similarity 67.8%; Score 12.2; DB 3; Length 36;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTC 17

Db 17 CTCATGCGAATGTC 1

## RESULT 38

US-09-013-406-16

Sequence 16, Application US/09013406

Patent No. 6252059

## GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

APPLICANT: Yeasing Yang

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/013,406

FILING DATE:

CLASSIFICATION:

QY 1 CTCATTGGAAATTTC 17

ACUUGGAUUGC 17

Application US/09013406

2059

INATION: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

VENTION: NUCLEIC ACID AMPLIFICATION

VENTION: OLIGONUCLEOTIDES AND PROBES

SEQUENCES: 139

ANCE ADDRESS:

Y: Lyon & Lyon

611 West Sixth Street

s Angeles

alifornia

USA

17

ADABLE FORM:

PE: 3.5" Diskette, 1.44 Mb storage

IBM PS/2 Model 50Z or 55SX

SYSTEM: IBM P.C. DOS (Version 3.30)

WordPerfect (Version 5.0)

PLICATION DATA:

ON NUMBER: US/09/013,406

TE:

ATION DATA:

ON NUMBER: 08/479,852

TE:

ON NUMBER: U.S. Serial No. 6252059 07/550,837

TE: 7/10/90

ON NUMBER: U.S. Serial No. 6252059 07/379,501

TE: 7/11/89

ENT INFORMATION:

burg, Richard J.

ION NUMBER: 32,327

/DOCKET NUMBER: 196/189

CATION INFORMATION:

: (213) 489-1600

7-3510

OR SEQ ID NO: 137:

ARACTERISTICS:

36

cleic acid

ESS: single

linear

7

67.8%; Score 12.2; DB 3; Length 36;

ilarity 82.4%; Pred.No.3.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGAATTTGC 17

ACTTTGGAATTTGC 20

pplication US/09766095

9749

INATION:

NT: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

F INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-JAN-01

APPLICATION NUMBER: U.S. Serial No. 6649749 07/550,837

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. 6649749 07/379,501

FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-766-095-16

Query Match 67.8%; Score 12.2; DB 4; Length 36;

Best Local Similarity 82.4%; Pred.No.3.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCAATTTGGAATTTGC 17

Db 1 CTACTTTGGAATTTGC 17

RESULT 43

US-09-766-095-96/c

; Sequence 96, Application US/09766095

; Patent No. 6649749

GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

```

APPLICATION DATA:
PPLICATION NUMBER: US/09/766,095
LING DATE: 18-Jan-2001
ASSIFICATION: <Unknown>
APPLICATION DATA:
PPLICATION NUMBER: 09/013,406
LING DATE: 26-JAN-01
PPLICATION NUMBER: U.S. Serial No. 6649749 07/550,837
LING DATE: 10-Jul-90
PPLICATION NUMBER: U.S. Serial No. 6649749 07/379,501
LING DATE: 11-Jul-89
Y/AGENT INFORMATION:
ME: Warburg, Richard J.
ISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
MUNICATION INFORMATION:
LEPHONE: (213) 489-1600
LEFAX: (213) 955-0440
LEX: 67-3510
FOR SEQ ID NO: 96:
E CHARACTERISTICS:
NGTH: 36
PE: nucleic acid
RANDEDNESS: single
POLOGY: linear
E DESCRIPTION: SEQ ID NO: 96:
67.8%; Score 12.2; DB 4; Length 36;
ilarity 82.4%; Pred. No. 3.4e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTGGAATTTCG 17
|||||
ACTTTGGAATATTCG 20

3 Application US/09766095
9749
RMATION:
NT: Sherrol H. McDonough, Thomas B. Ryder,
Yeasing Yang
F INVENTION: NUCLEIC ACID AMPLIFICATION
OLIGONUCLEOTIDES AND PROBES
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
OF SEQUENCES: 139
NDENCE ADDRESS:
DRESSEE: Lyon & Lyon
REET: 611 West Sixth Street
TY: Los Angeles
ATE: California
UNTRY: USA
P: 90017
R READABLE FORM:
DIUM TYPE: 3.5" Diskette, 1.44 Mb storage
MPUTER: IBM PS/2 Model 50Z or 55SX
ERATING SYSTEM: IBM P.C. DOS (Version 3.30)
FTWARE: WordPerfect (Version 5.0)
APPLICATION DATA:
PLICATION NUMBER: US/09/766,095
LING DATE: 18-Jan-2001
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: 09/013,406
LING DATE: 26-JAN-01
PLICATION NUMBER: U.S. Serial No. 6649749 07/550,837
LING DATE: 10-Jul-90
PLICATION NUMBER: U.S. Serial No. 6649749 07/379,501
LING DATE: 11-Jul-89
Y/AGENT INFORMATION:
ME: Warburg, Richard J.

```

```

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 196/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-766-095-133

Query Match 67.8%; Score 12.2; DB 4; Length 36;
Best Local Similarity 41.2%; Pred. No. 3.4e+03;
Matches 7; Conservative 7; Mismatches 3; Indels 0;

Qy 1 CTCAITTTGGAATTTTCG 17
|: :|||: :|||
Db 1 CUACUUGGAUAUUGC 17

RESULT 45
US-09-766-095-137/c
; Sequence 137, Application US/09766095
; Patent No. 6649749
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
; Yeasing Yang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; OLIGONUCLEOTIDES AND PROBES
; TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,095
; FILING DATE: 18-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,406
; FILING DATE: 26-JAN-01
; APPLICATION NUMBER: U.S. Serial No. 6649749 07/550,837
; FILING DATE: 10-Jul-90
; APPLICATION NUMBER: U.S. Serial No. 6649749 07/379,501
; FILING DATE: 11-Jul-89
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 196/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

1 09:38:22 2004

us-10-090-326-16.max.rni

37

67.8%; Score 12.2; DB 4; Length 36;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTTCG 17  
|||||  
TACTTGGGAATTTCG 20

i: February 29, 2004, 11:22:25  
61 secs





64.4	24	10	US-09-978-665A-372	Sequence 372, App	c 162	11.4	63.3	17	14	US-10-287-919-792	Sequence
64.4	24	10	US-09-978-802A-372	Sequence 372, App	c 163	11.4	63.3	17	14	US-10-287-919-792	Sequence
64.4	24	12	US-10-164-749A-372	Sequence 372, App	c 164	11.4	63.3	17	14	US-10-339-782-481	Sequence
64.4	24	14	US-10-017-081A-372	Sequence 372, App	c 165	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-167-749-372	Sequence 372, App	c 166	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-013-921A-372	Sequence 372, App	c 167	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-013-929A-372	Sequence 372, App	c 168	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-016-177A-372	Sequence 372, App	c 169	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-166-709A-372	Sequence 372, App	c 170	11.4	63.3	20	10	US-09-784-674-383	Sequence
64.4	24	14	US-10-143-031A-372	Sequence 372, App	c 171	11.4	63.3	21	15	US-10-349-143-977A	Sequence
64.4	24	14	US-10-143-030A-372	Sequence 372, App	c 172	11.4	63.3	21	14	US-10-349-143-977A	Sequence
64.4	24	14	US-10-143-030A-372	Sequence 372, App	c 173	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-002-967A-372	Sequence 372, App	c 174	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-017-083A-372	Sequence 372, App	c 175	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-128A-372	Sequence 372, App	c 176	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-017-191A-372	Sequence 372, App	c 177	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-143-028A-372	Sequence 372, App	c 178	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-143-029A-372	Sequence 372, App	c 179	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-124A-372	Sequence 372, App	c 180	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-160-502A-372	Sequence 372, App	c 181	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-087A-372	Sequence 372, App	c 182	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-067A-372	Sequence 372, App	c 183	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-017A-372	Sequence 372, App	c 184	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-164-728A-372	Sequence 372, App	c 185	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-164-728A-372	Sequence 372, App	c 186	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-013-926A-372	Sequence 372, App	c 187	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-165-247A-372	Sequence 372, App	c 188	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-124A-372	Sequence 372, App	c 189	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-160-502A-372	Sequence 372, App	c 190	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-145-087A-372	Sequence 372, App	c 191	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-017-086A-372	Sequence 372, App	c 192	11.4	63.3	25	10	US-10-349-143-977A	Sequence
64.4	24	14	US-10-164-829A-372	Sequence 372, App	c 193	11.4					

62.2	47	15	US-10-349-143-2845	Sequence 2845, Ap	308	10.8	60.0	25	14	US-10-098-263B-3283	Sequenc
62.2	47	15	US-10-349-143-2870	Sequence 2870, Ap	309	10.8	60.0	25	14	US-10-098-263B-37155	Sequenc
62.2	50	14	US-10-029-386-15382	Sequence 15382, A	310	10.8	60.0	25	14	US-10-098-263B-43484	Sequenc
62.2	50	15	US-10-131-827-3086	Sequence 3086, Ap	311	10.8	60.0	25	14	US-10-098-263B-48757	Sequenc
62.2	50	15	US-10-131-827-3138	Sequence 3138, Ap	312	10.8	60.0	25	14	US-10-098-263B-51065	Sequenc
62.2	50	15	US-10-131-827-5498	Sequence 5498, Ap	313	10.8	60.0	25	14	US-10-098-263B-54705	Sequenc
62.2	50	15	US-10-131-827-7751	Sequence 7751, Ap	314	10.8	60.0	25	14	US-10-098-263B-54706	Sequenc
62.2	50	15	US-10-131-827-7847	Sequence 7847, Ap	c 315	10.8	60.0	25	14	US-10-098-263B-59098	Sequenc
62.2	50	15	US-10-131-827-8026	Sequence 8026, Ap	c 316	10.8	60.0	25	14	US-10-098-263B-70537	Sequenc
62.2	60	9	US-09-886-900-3	Sequence 3, Appli	317	10.8	60.0	25	14	US-10-098-263B-81781	Sequenc
62.2	60	10	US-09-908-975-5332	Sequence 5332, Ap	318	10.8	60.0	25	14	US-10-098-263B-81781	Sequenc
62.2	60	10	US-09-908-975-6014	Sequence 6014, Ap	c 319	10.8	60.0	25	14	US-10-098-263B-93262	Sequenc
62.2	60	10	US-09-908-975-9693	Sequence 9693, Ap	c 320	10.8	60.0	25	14	US-10-098-263B-104996	Sequenc
62.2	60	10	US-09-908-975-10029	Sequence 10029, A	c 321	10.8	60.0	27	10	US-09-232-785-32	Sequenc
62.2	60	10	US-09-908-975-10606	Sequence 10606, A	322	10.8	60.0	27	10	US-10-312-273-384	Sequenc
62.2	60	10	US-09-908-975-12644	Sequence 12644, A	323	10.8	60.0	29	10	US-09-907-111-172	Sequenc
62.2	60	10	US-09-908-975-17258	Sequence 17258, A	c 324	10.8	60.0	29	14	US-10-310-507-17	Sequenc
62.2	60	10	US-09-908-975-19465	Sequence 19465, A	325	10.8	60.0	29	14	US-10-336-638-877	Sequenc
62.2	60	10	US-09-908-975-19731	Sequence 19731, A	326	10.8	60.0	30	14	US-10-218-654-146	Sequenc
62.2	60	10	US-09-908-975-21798	Sequence 21798, A	c 327	10.8	60.0	30	14	US-10-238-042-2	Sequenc
61.1	15	9	US-09-930-536-3	Sequence 3, Appli	328	10.8	60.0	30	14	US-10-262-439-146	Sequenc
61.1	17	15	US-10-300-683-138	Sequence 138, App	c 329	10.8	60.0	32	9	US-09-804-682-89	Sequenc
61.1	17	15	US-10-300-683-325	Sequence 325, App	330	10.8	60.0	32	13	US-10-006-009-41	Sequenc
61.1	17	15	US-10-300-683-503	Sequence 503, App	331	10.8	60.0	33	9	US-09-922-261-102	Sequenc
61.1	20	10	US-09-998-027-157	Sequence 157, App	332	10.8	60.0	33	9	US-09-428-122-4	Sequenc
61.1	20	14	US-10-165-099-157	Sequence 25, Appl	c 333	10.8	60.0	33	10	US-10-312-273-625	Sequenc
61.1	23	9	US-09-898-533-25	Sequence 48, Appl	c 334	10.8	60.0	33	15	US-10-194-550-22	Sequenc
61.1	27	14	US-10-219-850-48	Sequence 60, Appl	335	10.8	60.0	33	15	US-09-730-289B-2294	Sequenc
61.1	27	15	US-10-353-678-60	Sequence 4, Appli	336	10.8	60.0	37	14	US-09-780-533A-3099	Sequenc
61.1	40	14	US-10-200-013-4	Sequence 454, App	c 337	10.8	60.0	38	10	US-09-776-474-1730	Sequenc
61.1	47	15	US-10-349-143-454	Sequence 1707, Ap	c 338	10.8	60.0	38	10	US-09-776-474-1875	Sequenc
61.1	47	15	US-10-349-143-1724	Sequence 5338, Ap	c 339	10.8	60.0	38	10	US-09-792-818-921	Sequenc
61.1	50	15	US-10-131-827-816	Sequence 9070, Ap	c 340	10.8	60.0	39	15	US-10-027-632-5430	Sequenc
61.1	50	15	US-10-131-827-2704	Sequence 1390, Ap	c 341	10.8	60.0	40	15	US-10-027-632-175486	Sequenc
61.1	54	8	US-08-781-986A-1707	Sequence 14595, A	c 342	10.8	60.0	42	14	US-10-221-993-14	Sequenc
61.1	60	10	US-09-908-975-5338	Sequence 15050, A	c 343	10.8	60.0	44	15	US-10-373-090-3	Sequenc
61.1	60	10	US-09-908-975-9070	Sequence 18084, A	c 344	10.8	60.0	45	15	US-10-369-299-16	Sequenc
61.1	60	10	US-09-908-975-14595	Sequence 19090, A	c 345	10.8	60.0	47	9	US-09-732-914-122	Sequenc
61.1	60	10	US-09-908-975-15050	Sequence 629, App	c 346	10.8	60.0	47	14	US-10-137-473-43	Sequenc
61.1	60	10	US-09-908-975-18084	Sequence 1390, Ap	c 347	10.8	60.0	47	15	US-10-349-143-271	Sequenc
61.1	60	10	US-09-908-975-19090	Sequence 3165, Ap	c 348	10.8	60.0	47	15	US-10-349-143-517	Sequenc
61.1	60	10	US-09-908-975-2181	Sequence 3165, Ap	c 349	10.8	60.0	47	15	US-10-349-143-1657	Sequenc
61.1	60	10	US-10-287-919-764	Sequence 764, App	c 350	10.8	60.0	47	15	US-10-349-143-3212	Sequenc
61.1	60	10	US-10-287-919-2181	Sequence 2181, Ap	c 351	10.8	60.0	50	8	US-08-781-986A-2475	Sequenc
61.1	60	10	US-10-128-560-5	Sequence 5, Appli	c 352	10.8	60.0	50	14	US-10-322-360-45	Sequenc
61.1	60	10	US-10-128-560-18	Sequence 18, Appl	c 353	10.8	60.0	50	14	US-10-322-360-149	Sequenc
61.1	60	10	US-10-205-309-250	Sequence 250, App	c 354	10.8	60.0	50	15	US-10-322-360-149	Sequenc
61.1	60	10	US-09-828-344-59	Sequence 575, App	c 355	10.8	60.0	50	15	US-10-131-827-2	Sequenc
61.1	60	10	US-09-784-674-718	Sequence 59, Appl	c 356	10.8	60.0	50	15	US-10-131-827-3	Sequenc
61.1	60	10	US-09-784-674-719	Sequence 718, App	c 357	10.8	60.0	50	15	US-10-131-827-515	Sequenc
61.1	60	10	US-09-784-674-720	Sequence 719, App	c 358	10.8	60.0	50	15	US-10-131-827-1861	Sequenc
61.1	60	10	US-09-784-674-721	Sequence 720, App	c 359	10.8	60.0	50	15	US-10-131-827-2424	Sequenc
61.1	60	10	US-09-784-674-722	Sequence 721, App	c 360	10.8	60.0	50	15	US-10-131-827-2862	Sequenc
61.1	60	10	US-09-784-674-723	Sequence 722, App	c 361	10.8	60.0	50	15	US-10-131-827-5475	Sequenc
61.1	60	10	US-09-784-674-724	Sequence 723, App	c 362	10.8	60.0	50	15	US-10-131-827-6871	Sequenc
61.1	60	10	US-10-012-456A-30	Sequence 724, App	c 363	10.8	60.0	50	15	US-10-131-827-7605	Sequenc
61.1	60	10	US-10-331-907-331	Sequence 30, Appl	c 364	10.8	60.0	50	15	US-10-131-827-7844	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 331, App	c 365	10.8	60.0	57	8	US-08-781-986A-1668	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 4004, Ap	c 366	10.8	60.0	58	15	US-10-339-712-18	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 9573, Ap	c 367	10.8	60.0	59	9	US-09-796-071-10	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 165, App	c 368	10.8	60.0	59	9	US-09-796-071-11	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 31, Appl	c 369	10.8	60.0	60	10	US-09-907-111-66	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 939, App	c 370	10.8	60.0	60	10	US-09-908-975-5474	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 487, App	c 371	10.8	60.0	60	10	US-09-908-975-5513	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 1, Appli	c 372	10.8	60.0	60	10	US-09-908-975-11713	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 14, Appl	c 373	10.8	60.0	60	10	US-09-908-975-12403	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 13, Appl	c 374	10.8	60.0	60	10	US-09-908-975-13405	Sequenc
61.1	60	10	US-10-447-136-165	Sequence 808, App	c 375	10.8	60.0	60	10	US-09-908-975-13915	Sequenc
61.1	60	10	US-10-447-136-165		c 376	10.8	60.0	60	10	US-09-908-975-16004	Sequenc
61.1	60	10	US-10-447-136-165		c 377	10.8	60.0	60	10	US-09-908-975-16629	Sequenc
61.1	60	10	US-10-447-136-165		c 378	10.8	60.0	60	10		
61.1	60	10	US-10-447-136-165		c 379	10.8	60.0	60	10		
61.1	60	10	US-10-447-136-165		c 380	10.8	60.0	60	10		

60.0	60	10	US-09-908-975-16965	Sequence 16965, A	454	10.6	58.9	41	14	US-10-292-896-86	Sequenc
60.0	60	10	US-09-908-975-17447	Sequence 17447, A	C 455	10.6	58.9	43	14	US-10-193-960-10	Sequenc
60.0	60	10	US-09-908-975-17791	Sequence 17791, A	C 456	10.6	58.9	43	14	US-10-193-960-13	Sequenc
60.0	60	10	US-09-908-975-18564	Sequence 18564, A	C 457	10.6	58.9	43	14	US-10-193-960-16	Sequenc
60.0	60	10	US-09-908-975-19285	Sequence 19285, A	C 458	10.6	58.9	43	14	US-10-193-960-26	Sequenc
60.0	60	10	US-09-908-975-20722	Sequence 20722, A	C 459	10.6	58.9	45	9	US-09-915-182-3	Sequenc
60.0	60	10	US-09-908-975-22451	Sequence 22451, A	C 460	10.6	58.9	45	9	US-09-765-272-235	Sequenc
60.0	60	10	US-09-908-975-32164	Sequence 32164, A	C 461	10.6	58.9	45	10	US-09-967-301-12	Sequenc
60.0	60	14	US-10-205-009-125	Sequence 125, App	C 462	10.6	58.9	45	10	US-09-967-301-13	Sequenc
58.9	17	9	US-09-866-108-6223	Sequence 6223, App	C 463	10.6	58.9	46	10	US-09-453-234-7	Sequenc
58.9	16	10	US-09-306-333A-106	Sequence 106, App	C 464	10.6	58.9	47	14	US-10-076-802-49	Sequenc
58.9	19	15	US-10-349-143-7292	Sequence 7292, App	C 465	10.6	58.9	47	14	US-10-076-802-50	Sequenc
58.9	19	15	US-10-349-143-7338	Sequence 7338, App	C 466	10.6	58.9	47	15	US-10-367-169-49	Sequenc
58.9	20	15	US-10-349-143-6437	Sequence 6437, App	C 467	10.6	58.9	47	15	US-10-367-169-50	Sequenc
58.9	21	9	US-09-765-081-397	Sequence 397, App	C 468	10.6	58.9	47	15	US-10-349-143-201	Sequenc
58.9	21	14	US-10-084-839-3970	Sequence 3970, App	C 469	10.6	58.9	47	15	US-10-349-143-3787	Sequenc
58.9	21	15	US-10-349-143-4952	Sequence 4952, App	C 470	10.6	58.9	47	15	US-10-349-143-1579	Sequenc
58.9	22	14	US-10-084-839-3973	Sequence 3973, App	C 471	10.6	58.9	47	15	US-10-349-143-3787	Sequenc
58.9	24	14	US-09-992-665-262	Sequence 262, App	C 472	10.6	58.9	49	10	US-09-782-974C-95	Sequenc
58.9	24	14	US-10-236-745-13	Sequence 13, Appl	C 473	10.6	58.9	50	15	US-10-131-827-719	Sequenc
58.9	24	14	US-10-032-585-5531	Sequence 5531, App	C 474	10.6	58.9	50	15	US-10-131-827-719	Sequenc
58.9	24	15	US-10-309-775A-8	Sequence 8, Appli	C 475	10.6	58.9	50	15	US-10-131-827-719	Sequenc
58.9	25	9	US-09-866-108-11115	Sequence 11115, A	C 476	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11116	Sequence 11116, A	C 477	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11117	Sequence 11117, A	C 478	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11118	Sequence 11118, A	C 479	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11119	Sequence 11119, A	C 480	10.6	58.9	50	15	US-10-131-827-7102	Sequenc
58.9	25	9	US-09-866-108-11120	Sequence 11120, A	C 481	10.6	58.9	50	15	US-10-131-827-7600	Sequenc
58.9	25	9	US-09-866-108-11121	Sequence 11121, A	C 482	10.6	58.9	50	15	US-10-444-925-103	Sequenc
58.9	25	9	US-09-866-108-11122	Sequence 11122, A	C 483	10.6	58.9	52	9	US-10-444-925-105	Sequenc
58.9	25	9	US-09-866-108-11123	Sequence 11123, A	C 484	10.6	58.9	52	9	US-09-547-267-28	Sequenc
58.9	25	9	US-09-796-543-6	Sequence 6, Appli	C 485	10.6	58.9	52	10	US-09-920-923-7	Sequenc
58.9	25	10	US-09-992-665-261	Sequence 261, App	C 486	10.6	58.9	54	8	US-08-781-986A-1965	Sequenc
58.9	25	14	US-10-215-112-6100	Sequence 6100, App	C 487	10.6	58.9	55	15	US-10-444-925-107	Sequenc
58.9	25	14	US-10-215-112-8233	Sequence 8233, App	C 488	10.6	58.9	55	15	US-10-444-925-109	Sequenc
58.9	25	14	US-10-215-112-8359	Sequence 8359, App	C 489	10.6	58.9	58	9	US-09-790-317-3	Sequenc
58.9	25	14	US-10-215-112-8864	Sequence 8864, App	C 490	10.6	58.9	58	14	US-10-262-828A-3	Sequenc
58.9	25	14	US-10-098-263B-14709	Sequence 14709, A	C 491	10.6	58.9	60	10	US-09-908-975-6435	Sequenc
58.9	25	14	US-10-098-263B-19461	Sequence 19461, A	C 492	10.6	58.9	60	10	US-09-908-975-6842	Sequenc
58.9	25	14	US-10-098-263B-19462	Sequence 19462, A	C 493	10.6	58.9	60	10	US-09-908-975-8165	Sequenc
58.9	25	14	US-10-098-263B-19477	Sequence 19477, A	C 494	10.6	58.9	60	10	US-09-908-975-9323	Sequenc
58.9	25	14	US-10-098-263B-35884	Sequence 35884, A	C 495	10.6	58.9	60	10	US-09-908-975-10647	Sequenc
58.9	25	14	US-10-098-263B-41992	Sequence 41992, A	C 496	10.6	58.9	60	10	US-09-908-975-11096	Sequenc
58.9	25	14	US-10-098-263B-51148	Sequence 51148, A	C 497	10.6	58.9	60	10	US-09-908-975-13069	Sequenc
58.9	25	14	US-10-098-263B-60280	Sequence 60280, A	C 498	10.6	58.9	60	10	US-09-908-975-13754	Sequenc
58.9	25	14	US-10-098-263B-60966	Sequence 60966, A	C 499	10.6	58.9	60	10	US-09-908-975-13922	Sequenc
58.9	25	14	US-10-098-263B-95647	Sequence 95647, A	C 500	10.6	58.9	60	10	US-09-908-975-14334	Sequenc
58.9	25	14	US-10-098-263B-115695	Sequence 115695, A	C 501	10.6	58.9	60	10	US-09-908-975-14721	Sequenc
58.9	26	14	US-10-278-455-26	Sequence 26, Appl	C 502	10.6	58.9	60	10	US-09-908-975-17682	Sequenc
58.9	26	14	US-10-278-437-26	Sequence 26, Appl	C 503	10.6	58.9	60	10	US-09-908-975-19901	Sequenc
58.9	26	15	US-10-405-806-4	Sequence 4, Appli	C 504	10.6	58.9	60	10	US-09-908-975-20612	Sequenc
58.9	27	14	US-10-084-839-3967	Sequence 3967, App	C 505	10.6	58.9	60	10	US-09-908-975-22542	Sequenc
58.9	28	14	US-10-084-839-3971	Sequence 3971, App	C 506	10.6	58.9	60	10	US-09-908-975-23670	Sequenc
58.9	30	9	US-09-564-329A-23	Sequence 23, Appl	C 507	10.4	57.8	17	10	US-09-780-533A-397	Sequenc
58.9	30	9	US-09-855-153-23	Sequence 23, Appl	C 508	10.4	57.8	17	10	US-09-780-533A-2234	Sequenc
58.9	30	9	US-09-854-811-23	Sequence 23, Appl	C 509	10.4	57.8	17	10	US-09-780-533A-2573	Sequenc
58.9	30	9	US-09-934-773-23	Sequence 23, Appl	C 510	10.4	57.8	17	10	US-09-780-533A-2574	Sequenc
58.9	30	9	US-09-963-620-23	Sequence 23, Appl	C 511	10.4	57.8	17	10	US-09-740-332-1391	Sequenc
58.9	30	10	US-09-855-632-23	Sequence 23, Appl	C 512	10.4	57.8	17	10	US-09-817-879-1391	Sequenc
58.9	30	14	US-10-085-906-148	Sequence 148, App	C 513	10.4	57.8	17	14	US-10-060-998-936	Sequenc
58.9	30	14	US-10-225-784-23	Sequence 23, Appl	C 514	10.4	57.8	17	14	US-10-060-998-937	Sequenc
58.9	30	14	US-10-224-720-23	Sequence 23, Appl	C 515	10.4	57.8	17	14	US-10-060-998-938	Sequenc
58.9	30	14	US-10-225-779-23	Sequence 23, Appl	C 516	10.4	57.8	17	14	US-10-060-998-939	Sequenc
58.9	30	15	US-10-374-381-23	Sequence 23, Appl	C 517	10.4	57.8	17	14	US-10-060-998-940	Sequenc
58.9	30	15	US-10-446-542-23	Sequence 23, Appl	C 518	10.4	57.8	17	14	US-10-114-270-329	Sequenc
58.9	31	10	US-09-510-378-181	Sequence 181, App	C 519	10.4	57.8	19	12	US-10-114-270-329	Sequenc
58.9	32	9	US-09-824-286-8	Sequence 8, Appli	C 520	10.4	57.8	19	14	US-10-225-023-350	Sequenc
58.9	33	14	US-10-284-083-8	Sequence 8, Appli	C 521	10.4	57.8	19	14	US-10-225-023-395	Sequenc
58.9	33	14	US-10-199-937-144	Sequence 144, App	C 522	10.4	57.8	19	14	US-10-225-023-484	Sequenc
58.9	35	9	US-09-766-095-32	Sequence 32, Appl	C 523	10.4	57.8	19	14	US-10-225-023-505	Sequenc
58.9	35	9	US-09-766-095-112	Sequence 112, App	C 524	10.4	57.8	19	14	US-10-225-023-536	Sequenc
58.9	41	12	US-10-453-827-248	Sequence 248, App	C 525	10.4	57.8	19	14	US-10-225-023-565	Sequenc
58.9	41	14	US-10-080-299-43	Sequence 43, Appli	C 526	10.4	57.8	19	14	US-10-225-023-598	Sequenc

19	14	US-10-225-023-1088	Sequence 1088, Ap	c 600	10.4	57.8	34	15	US-10-283-024-7	Sequence
19	14	US-10-225-023-1133	Sequence 1133, Ap	c 601	10.4	57.8	34	15	US-10-283-024-10	Sequence
19	14	US-10-225-023-1222	Sequence 1222, Ap	c 602	10.4	57.8	34	15	US-10-449-710-1	Sequence
19	14	US-10-225-023-1243	Sequence 1243, Ap	c 603	10.4	57.8	35	14	US-10-259-197-1	Sequence
19	14	US-10-225-023-1274	Sequence 1274, Ap	c 604	10.4	57.8	35	14	US-10-259-164-1	Sequence
19	14	US-10-225-023-1303	Sequence 1303, Ap	c 605	10.4	57.8	36	9	US-09-912-787-40	Sequence
19	14	US-10-225-023-1336	Sequence 1336, Ap	c 606	10.4	57.8	36	9	US-09-912-787-42	Sequence
19	14	US-09-766-450-79	Sequence 79, Appl	c 607	10.4	57.8	36	13	US-10-014-326-26	Sequence
20	10	US-09-784-674-387	Sequence 387, Appl	c 608	10.4	57.8	36	13	US-10-014-326-28	Sequence
20	10	US-09-882-945A-65	Sequence 65, Appl	c 609	10.4	57.8	36	14	US-10-194-985-16	Sequence
20	14	US-10-181-107-154	Sequence 154, Appl	c 610	10.4	57.8	36	14	US-10-194-985-17	Sequence
20	14	US-10-238-443-62	Sequence 62, Appl	c 611	10.4	57.8	36	14	US-10-194-985-18	Sequence
20	14	US-10-309-362-62	Sequence 62, Appl	c 612	10.4	57.8	36	14	US-10-194-985-19	Sequence
20	15	US-10-189-256-13	Sequence 13, Appl	c 613	10.4	57.8	38	14	US-10-009-623A-5	Sequence
20	15	US-10-189-256-85	Sequence 85, Appl	c 614	10.4	57.8	47	15	US-10-349-143-221	Sequence
20	15	US-10-349-143-6395	Sequence 6395, Ap	c 615	10.4	57.8	47	15	US-10-349-143-559	Sequence
21	9	US-09-969-373-2678	Sequence 2678, Ap	c 616	10.4	57.8	47	15	US-10-349-143-732	Sequence
21	10	US-09-945-943-20	Sequence 20, Appl	c 617	10.4	57.8	47	15	US-10-349-143-842	Sequence
21	15	US-10-349-143-5641	Sequence 5641, Ap	c 618	10.4	57.8	47	15	US-10-349-143-3080	Sequence
22	14	US-10-084-555-44	Sequence 44, Appl	c 619	10.4	57.8	47	15	US-10-349-143-3364	Sequence
22	15	US-10-120-801-144	Sequence 144, Appl	c 620	10.4	57.8	47	15	US-10-349-143-3399	Sequence
22	15	US-10-099-322-204	Sequence 204, Appl	c 621	10.4	57.8	47	15	US-10-349-143-3528	Sequence
22	15	US-10-162-335-198	Sequence 198, Appl	c 622	10.4	57.8	47	15	US-10-349-143-3571	Sequence
22	15	US-10-044-564-204	Sequence 204, Appl	c 623	10.4	57.8	48	13	US-10-007-814-44	Sequence
23	9	US-09-982-610-2	Sequence 2, Appli	c 624	10.4	57.8	48	13	US-10-007-814-45	Sequence
23	12	US-10-373-406B-22	Sequence 22, Appl	c 625	10.4	57.8	48	14	US-10-315-515-113	Sequence
23	14	US-10-080-794-16	Sequence 16, Appl	c 626	10.4	57.8	50	15	US-10-131-827-258	Sequence
25	9	US-09-233-490-16	Sequence 16, Appl	c 627	10.4	57.8	50	15	US-10-131-827-1240	Sequence
25	11	US-09-236-939-16	Sequence 16, Appl	c 628	10.4	57.8	50	15	US-10-131-827-1242	Sequence
25	14	US-10-215-112-5811	Sequence 5811, Ap	c 629	10.4	57.8	50	15	US-10-131-827-2308	Sequence
25	14	US-10-098-263B-112263	Sequence 112263, Sequence	c 630	10.4	57.8	50	15	US-10-131-827-2809	Sequence
25	14	US-10-098-263B-119143	Sequence 119143, Sequence	c 631	10.4	57.8	50	15	US-10-131-827-3161	Sequence
25	14	US-10-060-998-2440	Sequence 2440, Ap	c 632	10.4	57.8	50	15	US-10-131-827-4467	Sequence
25	14	US-10-060-998-2441	Sequence 2441, Ap	c 633	10.4	57.8	50	15	US-10-131-827-6231	Sequence
25	14	US-10-060-998-2442	Sequence 2442							

56.7	19	14	US-10-225-023-510	Sequence 510, App	746	10.2	56.7	25	14	US-10-098-263B-112005	Sequence
56.7	19	14	US-10-225-023-1157	Sequence 1157, App	747	10.2	56.7	25	14	US-10-098-263B-115806	Sequence
56.7	19	14	US-10-225-023-1248	Sequence 1248, App	c 748	10.2	56.7	25	14	US-10-098-263B-124044	Sequence
56.7	20	9	US-09-820-339A-21	Sequence 21, Appl	749	10.2	56.7	25	14	US-10-098-263B-124487	Sequence
56.7	20	9	US-09-800-631-55	Sequence 55, Appl	c 750	10.2	56.7	25	14	US-10-098-263B-125789	Sequence
56.7	20	9	US-09-895-382-23	Sequence 23, Appl	c 751	10.2	56.7	25	14	US-10-098-263B-125797	Sequence
56.7	20	9	US-09-784-674-377	Sequence 377, App	c 752	10.2	56.7	25	14	US-10-098-263B-125930	Sequence
56.7	20	14	US-10-057-550-105	Sequence 105, App	c 753	10.2	56.7	27	10	US-09-888-326-56	Sequence
56.7	20	14	US-10-173-225B-83	Sequence 83, Appl	754	10.2	56.7	27	10	US-09-888-326-493	Sequence
56.7	20	14	US-10-293-783-55	Sequence 55, Appl	755	10.2	56.7	27	10	US-09-776-479-142	Sequence
56.7	20	15	US-10-388-263-703	Sequence 703, App	c 756	10.2	56.7	27	10	US-09-776-479-143	Sequence
56.7	20	15	US-10-343-143-8723	Sequence 8723, App	c 757	10.2	56.7	27	14	US-10-112-653-135	Sequence
56.7	20	15	US-10-289-762-2664	Sequence 2664, App	c 758	10.2	56.7	27	14	US-10-112-653-136	Sequence
56.7	20	15	US-10-289-762-2671	Sequence 2671, App	759	10.2	56.7	27	14	US-10-017-995-142	Sequence
56.7	20	15	US-10-289-762-4621	Sequence 4621, App	c 760	10.2	56.7	27	14	US-10-017-995-143	Sequence
56.7	20	15	US-10-289-762-4730	Sequence 4730, App	c 761	10.2	56.7	28	13	US-10-067-989-13	Sequence
56.7	21	9	US-09-969-373-2397	Sequence 2397, App	762	10.2	56.7	29	9	US-09-839-894-11	Sequence
56.7	21	9	US-09-969-373-2398	Sequence 2398, App	c 763	10.2	56.7	29	12	US-10-188-186-227	Sequence
56.7	21	9	US-09-969-373-2400	Sequence 2400, App	c 764	10.2	56.7	29	14	US-10-288-823-1	Sequence
56.7	21	9	US-09-969-373-2402	Sequence 2402, App	c 765	10.2	56.7	29	14	US-10-288-823-3	Sequence
56.7	21	9	US-09-969-373-2475	Sequence 2475, App	c 766	10.2	56.7	30	9	US-09-993-292A-17	Sequence
56.7	21	9	US-09-995-225-62	Sequence 62, Appl	c 767	10.2	56.7	30	14	US-10-156-275-45	Sequence
56.7	21	10	US-09-995-225-62	Sequence 62, Appl	c 768	10.2	56.7	31	9	US-09-766-399-51	Sequence
56.7	21	10	US-09-866-077-6	Sequence 6, Appli	769	10.2	56.7	31	9	US-09-376-940-33	Sequence
56.7	21	14	US-10-211-296-8	Sequence 8, Appli	770	10.2	56.7	31	14	US-10-319-130-41	Sequence
56.7	21	14	US-10-301-840-8	Sequence 8, Appli	c 771	10.2	56.7	31	14	US-10-319-130-42	Sequence
56.7	21	15	US-10-349-143-4378	Sequence 4378, App	c 772	10.2	56.7	31	15	US-10-603-642-51	Sequence
56.7	21	15	US-10-349-143-6173	Sequence 6173, App	c 773	10.2	56.7	33	9	US-09-940-308-11	Sequence
56.7	21	15	US-10-349-143-6574	Sequence 6574, App	c 774	10.2	56.7	33	13	US-10-115-701A-11	Sequence
56.7	22	8	US-08-913-322-11	Sequence 11, Appl	775	10.2	56.7	33	15	US-10-332-065-26	Sequence
56.7	22	9	US-09-771-938B-14	Sequence 14, Appl	c 776	10.2	56.7	34	14	US-10-146-327-17	Sequence
56.7	22	13	US-10-109-885-12	Sequence 12, Appl	c 777	10.2	56.7	34	14	US-10-160-385-1	Sequence
56.7	22	14	US-10-309-280-12	Sequence 12, Appl	c 778	10.2	56.7	34	14	US-10-186-042-18	Sequence
56.7	22	15	US-10-120-801-147	Sequence 147, App	c 779	10.2	56.7	35	13	US-10-007-805-557	Sequence
56.7	23	10	US-09-766-450-13	Sequence 13, Appl	c 780	10.2	56.7	35	14	US-10-076-622-557	Sequence
56.7	23	14	US-10-181-177-4	Sequence 4, Appli	c 781	10.2	56.7	35	14	US-10-068-174-3	Sequence
56.7	23	14	US-10-005-956-822	Sequence 822, App	c 782	10.2	56.7	35	14	US-10-124-805-557	Sequence
56.7	23	14	US-10-005-956-823	Sequence 823, App	c 783	10.2	56.7	35	15	US-10-332-065-14	Sequence
56.7	24	9	US-09-918-568-25	Sequence 25, Appl	c 784	10.2	56.7	36	14	US-10-322-656-31	Sequence
56.7	24	9	US-09-969-373-2382	Sequence 2382, App	c 785	10.2	56.7	36	14	US-10-102-239-12	Sequence
56.7	24	9	US-09-848-585-36	Sequence 36, Appl	c 786	10.2	56.7	36	14	US-10-102-239-16	Sequence
56.7	24	10	US-09-896-994-3	Sequence 3, Appli	c 787	10.2	56.7	36	14	US-10-102-239-16	Sequence
56.7	24	14	US-10-434-588-19	Sequence 19, Appl	c 788	10.2	56.7	36	15	US-10-440-850-1425	Sequence
56.7	24	14	US-10-032-585-5379	Sequence 5379, App	c 789	10.2	56.7	36	15	US-10-440-850-1673	Sequence
56.7	25	9	US-09-942-310-31	Sequence 45, Appl	c 790	10.2	56.7	36	15	US-10-440-850-1870	Sequence
56.7	25	11	US-09-730-559B-47	Sequence 31, Appl	c 791	10.2	56.7	37	10	US-09-877-478-6258	Sequence
56.7	25	14	US-10-177-987-3	Sequence 3, Appli	c 792	10.2	56.7	37	10	US-09-877-478-6354	Sequence
56.7	25	14	US-10-215-112-5606	Sequence 5606, App	793	10.2	56.7	37	14	US-10-072-975-34	Sequence
56.7	25	14	US-10-215-112-10258	Sequence 10258, A	794	10.2	56.7	37	15	US-10-360-275-34	Sequence
56.7	25	14	US-10-215-112-14387	Sequence 14387, A	c 795	10.2	56.7	38	10	US-09-730-289B-2204	Sequence
56.7	25	14	US-10-098-263B-1646	Sequence 1646, App	c 796	10.2	56.7	38	10	US-09-780-533A-3723	Sequence
56.7	25	14	US-10-098-263B-6258	Sequence 6258, App	c 797	10.2	56.7	38	10	US-09-877-478-3014	Sequence
56.7	25	14	US-10-098-263B-6349	Sequence 6349, App	c 798	10.2	56.7	38	10	US-09-877-478-3280	Sequence
56.7	25	14	US-10-098-263B-6350	Sequence 6350, App	c 799	10.2	56.7	38	10	US-09-848-754A-4133	Sequence
56.7	25	14	US-10-098-263B-6350	Sequence 6350, App	c 800	10.2	56.7	38	10	US-09-848-754A-4298	Sequence
56.7	25	14	US-10-098-263B-22324	Sequence 22324, A	c 801	10.2	56.7	38	10	US-09-848-754A-5589	Sequence
56.7	25	14	US-10-098-263B-29035	Sequence 29035, A	c 802	10.2	56.7	38	10	US-09-780-164-1358	Sequence
56.7	25	14	US-10-098-263B-29036	Sequence 29036, A	803	10.2	56.7	38	10	US-09-910-469-106	Sequence
56.7	25	14	US-10-098-263B-29036	Sequence 29036, A	804	10.2	56.7	38	10	US-09-910-469-116	Sequence
56.7	25	14	US-10-098-263B-30258	Sequence 30258, A	c 805	10.2	56.7	38	10	US-09-910-469-136	Sequence
56.7	25	14	US-10-098-263B-31487	Sequence 31487, A	c 806	10.2	56.7	38	14	US-10-156-306-670	Sequence
56.7	25	14	US-10-098-263B-44646	Sequence 44646, A	c 807	10.2	56.7	38	14	US-10-156-306-1095	Sequence
56.7	25	14	US-10-098-263B-56240	Sequence 56240, A	c 808	10.2	56.7	38	14	US-10-156-306-2235	Sequence
56.7	25	14	US-10-098-263B-61284	Sequence 61284, A	c 809	10.2	56.7	38	14	US-10-230-006-402	Sequence
56.7	25	14	US-10-098-263B-62453	Sequence 62453, A	c 810	10.2	56.7	38	15	US-10-407-079-47	Sequence
56.7	25	14	US-10-098-263B-75385	Sequence 75385, A	c 811	10.2	56.7	39	9	US-09-922-261-132	Sequence
56.7	25	14	US-10-098-263B-75617	Sequence 75617, A	c 812	10.2	56.7	39	14	US-10-102-239-14	Sequence
56.7	25	14	US-10-098-263B-81613	Sequence 81613, A	c 813	10.2	56.7	39	15	US-10-364-649-34	Sequence
56.7	25	14	US-10-098-263B-86552	Sequence 86552, A	814	10.2	56.7	40	9	US-09-998-130A-2	Sequence
56.7	25	14	US-10-098-263B-97200	Sequence 97200, A	c 815	10.2	56.7	40	14	US-10-005-956-1554	Sequence
56.7	25	14	US-10-098-263B-98069	Sequence 98069, A	c 816	10.2	56.7	40	14	US-10-187-253A-55	Sequence
56.7	25	14	US-10-098-263B-101114	Sequence 101114, A	817	10.2	56.7	40	14	US-10-199-820-143	Sequence
56.7	25	14	US-10-098-263B-106875	Sequence 106875, A	818	10.2	56.7	41	14	US-10-072-438-44	Sequence

56.7	43	9	US-09-962-628B-40	Sequence 40, Appl	C 892	10.2	56.7	60	10	US-09-908-975-13444	Sequenc
56.7	43	14	US-10-193-960-28	Sequence 28, Appl	893	10.2	56.7	60	10	US-09-908-975-15858	Sequenc
56.7	43	15	US-10-027-632-177267	Sequence 177267,	C 894	10.2	56.7	60	10	US-09-908-975-15877	Sequenc
56.7	44	9	US-09-988-899-60	Sequence 60, Appl	C 895	10.2	56.7	60	10	US-09-908-975-16317	Sequenc
56.7	44	15	US-09-822-698A-11	Sequence 11, Appl	896	10.2	56.7	60	10	US-09-908-975-16550	Sequenc
56.7	44	15	US-10-027-632-58555	Sequence 58555, A	897	10.2	56.7	60	10	US-09-908-975-17126	Sequenc
56.7	47	15	US-10-170-997-819	Sequence 819, App	C 898	10.2	56.7	60	10	US-09-908-975-17235	Sequenc
56.7	47	15	US-10-349-143-258	Sequence 258, App	C 899	10.2	56.7	60	10	US-09-908-975-17449	Sequenc
56.7	47	15	US-10-349-143-422	Sequence 422, App	900	10.2	56.7	60	10	US-09-908-975-17892	Sequenc
56.7	47	15	US-10-349-143-477	Sequence 477, App	C 901	10.2	56.7	60	10	US-09-908-975-18915	Sequenc
56.7	47	15	US-10-349-143-855	Sequence 855, App	902	10.2	56.7	60	10	US-09-908-975-19358	Sequenc
56.7	47	15	US-10-349-143-899	Sequence 899, App	903	10.2	56.7	60	10	US-09-908-975-19739	Sequenc
56.7	47	15	US-10-349-143-2498	Sequence 2498, Ap	C 904	10.2	56.7	60	10	US-09-908-975-20314	Sequenc
56.7	47	15	US-10-349-143-2621	Sequence 2621, Ap	C 905	10.2	56.7	60	10	US-09-908-975-20342	Sequenc
56.7	47	15	US-10-349-143-2927	Sequence 2927, Ap	906	10.2	56.7	60	10	US-09-908-975-20387	Sequenc
56.7	47	15	US-10-349-143-3406	Sequence 3406, Ap	907	10.2	56.7	60	10	US-09-908-975-20466	Sequenc
56.7	47	15	US-10-349-143-3744	Sequence 3744, Ap	908	10.2	56.7	60	10	US-09-908-975-22281	Sequenc
56.7	50	15	US-10-131-827-237	Sequence 237, App	C 909	10.2	56.7	60	10	US-09-908-975-22684	Sequenc
56.7	50	15	US-10-131-827-892	Sequence 892, App	910	10.2	56.7	60	10	US-09-908-975-22939	Sequenc
56.7	50	15	US-10-131-827-1086	Sequence 1086, Ap	911	10.2	56.7	60	10	US-09-908-975-23270	Sequenc
56.7	50	15	US-10-131-827-2187	Sequence 2187, Ap	912	10.2	56.7	60	10	US-09-908-975-23167	Sequenc
56.7	50	15	US-10-131-827-2458	Sequence 2458, Ap	913	10.2	56.7	60	15	US-10-423-847-27	Sequenc
56.7	50	15	US-10-131-827-2526	Sequence 2526, Ap	C 914	10	55.6	19	9	US-09-881-012-125	Sequenc
56.7	50	15	US-10-131-827-3115	Sequence 3115, Ap	915	10	55.6	19	15	US-10-349-143-4876	Sequenc
56.7	50	15	US-10-131-827-3485	Sequence 3485, Ap	916	10	55.6	19	15	US-10-349-143-6312	Sequenc
56.7	50	15	US-10-131-827-3667	Sequence 3667, Ap	C 917	10	55.6	19	15	US-10-444-925-127	Sequenc
56.7	50	15	US-10-131-827-3933	Sequence 3933, Ap	C 918	10	55.6	20	9	US-09-734-188-6	Sequenc
56.7	50	15	US-10-131-827-4765	Sequence 4765, Ap	C 919	10	55.6	20	9	US-09-995-598-4	Sequenc
56.7	50	15	US-10-131-827-5202	Sequence 5202, Ap	C 920	10	55.6	20	14	US-09-828-344-60	Sequenc
56.7	50	15	US-10-131-827-5369	Sequence 5369, Ap	921	10	55.6	20	14	US-10-007-010-77	Sequenc
56.7	50	15	US-10-131-827-5435	Sequence 5435, Ap	C 922	10	55.6	20	14	US-10-023-782A-84	Sequenc
56.7	50	15	US-10-131-827-6139	Sequence 6139, Ap	923	10	55.6	20	15	US-10-177-573-53	Sequenc
56.7	50	15	US-10-131-827-6346	Sequence 6346, Ap	924	10	55.6	20	15	US-10-104-047-3960	Sequenc
56.7	50	15	US-10-131-827-7898	Sequence 7898, Ap	925	10	55.6	20	15	US-10-349-143-6720	Sequenc
56.7	50	15	US-10-444-925-102	Sequence 102, App	926	10	55.6	20	15	US-10-447-136-186	Sequenc
56.7	51	10	US-09-747-377-402	Sequence 402, App	927	10	55.6	20	15	US-10-199-221-62	Sequenc
56.7	51	10	US-09-922-225A-37	Sequence 37, Appl	928	10	55.6	21	10	US-09-932-300-64	Sequenc
56.7	51	14	US-10-105-613-402	Sequence 402, App	929	10	55.6	21	14	US-10-058-597-2	Sequenc
56.7	51	14	US-10-321-039-393	Sequence 393, App	C 930	10	55.6	21	15	US-10-349-143-11600	Sequenc
56.7	54	9	US-09-938-744-11	Sequence 11, Appl	C 931	10	55.6	21	15	US-10-452-510-178	Sequenc
56.7	54	12	US-10-403-676-37	Sequence 37, Appl	932	10	55.6	22	14	US-10-246-581-20	Sequenc
56.7	54	12	US-10-403-676-39	Sequence 39, Appl	933	10	55.6	22	14	US-10-032-585-4669	Sequenc
56.7	54	12	US-10-403-676-39	Sequence 39, Appl	934	10	55.6	22	15	US-10-374-077-88	Sequenc
56.7	54	15	US-10-449-548-39	Sequence 39, Appl	C 935	10	55.6	22	15	US-10-457-839-63	Sequenc
56.7	55	10	US-09-866-925-243	Sequence 243, Appl	C 936	10	55.6	23	9	US-09-950-046A-3	Sequenc
56.7	55	15	US-10-040-539-4	Sequence 4, Appl	C 937	10	55.6	23	14	US-10-308-460-9	Sequenc
56.7	55	15	US-10-444-925-106	Sequence 106, App	938	10	55.6	23	16	US-10-309-290-222	Sequenc
56.7	55	15	US-10-444-925-108	Sequence 108, App	939	10	55.6	24	10	US-09-940-185-2492	Sequenc
56.7	55	15	US-10-444-925-108	Sequence 108, App	C 940	10	55.6	24	10	US-09-940-185-3382	Sequenc
56.7	56	8	US-08-781-986A-2085	Sequence 2085, Ap	C 941	10	55.6	24	14	US-10-072-094-104	Sequenc
56.7	56	14	US-10-219-227-12	Sequence 12, Appl	C 942	10	55.6	24	14	US-10-024-648-2	Sequenc
56.7	59	13	US-10-013-737-10	Sequence 10, Appl	943	10	55.6	24	14	US-10-172-094-104	Sequenc
56.7	59	15	US-10-027-632-176095	Sequence 176095,	C 944	10	55.6	25	9	US-09-834-956-17	Sequenc
56.7	60	9	US-09-922-261-4	Sequence 4, Appl	C 945	10	55.6	25	14	US-10-081-119-5	Sequenc
56.7	60	10	US-09-995-529-320	Sequence 320, App	C 946	10	55.6	25	14	US-10-215-112-2084	Sequenc
56.7	60	10	US-09-995-529-321	Sequence 321, App	947	10	55.6	25	14	US-10-215-112-5048	Sequenc
56.7	60	10	US-09-995-529-322	Sequence 322, App	C 948	10	55.6	25	14	US-10-287-919-1083	Sequenc
56.7	60	10	US-09-995-529-323	Sequence 323, App	C 949	10	55.6	25	14	US-10-098-263B-2785	Sequenc
56.7	60	10	US-09-995-529-324	Sequence 324, App	950	10	55.6	25	14	US-10-098-263B-15554	Sequenc
56.7	60	10	US-09-908-975-5150	Sequence 5150, Ap	C 951	10	55.6	25	14	US-10-098-263B-32822	Sequenc
56.7	60	10	US-09-908-975-6048	Sequence 6048, Ap	C 952	10	55.6	25	14	US-10-098-263B-37993	Sequenc
56.7	60	10	US-09-908-975-7273	Sequence 7273, Ap	C 953	10	55.6	25	14	US-10-098-263B-42334	Sequenc
56.7	60	10	US-09-908-975-7495	Sequence 7495, Ap	954	10	55.6	25	14	US-10-098-263B-59974	Sequenc
56.7	60	10	US-09-908-975-7729	Sequence 7729, Ap	955	10	55.6	25	14	US-10-098-263B-61207	Sequenc
56.7	60	10	US-09-908-975-9163	Sequence 9163, Ap	956	10	55.6	25	14	US-10-098-263B-63884	Sequenc
56.7	60	10	US-09-908-975-9775	Sequence 9775, Ap	957	10	55.6	25	14	US-10-098-263B-68254	Sequenc
56.7	60	10	US-09-908-975-10868	Sequence 10868, A	C 958	10	55.6	25	14	US-10-098-263B-76782	Sequenc
56.7	60	10	US-09-908-975-11737	Sequence 11737, A	C 959	10	55.6	25	14	US-10-098-263B-86319	Sequenc
56.7	60	10	US-09-908-975-11804	Sequence 11804, A	C 960	10	55.6	25	14	US-10-098-263B-86320	Sequenc
56.7	60	10	US-09-908-975-12128	Sequence 12128, A	C 961	10	55.6	25	14	US-10-098-263B-86937	Sequenc
56.7	60	10	US-09-908-975-12843	Sequence 12843, A	C 962	10	55.6	25	14	US-10-098-263B-86938	Sequenc
56.7	60	10	US-09-908-975-13068	Sequence 13068, A	C 963	10	55.6	25	14	US-10-098-263B-96434	Sequenc
56.7	60	10	US-09-908-975-13325	Sequence 13325, A	964	10	55.6	25	14	US-10-098-263B-102897	Sequenc

55.6 25 14 US-10-098-263B-115475  
 55.6 25 14 US-10-098-263B-125193  
 55.6 25 14 US-10-098-263B-125425  
 55.6 25 14 US-10-098-263B-127403  
 55.6 25 15 US-10-285-061-39  
 55.6 25 15 US-10-300-683-135  
 55.6 25 15 US-10-300-683-500  
 55.6 27 9 US-09-814-661A-23  
 55.6 28 9 US-09-037-657-31  
 55.6 28 9 US-09-851-129A-11  
 55.6 30 9 US-09-727-311-61  
 55.6 30 9 US-09-760-574-91  
 55.6 30 10 US-09-766-442A-91  
 55.6 30 14 US-10-287-919-1904  
 55.6 30 14 US-10-287-919-1905  
 55.6 31 10 US-09-862-393-16  
 55.6 31 14 US-10-193-784-79  
 55.6 33 9 US-09-833-555-27  
 55.6 35 9 US-09-784-990-43  
 55.6 35 14 US-10-229-412-43  
 55.6 37 14 US-10-133-133A-2  
 55.6 37 14 US-10-133-133A-3  
 55.6 38 10 US-09-780-533A-4747  
 55.6 39 10 US-09-155-106-45  
 55.6 39 10 US-09-969-748C-84  
 55.6 39 12 US-09-949-039-88  
 55.6 39 14 US-10-423-828-58  
 55.6 39 14 US-10-005-956-1446  
 55.6 39 15 US-10-457-839-80  
 55.6 41 14 US-10-005-956-934  
 55.6 43 9 US-09-753-574-1  
 55.6 44 9 US-09-968-355-9  
 55.6 45 9 US-09-912-787-50  
 55.6 45 9 US-09-957-641-10  
 55.6 45 9 US-09-957-641-18  
 55.6 45 10 US-09-884-465A-275

# ALIGNMENTS

13 Application US/10351157  
 3. US20030215838A1  
 WATION:  
 recher, Cindy A.  
 ao, Zeren  
 Kuipper, Joseph L.  
 Jasovich, Maria M.  
 Grant, Francis J.  
 Presnell, Scott R.  
 Whitmore, Theodore E.  
 Hammond, Angela K.  
 No. US20030215838A1ak, Julia E.  
 Gross, Jane A.  
 Dillon, Stacey R.  
 ENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
 CS: 02-02  
 ICATION NUMBER: US/10/351,157  
 NG DATE: 2003-01-21  
 ATION NUMBER: US 60/435,361  
 DATE: 2003-12-19  
 ATION NUMBER: US 60/389,108  
 DATE: 2002-06-14  
 ATION NUMBER: US 60/350,325  
 DATE: 2002-01-18  
 Q ID NOS: 183  
 st-SEQ for Windows Version 4.0

rtificial Sequence

FEATURE:  
 ; OTHER INFORMATION: Primer ZC40574  
 US-10-351-157-143  
 Query Match 100.0%; Score 18; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 50; Indels 0;  
 Matches 18; Conservative 0; Mismatches 0;  
 QY 1 CTCATTGGGAATTTGCC 18  
 |||||  
 Db 1 CTCATTGGGAATTTGCC 18  
 |||||  
 RESULT 2  
 US-10-367-438-198  
 ; Sequence 198, Application US/10367438  
 ; Publication No. US20030180773A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COHEN, Daniel  
 ; BLUMENFELD, Marta  
 ; TCHOUMAKOV, Ilia  
 ; TITLE OF INVENTION: Biallelic markers for use in  
 ; constructing a high density disequilib  
 ; the human genome.  
 ; NUMBER OF SEQUENCES: 336  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear  
 ; STREET: 550 West C Street  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Win95  
 ; SOFTWARE: Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/367,438  
 ; FILING DATE: 14-Feb-2003  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/463,075A  
 ; FILING DATE: 14-Jan-2000  
 ; INFORMATION FOR SEQ ID NO: 198:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: SINGLE  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: DNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: downstream amplification primer for SEQ ID:  
 ; LOCATION: 1..20  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 198:  
 US-10-367-438-198  
 Query Match 77.8%; Score 14; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CATTGGGAATTTG 16  
 |||||  
 Db 3 CATTGGGAATTTG 16  
 |||||  
 RESULT 3  
 US-10-349-143-11109  
 ; Sequence 11109, Application US/10349143  
 ; Publication No. US2004000584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Daniel

09:38:22 2004

us-10-090-326-16.max.rnpb

```
lumenfeld, Marta
humakov, Ilya
NTION: Biallelic markers for use in constructing a high density...
E: GENSET.020CP1
CATION NUMBER: US/10/349,143
G DATE: 2003-01-21
TION NUMBER: US/09/422,978
DATE: 1999-10-20
TION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
DATE: EARLIER FILING DATE: 1999-04-21
TION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
DATE: EARLIER FILING DATE: 1998-11-23
TION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
DATE: EARLIER FILING DATE: 1998-04-21
; ID NOS: 11796
;
mo Sapiens
imer_bind
.20
ATTION: downstream amplification primer 99-2645 for SEQ 3244, in compleme
109
77.8%; Score 14; DB 15; Length 20;
ilarity 100.0%; Pred. No. 3.8e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TTTGGAAATTGG 16
|||||
TTTGGAAATTGG 16
C
plication US/10193960
: US20030104477A1
ATION:
echler, Joe
alkirs, Gunars
ray, Jeff
iosite Diagnostics Inc.
NTION: Chimeric Polyclonal Antibodies
E: 014907-0027000US
CATION NUMBER: US/10/193,960
G DATE: 2002-07-12
TION NUMBER: US/09/410,903
DATE: 1999-10-02
TION NUMBER: US 08/832,985
DATE: 1997-04-04
TION NUMBER: US 08/835,159
DATE: 1997-04-04
TION NUMBER: WO PCT/US98/06704
DATE: 1998-04-03
ID NOS: 100
tSEQ for Windows Version 3.0
tifical Sequence
ATTION: oligo 50
73.3%; Score 13.2; DB 14; Length 43;
ilarity 83.3%; Pred. No. 1e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CATTGGAAATTTGCC 18
|||||
CATTTCGGCTTTGCC 11
```

```
RESULT 5
US-09-908-975-22707
; Sequence 22707, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22707
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-22707
Query Match 73.3%; Score 13.2; DB 10; Length 60;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;
QY 1 CTCATTGGAAATTTGCC 18
|||
DB 38 CTCATTGGAAATTCCTCC 55
RESULT 6
US-10-032-585-4803/c
; Sequence 4803, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4803
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4803
Query Match 72.2%; Score 13; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
QY 5 TTTGGAAATTTGCC 17
|||||
DB 14 TTTGGAAATTTGCC 2
RESULT 7
US-09-902-563-46/c
; Sequence 46, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
```



1 09:38:22 2004

us-10-090-326-16.max.rnpb

ENTION: Methods of Modulating Immune Coagulation  
CE: 9579-37  
ICATION NUMBER: US/09/902,563  
NG DATE: 2002-09-09  
ATION NUMBER: US 09/442,143  
DATE: 1999-11-15  
Q ID NOS: 53  
tentin version 3.1

rtificial Sequence

ATION: Primer

5

71.1%; Score 12.8; DB 10; Length 19;  
milarity 87.5%; Pred. No. 1.4e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTTGGCC 18

||||| |||||  
ATTAGATTTTGGCC 4

s/c

Application US/10096255  
US20030103974A1  
ATION:

svy, Gary

Clark, David A.  
ENTION: Methods of Modulating Immune Coagulation  
CE: 9579-52

ICATION NUMBER: US/10/096,255

NG DATE: 2002-03-13

ATION NUMBER: US 60/046,537

DATE: 1997-05-17

ATION NUMBER: US 60/061,684

DATE: 1997-10-10

Q ID NOS: 53

tentin version 3.1

rtificial Sequence

ATION: Primer

6

71.1%; Score 12.8; DB 14; Length 19;  
milarity 87.5%; Pred. No. 1.4e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTTGGCC 18

||||| |||||  
ATTAGATTTTGGCC 4

6

Application US/09863806  
US20020197608A1  
ORMATION:  
ANT: Sidransky, David  
OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA  
OF SEQUENCES: 195  
PONDENSE ADDRESS:  
DRESSEE: Fish & Richardson P.C.  
REET: 4225 Executive Square, Suite 1400  
ITY: La Jolla  
TATE: CA  
OUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/863,806  
FILING DATE: 22-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/038,637  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/152,313  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/146001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-09-863-806-66

Query Match 71.1%; Score 12.8; DB 9; Length 22;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGAATTTGGC 18

Db ||||| |||||  
6 CATCTGAATTTGGC 21

RESULT 10

US-09-908-975-6713  
Sequence 6713, Application US/09908975  
Publication NO. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6713  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-6713

Query Match 71.1%; Score 12.8; DB 10; Length 60;  
Best Local Similarity 87.5%; Pred. No. 1.6e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGAATTTGGC 18

||||| |||||

TTTGGAACTTTGCC 49

987  
Application US/09908975  
US20030165843A1

ATION:  
OSHAN, Avi  
ASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat

ALGER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME

TE: 36688-0005  
CATION NUMBER: US/09/908,975  
IG DATE: 2001-07-20  
TION NUMBER: US 60/287,724

DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0  
7

mo sapiens  
987

71.1%; Score 12.8; DB 10; Length 60;  
ilarity 87.5%; Pred. No. 1.6e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGAACTTTGCC 18  
|||||  
TTTGGTATTTGCC 37

04995  
5. Application US/10098263B  
US2003010410A1

ttman, Michael  
TION: Human Microarray  
E: 3118.1  
CATION NUMBER: US/10/098,263B  
IG DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
roarray Probe Sequence Listing Generator V 1.1  
95

mo sapien  
04995

68.9%; Score 12.4; DB 14; Length 25;  
ilarity 92.9%; Pred. No. 2.2e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TCATTGGAATTT 14  
|||||  
TCATCTGGAATTT 19

.034  
Application US/09754853A  
US20030005491A1  
ATION:

; APPLICANT: Hauge, Brian M.  
; APPLICANT: Parnell, Laurence D.  
; APPLICANT: Parsons, Jeremy D.  
; APPLICANT: Wang, Ming Li  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules A  
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance  
; FILE REFERENCE: 38-10(15810)B  
; CURRENT APPLICATION NUMBER: US/09/754,853A  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,880  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 1119  
; SEQ ID NO 1034  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 515002\_region\_G2\_70595\_13\_Reverse\_  
US-03-754-853A-1034

Query Match 68.9%; Score 12.4; DB 10; Length 27;  
Best Local Similarity 92.9%; Pred. No. 2.2e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCATTGGAATTTT 15  
|||||  
DB 14 TCATTGGAATTTAT 27

RESULT 14

US-10-131-827-958  
; Sequence 958, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND P  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 958  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-958

Query Match 68.9%; Score 12.4; DB 15; Length 50;  
Best Local Similarity 92.9%; Pred. No. 2.4e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 5 TTTGGAATTTGCC 18  
|||||  
DB 32 TTTGGAATTTGCC 45

RESULT 15

US-10-131-827-2943  
; Sequence 2943, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc

1 09:38:22 2004

us-10-090-326-16.max.rnpb

ENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
ENTION: CHRONIC INFLAMMATORY DISEASES  
E: 50661200120  
[CATION NUMBER: US/10/131,827  
G DATE: 2002-09-06  
ATION NUMBER: US 10/006,290  
DATE: 2001-10-22  
ATION NUMBER: US 60/296,764  
DATE: 2001-06-08  
ID NOS: 9090  
entIn version 3.1  
;

omo sapiens

143

68.9%; Score 12.4; DB 15; Length 50;  
ilarity 92.9%; Pred.No. 2.4e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TATTGGAATTTT 15  
|||||  
TATTGGAATTTT 43

1473/c

3. Application US/09908975  
3. US20030165843A1

ATION: HOSHAN, Avi

WASSERMAN, Alon

MINTZ, Eli

MINTZ, Eli

FAIGLER, Simchon

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
ENTION: THAT POPULATE A TRANSCRIPTOME

E: 36688-0005

ICATION NUMBER: US/09/908,975

G DATE: 2001-07-20

ATION NUMBER: US 60/287,724

DATE: 2001-05-02

ATION NUMBER: US 60/221,607

DATE: 2000-07-28

ID NOS: 32337

entIn version 3.0

73

omo sapiens

1473

68.9%; Score 12.4; DB 10; Length 60;  
ilarity 92.9%; Pred.No. 2.5e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TATTGGAATTTT 15  
|||||  
TATTGGCATTTT 31

1262/c

2. Application US/09908975  
2. US20030165843A1

ATION: HOSHAN, Avi

WASSERMAN, Alon

MINTZ, Eli

MINTZ, Eli

FAIGLER, Simchon

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21262  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-21262

Query Match 68.9%; Score 12.4; DB 10; Length 60;  
Best Local Similarity 92.9%; Pred.No. 2.5e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 5 TTGGGAATTTGCC 18  
|||||  
Db 43 TTGGGAATTTGCC 30

RESULT 18

US-09-784-674-379

; Sequence 379, Application US/09784674

; Publication No. US20030054346A1

; GENERAL INFORMATION:

; APPLICANT: Shannon, Karen W.

; Wolber, Paul K.

; Delenstarr, Glenda C.

; Webb, Peter G.

; Kincaid, Robert H.

; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

; NUMBER OF SEQUENCES: 1165

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Records Manager, Legal Department, Hewlett-

; Company M/S 2080

; STREET: 3000 Hanover Street

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/784,674

; FILING DATE: 15-Feb-2001

; CLASSIFICATION: No. US20030054346A1 available

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/021,701

; FILING DATE: 10-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Choi, Wendy A.

; REGISTRATION NUMBER: 36,697

; REFERENCE/DOCKET NUMBER: 10971464-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-236-2386

; TELEFAX: 650-852-8063

; INFORMATION FOR SEQ ID NO: 379:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

NSF: NO  
E DESCRIPTION: SEQ ID NO: 379:  
9

67.8%; Score 12.2; DB 10; Length 20;  
ilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CAATTGGAATTTGTC 17  
|||||  
'ACTTGGAAATATTGC 20

10  
Application US/09784674  
US20030054346A1

INVENTOR: Shannon, Karen W.  
Wolber, Paul K.  
Delenstarr, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.

OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

OF SEQUENCES: 1165

ONDENSE ADDRESS:

DRESSEE: Records Manager, Legal Department, Hewlett-Packard

Company M/S 20BO

REET: 3000 Hanover Street

TY: Palo Alto

ATE: CA

UNTRY: USA

P: 94304

R READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent In Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/784,674

LING DATE: 15-Feb-2001

ASSIFICATION: No. US20030054346A1 available

PLICATION DATA:

LING DATE: 10-FEB-1998

Y/AGENT INFORMATION:

ME: Choi, Wendy A.

ISTRATION NUMBER: 36,697

ERENCE/DOCKET NUMBER: 10971464-1

UNICATION INFORMATION:

LEPHONE: 650-236-2386

LEFAX: 650-852-8063

FOR SEQ ID NO: 380:

E CHARACTERISTICS:

NGTH: 20 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E TYPE: cDNA

TICAL: NO

NSF: NO

E DESCRIPTION: SEQ ID NO: 380:

0

67.8%; Score 12.2; DB 10; Length 20;  
ilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CAATTGGAATTTGTC 17  
|||||  
ACTTGGAAATATTGC 19

RESULT 20

US-09-784-674-381

; Sequence 381, Application US/09784674

; Publication No. US20030054346A1

; GENERAL INFORMATION:

; APPLICANT: Shannon, Karen W.

; Wolber, Paul K.

; Delenstarr, Glenda C.

; Webb, Peter G.

; Kincaid, Robert H.

; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

; NUMBER OF SEQUENCES: 1165

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Records Manager, Legal Department, Hewlett-

; COMPANY M/S 20BO

; STREET: 3000 Hanover Street

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/784,674

; FILING DATE: 15-Feb-2001

; CLASSIFICATION: No. US20030054346A1 available

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/021,701

; FILING DATE: 10-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Choi, Wendy A.

; REGISTRATION NUMBER: 36,697

; REFERENCE/DOCKET NUMBER: 10971464-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-236-2386

; TELEFAX: 650-852-8063

; INFORMATION FOR SEQ ID NO: 381:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHEICAL: NO

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 381:

US-09-784-674-381

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 10; Length 20;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTTGGAATTTGTC 17

Db 2 CTACTTTGGAATATTGC 18

RESULT 21

US-09-784-674-382

; Sequence 382, Application US/09784674

; Publication No. US20030054346A1

; GENERAL INFORMATION:

; APPLICANT: Shannon, Karen W.

; Wolber, Paul K.

; Delenstarr, Glenda C.

; Webb, Peter G.

; Kincaid, Robert H.

; TITLE OF INVENTION: Methods for evaluating oligonucleotide

1 09:38:22 2004

us-10-090-326-16.max.rnpb

probe sequences

OF SEQUENCES: 1165  
PONDENCE ADDRESS:  
DRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 20BO  
TREET: 3000 Hanover Street  
ITY: Palo Alto  
TATE: CA  
COUNTRY: USA  
IP: 94304  
ER READABLE FORM:  
EDIUM TYPE: Floppy disk  
OMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
FTWARE: Patentin Release #1.0, Version #1.30  
T APPLICATION DATA:  
PLICATION NUMBER: US/09/784,674  
ILING DATE: 15-Feb-2001  
ASSIFICATION: No. US20030054346A1 available  
APPLICATION DATA:  
PLICATION NUMBER: 09/021,701  
ILING DATE: 10-FEB-1998  
Y/AGENT INFORMATION:  
AME: Choi, Wendy A.  
EGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
MMUNICATION INFORMATION:  
ELEPHONE: 650-236-2386  
ELEFAX: 650-852-8063  
FOR SEQ ID NO: 382:  
CE CHARACTERISTICS:  
ENGTH: 20 base pairs  
YPE: nucleic acid  
TRANDEDNESS: single  
POLOGY: linear  
LE TYPE: cDNA  
ETICAL: NO  
ENSE: NO  
CE DESCRIPTION: SEQ ID NO: 382:  
92

67.8%; Score 12.2; DB 10; Length 20;  
nilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTGTC 17  
|||||  
TACTTGGGAATTGTC 17

Application US/10177573  
S. US20030236206A1  
ATION:  
asan M. Freier  
ENTION: ANTISENSE MODULATION OF PPP3R1 EXPRESSION  
TE: PTS-0364  
ICATION NUMBER: US/10/177,573  
NG DATE: 2002-06-20  
Q ID NOS: 104

Artificial Sequence

ATION: Antisense Oligonucleotide

67.8%; Score 12.2; DB 15; Length 20;  
nilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTCATTGGGAATTGTC 17  
|||||  
Db 3 CTCATTGCCAATTGTC 19

RESULT 23  
US-10-253-904-28  
; Sequence 28, Application US/10253904  
; Publication No. US20030158135A1  
; GENERAL INFORMATION:  
; APPLICANT: EL SOLH, NEVINE  
; APPLICANT: ALLIGNET, JEANINE  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING  
; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AN  
; TITLE OF INVENTION: COMPOUNDS  
; FILE REFERENCE: 03715-0059  
; CURRENT APPLICATION NUMBER: US/10/253,904  
; CURRENT FILING DATE: 2002-09-25  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-253-904-28

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTGGGAATTGTC 18  
|||||  
Db 2 TCGTTTGTAACTTGCC 18

RESULT 24  
US-10-392-970-26  
; Sequence 26, Application US/10392970  
; Publication No. US20030176679A1  
; GENERAL INFORMATION:  
; APPLICANT: El Solh, Nevine  
; APPLICANT: Allignet, Jeanine  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING  
; TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AN  
; TITLE OF INVENTION: COMPOUNDS  
; FILE REFERENCE: 03495.0173-00000  
; CURRENT APPLICATION NUMBER: US/10/392,970  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/099,932  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/050,380  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-10-392-970-26

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTGGGAATTGTC 18  
|||||  
Db 2 TCGTTTGTAACTTGCC 18

09:38:22 2004

us-10-090-326-16.max.rnpb

publication US/10082546  
US20030165868A1  
RMATION:

NT:

Lacroix, Jean-Michel

F INVENTION: METHOD AND KIT FOR QUANTITATION AND

OF SEQUENCES: 7 NUCLEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPL

ONDENCE ADDRESS:

DRESSEE: Oppedahl & Larson

REET: PO Box 5088

TY: Dillon

ATE: CO

UNTRY: US

P: 80435-5068

R READABLE FORM:

DUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

MPUTER: IBM compatible

ERATING SYSTEM: MS DOS

FTWARE: Word Perfect

APPLICATION DATA:

PLICATION NUMBER: US/10/082,546

LING DATE: 25-Feb-2002

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: <Unknown>

LING DATE: <Unknown>

Y/AGENT INFORMATION:

ME: Larson, Marina T.

ISTRATION NUMBER: 32,038

ERENCE/DOCKET NUMBER: VGEN.P-054

MUNICATION INFORMATION:

LEPHONE: 970 468 6600

LEFAX: 970 468 0104

LEX: <Unknown>

FOR SEQ ID NO: 5:

E CHARACTERISTICS:

NGTH: 27

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E TYPE: other nucleic acid

TICAL: NO

NSE: NO

T TYPE: internal

L SOURCE:

GANISM: HIV-1

E DESCRIPTION: SEQ ID NO: 5:

ilarity 67.8%; Score 12.2; DB 14; Length 27;

Conservative 0; Pred. No. 2.8e+04;

Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTCG 17

|||||

ACTTTGGATATTCG 18

publication US/09766095  
0020062016A1  
RMATION:

NT:

Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

F INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

OF SEQUENCES: 139

ONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-JAN-01

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07

FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-766-095-16

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 9; Length 36;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTGGGAATTTCG 17

|||||

Db 1 CTACTTTGGATATTCG 17

RESULT 27

US-09-766-095-96/c

; Sequence 96, Application US/09766095

; Patent No. US20020062016A1

; GENERAL INFORMATION:

; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

; Yeasing Yang

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

; OLIGONUCLEOTIDES AND PROBES

; TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

; SOFTWARE: WordPerfect (Version 5.0)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/766,095

us-10-090-326-16.max.rnpb

REPLICATION DATA:  
 REPLICATION NUMBER: 09/013, 406  
 FILING DATE: 26-JAN-01  
 REPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837  
 FILING DATE: 10-Jul-90  
 REPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501  
 FILING DATE: 11-Jul-89  
 REPLICATION INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 196/189

US-C9-766-095-137

67.8%; Score 12.2; DB 9; Length 36;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
TCATTGGAATTTGTC 17  
|||||  
ACTTTGGAATTTGTC 20  
/c  
application US/10379836  
US20030215850A1  
ATION:  
iscol-Myers Squibb Company  
TION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
TION: TAFI  
E: D0214NP  
CATION NUMBER: US/10/379,836  
G DATE: 2003-03-04  
TION NUMBER: U.S. 60/361,523  
DATE: 2002-03-04  
ID NOS: 24  
entIn version 3.2

## pio hamadryas

67.8%; Score 12.2; DB 15; Length 37;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
ATTGGAATTTGCC 18  
|||||  
ATTAGGAATTTGTC 10

2/c  
Application US/09747377  
US20030022255A1  
ATION:

ris, David  
TION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

E: A-69959/RMS/DCF  
CATION NUMBER: US/09/747,377  
3 DATE: 2000-12-22  
ID NOS: 493  
entIn version 3.0

s sp.  
2

67.8%; Score 12.2; DB 10; Length 39;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
TCATTGGAATTTGTC 17  
|||||  
CATTATAATTTGTC 14

2/c  
Application US/10105613  
US2003009963A1  
ATION:

ris, David  
TION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

FILE REFERENCE: A-69959/RMS/DCF  
CURRENT APPLICATION NUMBER: US/10/105,613  
CURRENT FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: US/09/747,377  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 493  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 472  
LENGTH: 39  
TYPE: DNA  
ORGANISM: Mus sp.  
US-10-105-613-472

Query Match 67.8%; Score 12.2; DB 14; Length 39;  
Best Local Similarity 82.4%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGTC 17  
|||||  
Db 30 CACATTATAATTTGTC 14

## RESULT 33

US-10-443-694-80  
Sequence 80, Application US/10443694  
Publication No. US20040001846A1  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R  
APPLICANT: Overfelli, Ouathek  
APPLICANT: Pinto, John  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES T  
FILE REFERENCE: 1769/41426-GB  
CURRENT APPLICATION NUMBER: US/10/443,694  
CURRENT FILING DATE: 2003-05-21  
PRIOR APPLICATION NUMBER: US 08/705,477  
PRIOR FILING DATE: 1996-08-29  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 80  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-443-694-80

Query Match 67.8%; Score 12.2; DB 15; Length 40;  
Best Local Similarity 82.4%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGAAATTTGCC 18  
|||||  
Db 8 TCATTGGTATGTACC 24

## RESULT 34

US-10-131-827-2575/c  
Sequence 2575, Application US/10131827  
Publication No. US20040009479A1  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND M  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08



. 09:38:22 2004

us-10-090-326-16.max.rnpb

```
; ID NOS: 9090
; entIn version 3.1

amo sapiens
175
    67.8%; Score 12.2; DB 15; Length 50;
    ilarity 82.4%; Pred. No. 3e+04; 3; Indels 0; Gaps 0;
    Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; CATTGGAAATTTGC 17
; CTTTAGAATTTAC 25.

;47
; Application US/10131827
; . US20040009479A1
; IATION:
; hlgemuth, Jay
; Fry, Kirk
; Woodward, Robert
; Y, Ngoc
; IENT: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; ENTION: CHRONIC INFLAMMATORY DISEASES
; E: 506612000120
; IATION NUMBER: US/10/131,827
; NG DATE: 2002-09-06
; ATION NUMBER: US 10/006,290
; DATE: 2001-10-22
; ATION NUMBER: US 60/296,764
; DATE: 2001-06-08
; ID NOS: 9090
; :entIn version 3.1
;
```

```
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5482

Query Match      67.8%; Score 12.2; DB 15; Length 50;
Best Local Similarity 82.4%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGC 17
   ||||| ||||| |||||
DB 49 CTCATTGGCAAGTTTC 33

RESULT 37
US-10-131-827-6631
; Sequence 6631, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND
; FILE REFERENCE: 506612000120
; CURRENT FILING DATE: 2002-09-06
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6631
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6631

Query Match      67.8%; Score 12.2; DB 15; Length 50;
Best Local Similarity 82.4%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGC 17
   ||||| ||||| |||||
DB 3 CTGATTGGATTTCTTC 19

RESULT 38
US-10-131-827-7021/c
; Sequence 7021, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND
; FILE REFERENCE: 506612000120
; CURRENT FILING DATE: 2002-09-06
; CURRENT APPLICATION NUMBER: US/10/131,827
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7021
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
21
67.8%; Score 12.2; DB 15; Length 50;
ilarity 82.4%; Pred. No. 3e+04; 3; Indels C; Gaps 0;
Conservative 0; Mismatches 3; Indels 3; Gaps 0;

CATTTGGAATTTGTC 17
|||||
3ATTTGGAATTTGTC 32

/c
plication US/10298796
. US20030220490A1
ATION:
RIYAMA, Shinichi
ASEGAWA, Takashi
NTION: CELL MEMBRANE DIRECTED DRUGS
E: 1110-253P
CATION NUMBER: US/10/298,796
3 DATE: 2002-11-19
TION NUMBER: US/09/331,793
DATE: 1999-06-25
ID NOS: 67
entIn version 3.0

nthetic DNA Primers

67.8%; Score 12.2; DB 15; Length 59;
ilarity 82.4%; Pred. No. 3.1e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTGGAATTTGTC 17
|||||
TTTTCGAATTTGTC 37

79
Application US/09908975
. US20030165843A1
ATION:
OSHAN, Avi
ASSERMAN, Alon
INTZ, Eli
INTZ, Liat
AIGLER, Simchon
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TION: THAT POPULATE A TRANSCRIPTOME
E: 36688-0005
CATION NUMBER: US/09/908,975
G DATE: 2001-07-20
TION NUMBER: US 60/287,724
DATE: 2001-05-02
TION NUMBER: US 60/221,607
DATE: 2000-07-28
ID NOS: 32337
entIn version 3.0

amo sapiens
:79

67.8%; Score 12.2; DB 10; Length 60;
ilarity 82.4%; Pred. No. 3.1e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTGGAATTTGTC 17

Db 34 CACCATTTGGAATTTGTC 50

RESULT 41
US-09-908-975-19813/c
; Sequence 19813, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19813
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19813

Query Match 67.8%; Score 12.2; DB 10; Length 60;
Best Local Similarity 82.4%; Pred. No. 3.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTTGGAATTTGTC 18
|||||
Db 45 TCACTTAGAATTTTACC 29

RESULT 42
US-10-123-101-75/c
; Sequence 75, Application US/10123101
; Publication No. US20030148262A1
; GENERAL INFORMATION:
; APPLICANT: POLO, John
; APPLICANT: PERRI, Silvia
; APPLICANT: THUDIUM, Kent
; TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES
; FILE REFERENCE: 2300-17924 / PFI7924.002
; CURRENT APPLICATION NUMBER: US/10/123,101
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 60/295,451
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 60
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: WEE
US-10-123-101-75

Query Match 67.8%; Score 12.2; DB 14; Length 60;
Best Local Similarity 82.4%; Pred. No. 3.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTTGGAATTTGTC 18
|||||
Db 18 TCAGTTGGAATGTTGAC 2
```

09:38:22 2004

us-10-090-326-16.max.rnpb

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,445  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2738:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2738  
Query Match 66.7%; Score 12; DB 8; Length 53;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 4 ATTTGGGAATTTT 15  
|||,|||  
Db 29 ATTTGGGAATTTT 40

Search completed: February 29, 2004, 13:42:55  
Job time : 121.571 secs

Application US/10298796  
. US20030220490A1  
ATTON:  
RIYAMA, Shinichi  
ASEGAWA, Takashi  
NTION: CELL MEMBRANE DIRECTED DRUGS  
E: 1110-253P  
CATION NUMBER: US/10/298,796  
G DATE: 2002-11-19  
TION NUMBER: US/09/331,793  
DATE: 1999-06-25  
ID NOS: 67  
entIn version 3.0

nthetic Synthetic DNA Primers

67.8%; Score 12.2; DB 15; Length 60;  
ilarity 82.4%; Pred. No. 3.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTCGAATTTGTC 17  
|||||  
TTTTTCGAATTTGTC 27

5/c  
Application US/10310734  
. US20030232324A1  
ATTON:  
LO, John  
ERRI, Silvia  
HUDIUM, Kent  
ANG, Zequn  
NTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES  
E: CHR-17924/02US (2300-17924.20)  
CATION NUMBER: US/10/310,734  
G DATE: 2002-12-04  
TION NUMBER: 10/123,101  
DATE: 2002-04-11  
ID NOS: 125  
entIn Ver. 2.0

rtificial Sequence

ATTON: Description of Artificial Sequence: WEE  
35

67.8%; Score 12.2; DB 15; Length 60;  
milarity 82.4%; Pred. No. 3.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTCGAATTTGTC 18  
|||||  
CAGTTTGAATGTTGAC 2

2738  
, Application US/08781986A  
O. US20030054436A1  
RMATION:  
Charles Kunsch  
NVENTION: Staphylococcus aureus Polynucleotides and Sequences  
SEQUENCES: 5255  
ENCE ADDRESS:

09:38:23 2004

us-10-090-326-16.max.rst

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1351.17 Seconds  
(without alignments)  
397.818 Million cell updates/sec

JS-10-090-326-16

l ctcatttgaatttgc 18

IDENTITY NUC

hapop 10.0 , Gapext 1.0

37513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0

angth: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vit:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB ID	Description
74.4	29	28	BZ770903
74.4	40	28	A2345478
74.4	56	29	AL752501
74.4	60	10	BE491325



22	13	BQ585082	E011827-0	297	10.4	57.8	41	29	AL751958
30	28	BH814304	SALK_0661	298	10.4	57.8	42	29	AG227149
32	28	BH902037	SALK_0911	299	10.4	57.8	43	28	BZ5292815
33	28	BZ594009	SALK_0825	300	10.4	57.8	45	9	AU007314
33	28	BZ594009	SALK_0825	301	10.4	57.8	45	29	AL942241
34	28	BH810792	SALK_0512	302	10.4	57.8	45	29	BX651940
35	28	BH813890	SALK_0654	303	10.4	57.8	46	28	AZ767539
35	28	BH864447	SALK_0960	304	10.4	57.8	46	28	BH810374
37	28	BZ356214	SALK_1284	305	10.4	57.8	46	28	BH909441
37	28	BZ356214	SALK_1284	306	10.4	57.8	47	29	TA2390H07P
39	28	BZ664670	SALK_0997	307	10.4	57.8	48	14	D18685
39	29	CC887215	SALK_1497	308	10.4	57.8	48	14	D18685
39	29	AA936922	cm55c08.s	309	10.4	57.8	48	14	D18685
42	9	AA936922	cm55c08.s	310	10.4	57.8	48	14	D18685
42	28	BZ766600	SALK_1376	311	10.4	57.8	48	28	BH903352
45	28	BZ597593	SALK_1099	312	10.4	57.8	48	28	BH903352
46	9	AA015178	AA015178	313	10.4	57.8	48	28	BH903352
46	9	AA023270	mh69g09.r	314	10.4	57.8	48	28	BH903352
46	9	AA291212	zs18b12.s	315	10.4	57.8	48	28	BH903352
46	9	AA291212	zs18b12.s	316	10.4	57.8	48	28	BH903352
46	29	BX651777	ArabiDops	317	10.4	57.8	49	13	BQ625383
47	28	BH792501	SALK_0646	318	10.4	57.8	49	13	BQ625383
47	28	BH792501	SALK_0646	319	10.4	57.8	49	13	BQ625383
48	28	BZ379658	SALK_1136	320	10.4	57.8	49	13	BQ625383
48	28	BH807683	1008073A0	321	10.4	57.8	49	13	BQ625383
48	28	BH851465	SALK_0730	322	10.4	57.8	49	13	BQ625383
48	28	BH851465	SALK_0730	323	10.4	57.8	49	13	BQ625383
48	28	TA373C08P	TA373C08P	324	10.4	57.8	49	13	BQ625383
49	9	AI747625	ul19d03.x	325	10.4	57.8	49	13	BQ625383
49	29	AL767455	ArabiDops	326	10.4	57.8	49	13	BQ625383
49	29	AL767455	ArabiDops	327	10.4	57.8	49	13	BQ625383
49	29	AL767455	ArabiDops	328	10.4	57.8	49	13	BQ625383
49	29	AL767455	ArabiDops	329	10.4	57.8	49	13	BQ625383
50	28	BH904193	SALK_1041	330	10.4	57.8	49	13	BQ625383
50	28	CC020659	3591.1.20	331	10.4	57.8	49	13	BQ625383
50	28	CC020659	3591.1.20	332	10.4	57.8	49	13	BQ625383
50	29	BX004572	ArabiDops	333	10.4	57.8	49	13	BQ625383
52	12	BG153633	lgs15h03	334	10.4	57.8	49	13	BQ625383
52	12	BG153633	lgs15h03	335	10.4	57.8	49	13	BQ625383
52	12	BG153633	lgs15h03	336	10.4	57.8	49	13	BQ625383
52	14	H04947	YJ51d09.sl	337	10.4	57.8	49	13	BQ625383
52	14	H04947	YJ51d09.sl	338	10.4	57.8	49	13	BQ625383
52	14	H04947	YJ51d09.sl	339	10.4	57.8	49	13	BQ625383
53	28	BZ292415	SALK_1242	340	10.4	57.8	49	13	BQ625383
53	28	CC458856	SALK_1222	341	10.4	57.8	49	13	BQ625383
53	28	CC458856	SALK_1222	342	10.4	57.8	49	13	BQ625383
53	28	AL767456	ArabiDops	343	10.4	57.8	49	13	BQ625383
53	29	BX890894	ArabiDops	344	10.4	57.8	49	13	BQ625383
53	29	BX890894	ArabiDops	345	10.4	57.8	49	13	BQ625383
54	28	BH848588	SALK_0885	346	10.4	57.8	49	13	BQ625383
55	10	AW168527	xi88a12.x	347	10.4	57.8	49	13	BQ625383
55	10	AW168527	xi88a12.x	348	10.4	57.8	49	13	BQ625383
55	12	BI451246	kd21f05.Y	349	10.4	57.8	49	13	BQ625383
55	12	BI451246	kd21f05.Y	350	10.4	57.8	49	13	BQ625383
56	14	TI7618	mps v40 The	351	10.4	57.8	49	13	BQ625383
56	28	AZ485389	IM0312H16	352	10.4	57.8	49	13	BQ625383
56	28	AZ485389	IM0312H16	353	10.4	57.8	49	13	BQ625383
56	28	AZ514492	IM0361G23	354	10.4	57.8	49	13	BQ625383
56	28	AZ514492	IM0361G23	355	10.4	57.8	49	13	BQ625383
56	29	AL760048	ArabiDops	356	10.4	57.8	49	13	BQ625383
56	29	AL760048	ArabiDops	357	10.4	57.8	49	13	BQ625383
57	29	BX002873	ArabiDops	358	10.4	57.8	49	13	BQ625383
57	9	AU264614	AU264614	359	10.4	57.8	49	13	BQ625383
57	12	BI676989	ic67h08.Y	360	10.4	57.8	49	13	BQ625383
57	12	BI676989	ic67h08.Y	361	10.4	57.8	49	13	BQ625383
57	28	BZ358275	SALK_1321	362	10.4	57.8	49	13	BQ625383
58	9	AU007255	AU007255	363	10.4	57.8	49	13	BQ625383
58	12	BJ035240	BJ035240	364	10.4	57.8	49	13	BQ625383
58	12	BJ035240	BJ035240	365	10.4	57.8	49	13	BQ625383
58	12	B44722	HS-1059-B2-	366	10.4	57.8	49	13	BQ625383
58	28	BH229733	SALK_0654	367	10.4	57.8	49	13	BQ625383
58	28	BH229733	SALK_0654	368	10.4	57.8	49	13	BQ625383
58	28	BH813934	SALK_0654	369	10.4	57.8	49	13	BQ625383
58	28	BH813934	SALK_0654	370	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	371	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	372	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	373	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	374	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	375	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	376	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	377	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	378	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	379	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	380	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	381	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	382	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	383	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	384	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	385	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	386	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	387	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	388	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	389	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	390	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	391	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	392	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	393	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	394	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	395	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	396	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	397	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	398	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	399	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	400	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	401	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	402	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	403	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	404	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	405	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	406	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	407	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	408	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	409	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	410	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	411	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	412	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	413	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	414	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	415	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	416	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	417	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	418	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	419	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	420	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	421	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	422	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	423	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	424	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	425	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	426	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	427	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	428	10.4	57.8	49	13	BQ625383
58	28	BH852423	SALK_0746	429	10.4	57.8	49	13	BQ625383
58	2								

56.7	30	13	BX625353	443	10.2	56.7	51	28	BZ380783	BZ380783
56.7	30	28	AZ401335	C 444	10.2	56.7	52	9	AI654461	AI654461
56.7	30	29	DM546253	C 445	10.2	56.7	52	10	BF636249	BF636249
56.7	31	9	AI057173	C 446	10.2	56.7	52	10	BF213416	BF213416
56.7	31	28	BZ290702	C 447	10.2	56.7	52	14	T80648	T80648
56.7	32	29	DM545760	C 448	10.2	56.7	52	28	AZ776478	AZ776478
56.7	32	29	AG253538	C 449	10.2	56.7	53	28	AZ447221	AZ447221
56.7	33	29	AL760357	C 450	10.2	56.7	53	28	AZ487502	AZ487502
56.7	33	29	AI132693	C 451	10.2	56.7	53	28	BH812711	BH812711
56.7	34	28	CC457308	C 452	10.2	56.7	53	28	BH849882	BH849882
56.7	35	10	BF531141	C 453	10.2	56.7	53	28	BZ355814	BZ355814
56.7	35	10	BF581828	C 454	10.2	56.7	53	28	BZ355814	BZ355814
56.7	35	29	BX654143	C 455	10.2	56.7	53	28	BZ660680	BZ660680
56.7	36	28	BH848146	C 456	10.2	56.7	53	29	CC885074	CC885074
56.7	36	29	BX890659	C 457	10.2	56.7	54	9	AU269158	AU269158
56.7	37	28	AZ466754	C 458	10.2	56.7	54	9	AA224858	AA224858
56.7	37	28	BZ665596	C 459	10.2	56.7	54	9	AA279907	AA279907
56.7	38	12	BJ077725	C 460	10.2	56.7	54	9	AA617305	AA617305
56.7	38	12	AZ621261	C 461	10.2	56.7	54	12	BM434926	BM434926
56.7	39	28	AZ417124	C 462	10.2	56.7	54	28	BH759557	BH759557
56.7	39	28	AZ431347	C 463	10.2	56.7	54	28	BH866169	BH866169
56.7	39	28	AL754813	C 464	10.2	56.7	54	29	CC179501	CC179501
56.7	39	29	AL754813	C 465	10.2	56.7	54	29	BX121288	BX121288
56.7	40	9	AI153860	C 466	10.2	56.7	55	13	BQ548203	BQ548203
56.7	40	28	AZ336797	C 467	10.2	56.7	55	13	BU663325	BU663325
56.7	40	28	BH146179	C 468	10.2	56.7	55	14	W89596	W89596
56.7	40	29	AL937697	C 469	10.2	56.7	55	29	CG710511	CG710511
56.7	41	10	BF207504	C 470	10.2	56.7	55	29	EX531700	EX531700
56.7	41	28	AZ747055	C 471	10.2	56.7	56	9	AA816098	AA816098
56.7	41	28	BH911711	C 472	10.2	56.7	56	9	AU258314	AU258314
56.7	43	9	AI130593	C 473	10.2	56.7	56	9	AV557704	AV557704
56.7	43	28	AZ327870	C 474	10.2	56.7	56	14	CB225832	CB225832
56.7	43	28	AZ937730	C 475	10.2	56.7	56	14	CB258411	CB258411
56.7	44	28	AQ026331	C 476	10.2	56.7	56	14	CF358645	CF358645
56.7	44	28	AZ339849	C 477	10.2	56.7	56	28	AZ496413	AZ496413
56.7	44	28	BH910335	C 478	10.2	56.7	56	28	AZ818221	AZ818221
56.7	44	29	AL769592	C 479	10.2	56.7	56	28	BH758325	BH758325
56.7	45	10	BF665932	C 480	10.2	56.7	56	28	BZ594242	BZ594242
56.7	45	28	AZ490987	C 481	10.2	56.7	56	28	CC458332	CC458332
56.7	45	28	AZ662681	C 482	10.2	56.7	57	10	BF542036	BF542036
56.7	45	28	BZ286360	C 483	10.2	56.7	57	10	AW424384	AW424384
56.7	45	28	BZ583559	C 484	10.2	56.7	57	14	CB931735	CB931735
56.7	46	9	AG922456	C 485	10.2	56.7	57	28	BH908477	BH908477
56.7	46	12	BG614289	C 486	10.2	56.7	57	28	BH911534	BH911534
56.7	46	14	H95347	C 487	10.2	56.7	57	28	BZ590841	BZ590841
56.7	46	28	BZ662482	C 488	10.2	56.7	58	9	AI828536	AI828536
56.7	46	28	BZ383830	C 489	10.2	56.7	58	10	BF634202	BF634202
56.7	46	28	CC057315	C 490	10.2	56.7	58	10	BE320889	BE320889
56.7	47	28	CC057317	C 491	10.2	56.7	58	14	CF099493	CF099493
56.7	47	28	CC455141	C 492	10.2	56.7	58	14	CK136840	CK136840
56.7	48	12	BJ062280	C 493	10.2	56.7	58	14	CK136840	CK136840
56.7	48	28	AZ598674	C 494	10.2	56.7	58	28	BH609701	BH609701
56.7	48	28	AZ656367	C 495	10.2	56.7	58	28	BZ379244	BZ379244
56.7	48	28	AZ782497	C 496	10.2	56.7	58	28	BX895854	BX895854
56.7	49	9	AI287232	C 497	10.2	56.7	58	28	CB294111	CB294111
56.7	49	9	AU268820	C 498	10.2	56.7	59	14	AQ103610	AQ103610
56.7	49	9	AV836810	C 499	10.2	56.7	59	28	AZ484130	AZ484130
56.7	49	12	BJ049535	C 500	10.2	56.7	59	28	AZ485555	AZ485555
56.7	49	28	AZ401521	C 501	10.2	56.7	59	28	AZ773992	AZ773992
56.7	49	28	BH846378	C 502	10.2	56.7	59	28	AZ806084	AZ806084
56.7	49	28	BZ770783	C 503	10.2	56.7	59	28	BH857040	BH857040
56.7	49	29	AL952708	C 504	10.2	56.7	59	28	BH902574	BH902574
56.7	50	9	AU103183	C 505	10.2	56.7	59	28	BH906359	BH906359
56.7	50	28	AZ801849	C 506	10.2	56.7	59	28	CG806861	CG806861
56.7	50	29	BX536405	C 507	10.2	56.7	59	29	TA101F03P	TA101F03P
56.7	51	9	AI988342	C 508	10.2	56.7	59	29	BM568451	BM568451
56.7	51	10	BF208869	C 509	10.2	56.7	60	12	CD950504	CD950504
56.7	51	14	CB274969	C 510	10.2	56.7	60	14	CF025058	CF025058
56.7	51	28	AZ694064	C 511	10.2	56.7	60	14	CF776186	CF776186
56.7	51	28	AZ760001	C 512	10.2	56.7	60	14	CF776615	CF776615
56.7	51	28	AZ836163	C 513	10.2	56.7	60	14	CF776672	CF776672
56.7	51	28	B00433	C 514	10.2	56.7	60	14		
56.7	51	28	BH909805	C 515	10.2	56.7	60	14		

56.7	60	14	CF776686	CF776686 jaa33f01.	589	10	55.6	56	13	BQ666073	BQ666073
56.7	60	28	AZ778391	AZ778391 2M0013006	590	10	55.6	56	14	CD683163	CD683163
56.7	60	29	CH88759	CH88759 SALK_1523	591	10	55.6	56	28	B01312	B01312
55.6	23	28	BH846934	BH846934 SALK_0120	C 592	10	55.6	56	28	BH229493	BH229493
55.6	24	28	AZ355269	AZ355269 1M0054E03	C 593	10	55.6	57	29	CG917991	CG917991
55.6	24	28	AZ514241	AZ514241 1M0360H21	C 594	10	55.6	57	29	TA356E01P	TA356E01P
55.6	25	28	AZ391004	AZ391004 1M0152J17	595	10	55.6	58	9	AA179009	AA179009
55.6	25	28	AZ504995	AZ504995 1M0345A02	596	10	55.6	58	9	BH906702	BH906702
55.6	25	29	CH304007	CH304007 Plasmodiu	597	10	55.6	59	28	AU255386	AU255386
55.6	28	29	CG724685	CG724685 1119082C0	598	10	55.6	59	28	AZ630895	AZ630895
55.6	28	28	AZ833718	AZ833718 2M0116D04	599	10	55.6	59	28	BH853618	BH853618
55.6	30	14	CF269581	CF269581 Fcy1col37	600	10	55.6	59	28	BH853683	BH853683
55.6	30	28	AZ664841	AZ664841 1M0545P19	601	10	55.6	59	28	BH904715	BH904715
55.6	34	28	AZ762569	AZ762569 1M0557O04	602	10	55.6	59	29	CC471273	CC471273
55.6	34	28	BZ768900	BZ768900 SALK_1412	C 603	10	55.6	59	29	AL766857	AL766857
55.6	34	29	CG723119	CG723119 1119074G1	C 604	10	55.6	60	9	AV833379	AV833379
55.6	35	28	BH852456	BH852456 SALK_0746	605	10	55.6	60	12	BM126375	BM126375
55.6	36	28	AZ499855	AZ499855 1M0337G22	C 606	10	55.6	60	12	BM513770	BM513770
55.6	37	9	AU263716	AU263716 AU263716	C 607	10	55.6	60	28	BH895321	BH895321
55.6	38	9	AV840044	AV840044 AV840044	C 608	10	55.6	60	29	CNS02FJ2	CNS02FJ2
55.6	38	28	BZ425325	BZ425325 100029638	C 609	9.8	54.4	22	28	AZ799717	AZ799717
55.6	39	9	AU259565	AU259565 AU259565	C 610	9.8	54.4	23	28	BH846974	BH846974
55.6	39	29	AG256137	AG256137 Lotus cor	C 611	9.8	54.4	24	28	AZ415688	AZ415688
55.6	40	28	CC025737	CC025737 3591_1_47	612	9.8	54.4	24	28	AZ443637	AZ443637
55.6	41	12	BJ049370	BJ049370 BJ049370	613	9.8	54.4	25	9	AA916478	AA916478
55.6	42	10	AW455805	AW455805 2D2 Neuro	614	9.8	54.4	25	29	CC886538	CC886538
55.6	42	14	D67708	D67708 CELK076G7F	C 615	9.8	54.4	27	28	AZ345858	AZ345858
55.6	42	28	BZ586955	BZ586955 3590_1_24	C 616	9.8	54.4	27	28	AZ782590	AZ782590
55.6	42	29	BX897196	BX897196 Arabidops	C 617	9.8	54.4	27	29	TA129H02P	TA129H02P
55.6	43	9	AA509550	AA509550 vH50d03.x	C 618	9.8	54.4	28	28	AZ346727	AZ346727
55.6	43	14	CA851085	CA851085 D10A01_B0	C 619	9.8	54.4	28	28	BH904375	BH904375
55.6	43	29	CG724749	CG724749 1119082E0	C 620	9.8	54.4	29	9	AU256382	AU256382
55.6	43	29	BX170734	BX170734 Panio rer	C 621	9.8	54.4	29	28	AZ313355	AZ313355
55.6	44	9	AU006731	AU006731 AU006731	C 622	9.8	54.4	31	28	AZ345457	AZ345457
55.6	44	14	CD029205	CD029205 mgn5007XA	623	9.8	54.4	31	28	BH903720	BH903720
55.6	44	28	BZ384717	BZ384717 SALK_1359	624	9.8	54.4	32	9	AU007928	AU007928
55.6	45	28	BH789555	BH789555 SALK_0378	625	9.8	54.4	32	28	BH907230	BH907230
55.6	45	28	BH865166	BH865166 SALK_0974	626	9.8	54.4	33	14	CF269589	CF269589
55.6	46	9	AI667606	AI667606 fdi6ell.x	627	9.8	54.4	33	28	AZ483388	AZ483388
55.6	46	28	BZ352539	BZ352539 SALK_0809	C 628	9.8	54.4	33	29	BX532756	BX532756
55.6	47	28	AZ783942	AZ783942 2M0026P03	C 629	9.8	54.4	33	29	TA61D02P	TA61D02P
55.6	47	28	BH633020	BH633020 1007058D0	C 630	9.8	54.4	34	12	B1145382	B1145382
55.6	47	28	CC022052	CC022052 3591_1_27	C 631	9.8	54.4	34	12	BJ055305	BJ055305
55.6	47	29	CG724664	CG724664 1119082B1	632	9.8	54.4	34	14	CF333374	CF333374
55.6	47	29	CL002272	CL002272 02S0105-0	633	9.8	54.4	34	29	AL944704	AL944704
55.6	48	28	BH814607	BH814607 SALK_0667	634	9.8	54.4	34	29	AL722216	AL722216
55.6	48	28	BZ762779	BZ762779 SALK_1069	C 635	9.8	54.4	35	28	BH906663	BH906663
55.6	48	29	TA263H04Q	TA263H04Q T. brucei	636	9.8	54.4	35	29	CG893855	CG893855
55.6	49	9	AA123717	AA123717 mq76d09.x	637	9.8	54.4	35	29	AL753362	AL753362
55.6	49	9	AI889232	AI889232 wms36D09.x	C 638	9.8	54.4	35	29	CNSC06SA	CNSC06SA
55.6	49	28	BH641431	BH641431 1008047F0	C 639	9.8	54.4	36	28	AZ807406	AZ807406
55.6	49	28	BH911354	BH911354 SALK_0678	640	9.8	54.4	36	28	BH904644	BH904644
55.6	49	28	BZ356313	BZ356313 SALK_1287	C 641	9.8	54.4	36	29	AG217240	AG217240
55.6	49	29	DME546797	DME546797 Drosophila	C 642	9.8	54.4	36	29	AG218041	AG218041
55.6	50	9	AI988040	AI988040 sc33a11.x	643	9.8	54.4	36	29	BX660749	BX660749
55.6	50	29	CG427403	CG427403 01S0749-0	C 644	9.8	54.4	37	14	R02052	R02052
55.6	51	9	AA614531	AA614531 np49c06.s	645	9.8	54.4	37	28	AQ254776	AQ254776
55.6	51	14	CD682301	CD682301 r749d02.y	646	9.8	54.4	37	28	BZ287003	BZ287003
55.6	51	28	AZ633366	AZ633366 1M048L03	C 647	9.8	54.4	37	28	AL751513	AL751513
55.6	51	28	BZ377421	BZ377421 SALK_0808	648	9.8	54.4	38	9	AA910311	AA910311
55.6	52	9	AI789302	AI789302 uk53e04.y	C 649	9.8	54.4	38	28	AZ837547	AZ837547
55.6	52	14	CA955020	CA955020 k134f11.y	650	9.8	54.4	38	28	BH792610	BH792610
55.6	52	14	CD683281	CD683281 r741f08.y	C 651	9.8	54.4	38	29	EX001766	EX001766
55.6	52	28	BH629312	BH629312 100707C0	652	9.8	54.4	38	29	EX662374	EX662374
55.6	52	29	CC796941	CC796941 SALK_1442	C 653	9.8	54.4	38	29	DR102F1S	DR102F1S
55.6	53	9	AV856132	AV856132 AV856132	C 654	9.8	54.4	39	9	AV853005	AV853005
55.6	53	28	BH411420	BH411420 1007022F0	C 655	9.8	54.4	39	13	C21308	C21308
55.6	53	28	BH902250	BH902250 SALK_0915	656	9.8	54.4	39	28	AZ775786	AZ775786
55.6	53	29	AL770198	AL770198 Arabidops	C 657	9.8	54.4	39	28	BH906670	BH906670
55.6	54	28	AQ902860	AQ902860 O661117-T	C 658	9.8	54.4	40	12	B033972	B033972
55.6	54	28	CL182349	CL182349 02S0205-0	659	9.8	54.4	40	14	CF328543	CF328543
55.6	55	9	A1914859	A1914859 tr36c02.x	660	9.8	54.4	40	14	H92455	H92455
55.6	55	28	BH910550	BH910550 SALK_0601	C 661	9.8	54.4	40	28	AZ424144	AZ424144



54.4	40	28	AZ590926	1M0400G15	735	9.8	54.4	52	28	BZ765415	BZ765415
54.4	40	28	AZ848456	2M0149020	736	9.8	54.4	52	29	BX536573	BX536573
54.4	40	28	BH864615	SALK_0963	737	9.8	54.4	53	14	H53365	H53365
54.4	40	28	BZ588133	3590_1.5	738	9.8	54.4	53	29	BX656514	BX656514
54.4	40	29	CC886423	SALK_1485	739	9.8	54.4	53	29	BX661868	BX661868
54.4	40	29	AG218522	Drosophila	740	9.8	54.4	54	9	AU255002	AU255002
54.4	40	29	AG218577	Drosophila	741	9.8	54.4	54	9	AV833768	AV833768
54.4	41	28	BH901464	SALK_0793	742	9.8	54.4	54	9	AA621269	AA621269
54.4	41	28	BH906771	SALK_0357	743	9.8	54.4	54	10	BE249013	BE249013
54.4	42	14	T17555	mps v112 Th	744	9.8	54.4	54	12	BM529183	BM529183
54.4	42	28	AZ826326	2M0102A03	745	9.8	54.4	54	14	CF776279	CF776279
54.4	42	28	BH791460	SALK_0599	746	9.8	54.4	54	28	BH863218	BH863218
54.4	42	28	BH847647	SALK_0551	747	9.8	54.4	54	28	BH902316	BH902316
54.4	42	28	CC455293	SALK_0802	748	9.8	54.4	54	28	BH902317	BH902317
54.4	43	9	AA921819	om40d12.s	749	9.8	54.4	54	28	BH902323	BH902323
54.4	43	28	AZ432623	1M0218D08	750	9.8	54.4	54	28	BH909991	BH909991
54.4	43	28	BZ662828	SALK_0263	751	9.8	54.4	54	28	BZ384156	BZ384156
54.4	43	28	BZ662833	SALK_0263	752	9.8	54.4	54	28	BZ596694	BZ596694
54.4	43	29	AG216392	Drosophila	753	9.8	54.4	55	9	AU254157	AU254157
54.4	43	29	BX656823	Arabidops	754	9.8	54.4	55	9	AV742610	AV742610
54.4	44	9	AA508066	ng92f11.s	755	9.8	54.4	55	12	BJ051885	BJ051885
54.4	44	9	AA545630	vj65g10.r	756	9.8	54.4	55	13	BQ568246	BQ568246
54.4	44	14	CF3335059	JMT--04-J	757	9.8	54.4	55	14	CB098745	CB098745
54.4	44	28	BH908609	SALK_0495	758	9.8	54.4	55	14	D19548 M	D19548 M
54.4	44	28	BX534980	Arabidops	759	9.8	54.4	55	14	W19160	W19160
54.4	45	28	AZ661549	1M0540M06	760	9.8	54.4	55	14	W31056	W31056
54.4	45	29	BX891955	Arabidops	761	9.8	54.4	55	14	AZ345660	AZ345660
54.4	46	9	AI636188	tz06e08.x	762	9.8	54.4	55	28	BZ767278	BZ767278
54.4	46	12	B1083327	602875594	763	9.8	54.4	55	29	CC795056	CC795056
54.4	46	28	BZ596536	SALK_0927	764	9.8	54.4	55	29	AL761596	AL761596
54.4	46	28	BZ665286	SALK_1109	765	9.8	54.4	55	29	AL952570	AL952570
54.4	46	28	BZ768917	SALK_1413	766	9.8	54.4	56	9	AA634526	AA634526
54.4	46	29	AG232605	Lotus cor	767	9.8	54.4	56	10	AW474036	AW474036
54.4	47	9	AV956026	AV956026	768	9.8	54.4	56	13	BQ472999	BQ472999
54.4	47	28	AZ321991	1M0042014	769	9.8	54.4	56	13	BQ762054	BQ762054
54.4	47	28	AZ386189	1M0145H04	770	9.8	54.4	56	13	BX718070	BX718070
54.4	47	28	AZ804274	2M0065N07	771	9.8	54.4	56	13	C21239 F	C21239 F
54.4	47	29	AL770737	Arabidops	772	9.8	54.4	56	14	CB274928	CB274928
54.4	48	28	AZ458214	1M0262A08	773	9.8	54.4	56	14	CF358797	CF358797
54.4	48	28	BH909255	SALK_0526	774	9.8	54.4	56	28	AQ025208	AQ025208
54.4	48	28	CC458944	SALK_1230	775	9.8	54.4	56	29	CC794651	CC794651
54.4	49	9	AU260260	AU260260	776	9.8	54.4	57	10	BF057873	BF057873
54.4	49	12	B1701273	84956605	777	9.8	54.4	57	12	BG885365	BG885365
54.4	49	14	CA995110	rg24c03.Y	778	9.8	54.4	57	12	BM128852	BM128852
54.4	49	14	CF312600	ABF--08-G	779	9.8	54.4	57	14	CB274909	CB274909
54.4	49	28	AZ786047	2M0030D19	780	9.8	54.4	57	14	CF801546	CF801546
54.4	49	28	BZ382085	SALK_1178	781	9.8	54.4	57	28	AZ463500	AZ463500
54.4	49	29	CC886429	SALK_1485	782	9.8	54.4	57	28	BH812817	BH812817
54.4	49	29	AL941925	Arabidops	783	9.8	54.4	57	28	BZ287127	BZ287127
54.4	49	29	BX531176	Arabidops	784	9.8	54.4	57	28	BZ384117	BZ384117
54.4	50	9	AU102299	AU102299	785	9.8	54.4	57	29	AL765755	AL765755
54.4	50	9	AU102299	AU102299	786	9.8	54.4	57	29	BX286419	BX286419
54.4	50	9	AU103189	AU103189	787	9.8	54.4	57	29	BX533727	BX533727
54.4	50	9	AA615310	vo01h08.r	788	9.8	54.4	58	10	AW246501	AW246501
54.4	50	10	AW783902	5.AL2.Gil	789	9.8	54.4	58	12	B1438036	B1438036
54.4	50	12	BM069725	ie88d07.Y	790	9.8	54.4	58	13	BX549853	BX549853
54.4	50	13	BQ125541	rc89f06.Y	791	9.8	54.4	58	28	BH416669	BH416669
54.4	50	14	CA795302	CA795302	792	9.8	54.4	58	28	BH791190	BH791190
54.4	50	14	CF301799	7LEAF--06	793	9.8	54.4	58	28	BH862804	BH862804
54.4	50	28	BH636136	1008009D0	794	9.8	54.4	58	28	BZ287603	BZ287603
54.4	50	29	CC493346	CH240_327	795	9.8	54.4	58	29	BX535617	BX535617
54.4	51	9	AL644395	AL644395	796	9.8	54.4	59	29	BX660313	BX660313
54.4	51	12	B1174734	OSTF052F1	797	9.8	54.4	59	29	AA458427	AA458427
54.4	51	28	AZ838224	2M0133018	798	9.8	54.4	59	10	BF036854	BF036854
54.4	52	9	AI326324	ml57g04.x	799	9.8	54.4	59	28	BH790538	BH790538
54.4	52	9	AL872200	AL872200	800	9.8	54.4	59	28	BZ768804	BZ768804
54.4	52	10	BF631825	NF026C09D	801	9.8	54.4	59	29	BX534620	BX534620
54.4	52	10	BM692095	NF052B07S	802	9.8	54.4	60	9	AI824783	AI824783
54.4	52	10	BE320772	NF028E03R	803	9.8	54.4	60	9	AV521053	AV521053
54.4	52	12	BM893619	1j27d05.x	804	9.8	54.4	60	9	AV8337197	AV8337197
54.4	52	13	BU497340	PfESToab6	805	9.8	54.4	60	10	BF638495	BF638495
54.4	52	28	AZ576597	AST-TD1.2	806	9.8	54.4	60	10	BF639003	BF639003
54.4	52	28	BZ288336	SALK_0217	807	9.8	54.4	60	14	D18195	D18195

54.4	60	28	AZ7822310	AZ7822310	2M0222C03	C 881	3.6	53.3	41	28	AZ467036
54.4	60	28	BZ354346	BZ354346	SALK_1248	882	9.6	53.3	41	28	AZ762719
54.4	60	28	BZ762244	BZ762244	SALK_0925	883	9.6	53.3	41	28	BZ381303
54.4	60	29	AL940665	AL940665	ArabiDops	884	9.6	53.3	41	29	AG217208
53.3	19	28	AZ769438	AZ769438	1M0570F09	C 885	9.6	53.3	42	28	AZ309889
53.3	19	28	AZ973582	AZ973582	2M0247C20	C 886	9.6	53.3	42	28	BH906566
53.3	20	28	AZ421329	AZ421329	1M0199J003	C 887	9.6	53.3	43	28	AZ378285
53.3	21	9	AL585535	AL585535	AL585535	888	9.6	53.3	43	28	AZ992855
53.3	22	28	AZ366186	AZ366186	1M0115L21	889	9.6	53.3	43	28	BH809878
53.3	22	28	AZ479849	AZ479849	1M0300E20	890	9.6	53.3	43	28	BZ352990
53.3	23	14	CF312348	CF312348	ABF--08-A	C 891	9.6	53.3	43	28	BZ763952
53.3	23	28	AZ345552	AZ345552	1M080E15	892	9.6	53.3	43	29	CG722753
53.3	23	28	AZ826455	AZ826455	2M0102P09	893	9.6	53.3	44	9	AA926720
53.3	24	28	AZ320835	AZ320835	1M0041I17	894	9.6	53.3	44	10	BE311212
53.3	24	28	AZ345509	AZ345509	1M080I03	895	9.6	53.3	44	28	AZ492304
53.3	24	29	TA208D09P	TA208D09P	AL479445 T. brucei	896	9.6	53.3	44	28	AZ601755
53.3	25	28	AZ427760	AZ427760	1M0209P22	C 897	9.6	53.3	44	28	BH789833
53.3	25	28	AZ829708	AZ829708	2M0107G19	C 898	9.6	53.3	45	9	AA778766
53.3	25	28	AZ950699	AZ950699	2M0214F20	C 899	9.6	53.3	45	9	AI471721
53.3	25	28	BH792245	BH792245	SALK_0631	900	9.6	53.3	45	28	AZ387836
53.3	25	29	TA62D04Q	TA62D04Q	AL464606 T. brucei	901	9.6	53.3	45	28	AZ954848
53.3	26	28	AZ309024	AZ309024	1M0012H07	902	9.6	53.3	45	28	BH789570
53.3	26	28	AZ410119	AZ410119	1M0182P08	C 903	9.6	53.3	45	29	CC883051
53.3	26	28	AZ478344	AZ478344	1M0298A22	C 904	9.6	53.3	46	9	AA654894
53.3	27	28	AZ443035	AZ443035	1M0237G06	C 905	9.6	53.3	46	9	AI033006
53.3	27	28	AZ949965	AZ949965	2M0213L16	C 906	9.6	53.3	46	9	AI744366
53.3	28	28	AZ343935	AZ343935	1M0077K12	907	9.6	53.3	46	10	BF123084
53.3	28	28	AZ774261	AZ774261	2M0003N21	908	9.6	53.3	46	28	AZ336053
53.3	28	28	BH905737	BH905737	SALK_1076	909	9.6	53.3	46	28	AZ418890
53.3	28	28	BZ664534	BZ664534	SALK_0759	C 910	9.6	53.3	46	28	AZ595876
53.3	29	28	AZ419920	AZ419920	1M0196E12	911	9.6	53.3	46	28	AZ808188
53.3	29	28	BZ596327	BZ596327	SALK_0923	912	9.6	53.3	46	28	BH906372
53.3	30	9	AV856232	AV856232	AV856232	913	9.6	53.3	46	29	EX125703
53.3	30	13	C01051	HUMGS00720	C01051 HUMGS00720	914	9.6	53.3	46	29	EX534722
53.3	30	28	AQ025784	AQ025784	1(2)k0620	C 915	9.6	53.3	47	28	AZ633235
53.3	30	28	AQ025785	AQ025785	1(2)k0620	916	9.6	53.3	47	28	AZ946143
53.3	30	28	AZ428907	AZ428907	1M0212C15	C 917	9.6	53.3	47	28	BH813635
53.3	31	9	A1002013	A1002013	ot40e08.s	C 918	9.6	53.3	47	28	BH906478
53.3	31	28	AZ827463	AZ827463	2M0103H19	C 919	9.6	53.3	47	29	AG019636
53.3	31	28	BH906412	BH906412	SALK_1098	920	9.6	53.3	47	29	BX654811
53.3	31	28	BZ597449	BZ597449	SALK_1050	C 921	9.6	53.3	48	14	D12328
53.3	31	28	BZ763070	BZ763070	SALK_1118	C 922	9.6	53.3	48	14	D12328
53.3	31	29	AL761476	AL761476	ArabiDops	C 923	9.6	53.3	48	29	CC795453
53.3	31	29	AL943189	AL943189	ArabiDops	924	9.6	53.3	48	29	CC795453
53.3	32	28	AZ485437	AZ485437	1M0312B19	925	9.6	53.3	49	9	AA496619
53.3	32	28	AZ602044	AZ602044	1M0420B12	C 926	9.6	53.3	49	9	AA594397
53.3	34	28	AZ462024	AZ462024	1M0269E12	C 927	9.6	53.3	49	12	BM281964
53.3	34	28	BH792264	BH792264	SALK_0632	C 928	9.6	53.3	49	14	CB277378
53.3	34	29	TA202F08P	TA202F08P	T. brucei	929	9.6	53.3	49	28	BH846326
53.3	35	28	BZ353611	BZ353611	SALK_1205	C 930	9.6	53.3	49	29	AB082215
53.3	35	29	TA336F08Q	TA336F08Q	T. brucei	C 931	9.6	53.3	50	9	AI126970
53.3	36	9	AU258465	AU258465	AU258465	932	9.6	53.3	50	9	AI102957
53.3	36	28	AZ425719	AZ425719	1M0205N21	C 933	9.6	53.3	50	9	AU103002
53.3	37	28	AZ423769	AZ423769	1M0203G22	C 934	9.6	53.3	50	12	BG526086
53.3	37	28	AZ586716	AZ586716	1M0392B19	C 935	9.6	53.3	50	12	BI749153
53.3	37	28	DR6865T	DR6865T	Dario rer	C 936	9.6	53.3	50	12	BI749153
53.3	37	29	TA35D05P	TA35D05P	T. brucei	937	9.6	53.3	50	13	BQ590343
53.3	38	28	AZ334854	AZ334854	1M0064X20	C 938	9.6	53.3	50	14	CB274908
53.3	38	28	AZ453551	AZ453551	1M0255E06	C 939	9.6	53.3	50	14	CB858064
53.3	38	28	BH847845	BH847845	SALK_0605	C 940	9.6	53.3	50	28	AZ427184
53.3	38	28	BH863567	BH863567	SALK_0941	941	9.6	53.3	50	28	AZ769352
53.3	38	28	BH903283	BH903283	SALK_0527	942	9.6	53.3	50	28	BH900918
53.3	38	28	CC456487	CC456487	SALK_0987	943	9.6	53.3	50	28	CC182113
53.3	38	28	BX659120	BX659120	ArabiDops	944	9.6	53.3	50	29	CC795807
53.3	38	29	TA115F10Q	TA115F10Q	T. brucei	C 945	9.6	53.3	50	29	CC941572
53.3	39	28	AZ798493	AZ798493	2M0055P15	946	9.6	53.3	50	29	CG400426
53.3	39	28	BZ593768	BZ593768	SALK_0820	947	9.6	53.3	50	29	CG400440
53.3	40	9	AI032824	AI032824	ox17F07.x	948	9.6	53.3	50	29	CG729919
53.3	40	9	AV845525	AV845525	AV845525	949	9.6	53.3	50	29	AL763583
53.3	40	28	AZ775335	AZ775335	2M0007G07	950	9.6	53.3	50	29	BX897057
53.3	40	28	BZ358998	BZ358998	SALK_1336	951	9.6	53.3	51	29	CC884509
53.3	41	9	AU013901	AU013901	AU013901	952	9.6	53.3	52	9	AI307707
53.3	41	28	AZ457981	AZ457981	1M0261B12	C 953	9.6	53.3	52	9	AI598081

```

FEATURES
source
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

```

ns, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
rinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednits, L.,  
nn, P., Zimmerman, J., and Ecker, J.R.  
sequence-indexed library of insertion mutations in the  
bidopsis Genome  
published (2001)

10003 20 bp DNA linear GSS 13-MAR-2003

ns, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
rinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednits, L.,  
nn, P., Zimmerman, J., and Ecker, J.R.  
sequence-indexed library of insertion mutations in the  
bidopsis Genome  
published (2001)

```

/db xref="taxon:10090"
/clone="UUGC1M0080A01"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
74.4%; Score 13.4; DB 28; Length 40;
ilarity 93.3%; Pred. No. 6.8e+04;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
ATTGGAATTTCG 16
|||||
ATTGGAATTTCG 17

2501 56 bp DNA linear GSS 17-JUN-2002
idopsis thaliana T-DNA flanking sequence GK-013F10-011902,
mic survey sequence.
2501
2501.1 GI:21484999
idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
db; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
zhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
Weisshaar,B.
peline for automated high-throughput generation of FSTs
nking sequence tags) from Arabidopsis thaliana T-DNA
sformed lines
blished
O.M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
flanking sequence tag based reverse genetics
blished
bases 1 to 56)
zhov,N., Li,Y., Rosso,M. and Weisshaar,B.
ct Submission
itted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
hntungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
sequence is recovered from the left border of the T-DNA. It
cates an insertion close to or within gene At5g08400. The
ences are generated at the MPI for Plant Breeding Research in
context of the GABI-Kat project. GABI-Kat is part of the German
t Genomics program designated 'GABI'. Information on line
lability can be found at:
://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers

```

```

source
1.56
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
/db xref="taxon:3702"
/clone="GK-013F10-011902"
/clone_lib="Arabidopsis thaliana T-DNA insertio
/notes="PCR was performed on DNA from Arabidopsi
plants (T1) which were transformed with the T-D
vector pAC106. The lines contain one or more T-
insertions. The DNA fragment(s) resulting from
were directly sequenced to determine the genom
flanking the insertion. Sequences displaying si
similarity to the A. thaliana nuclear genome se
processed for submission. T-DNA derived sequenc
removed"
ORIGIN
Query Match 74.4%; Score 13.4; DB 29; Length 56;
Best Local Similarity 93.3%; Pred. No. 6.7e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0;
Qy 3 CATTTGGAATTTCG 17
|||||
Db 43 CATTTGGAATTTCG 29

RESULT 4
BE491325
LOCUS BE491325 60 bp mRNA linear EST
DEFINITION db71e06.y1 Wellcome CRC psk egg Xenopus laevis cDNA clon
IMAGE:3378466 5' similar to SW:TRCB_XENLA_Q91854 BETA-TR
sequence.
ACCESSION BE491325
VERSION BE491325.1 GI:9610858
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
REFERENCE 1 (bases 1 to 60)
AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B.,
Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
COMMENT Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn
Gordon (Wellcome/CRC Institute). DNA Sequencing by: Wash
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library ar
through the I.M.A.G.E. Consortium/LLNL at: info@image.ll
Seq primer: -40RP from Gibco.
Location/Qualifiers
1.60
/organism="Xenopus laevis"
/mol type="mRNA"
/db xref="taxon:8355"
/clone="IMAGE:3378466"
/tissue_type="egg"
/lab host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC psk egg"
/notes="Vector: pBluescript SK-; Site 1: NotI; S
EcoRI; cDNAs were oligo-dT primed and direction
cloned. Library was constructed by N. Garrett,

```

A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).  
Note: This is a Xenopus Gene Collection (XGC) library."

74.4%; Score 13.4; DB 10; Length 60;  
ilarity 93.3%; Pred. No. 6.7e+04;  
Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
TCATTGGAAATTTT 15  
|||||  
TCATTGGCAATTTT 38

13284 37 bp DNA linear GSS 04-SEP-2002  
102372.19.30.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_102372.19.30.x; genomic  
ey sequence.

13284  
13284.1 GI:22714450

idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 37)  
iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
m,P., Zimmerman,J., and Ecker,J.R.

quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
inished (2001)

act: Joseph R. Ecker  
c Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA

: 858 453 4300 x1752  
: 858 558 6379

il: ecker@salk.edu  
s is single pass sequence recovered from the left border of  
A. This sequence lies within an annotated exon of At3g23970.  
ss: TDNA tagged.

Location/Qualifiers  
1..37  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_102372.19.30.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

73.3%; Score 13.2; DB 28; Length 37;  
milarity 83.3%; Pred. No. 8.4e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGAAATTTGCC 18  
|||||  
TCATTGGATGATTGCC 26

11561  
4a01.x1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1916136 3',

similar to TR:014597 014597 NON-FUNCTIONAL FOLATE BINDIN  
/, mRNA sequence.

ACCESSION  
Al3111561  
VERSION  
Al3111561.1 GI:4006432

KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Hom  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

REFERENCE  
1 (bases 1 to 52)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., N

Emmerit-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequenc

Clone distribution: NCI-CGAP clone distribution inform  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 539 Std Error: 0.00

Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
Location/Qualifiers  
1..52

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="IMAGE:1916136"

/tissue\_type="2 pooled tumors (clear cell type  
/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Kid5"  
/note="Organ: kidney; Vector: pT73D-Pac (Phar

a modified polylinker; Site 1: Not I; Site 2:  
strand cDNA was primed with a Not I - oligo(dt

RACCGAAGAAATTCGCGCGCAATATTTTATTTTATTTT  
double-stranded cDNA was ligated to Eco RI ada

(Pharmacia), digested with Not I and cloned in  
and Eco RI sites of the modified pT73 vector.

went through one round of normalization. Libra  
constructed by Bento Soares and M. Fatima Bona

# ORIGIN

Query Match 73.3%; Score 13.2; DB 9; Length 52;  
Best Local Similarity 83.3%; Pred. No. 8.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTGCC 18

Db 50 CCATTGTGAAGTTGCC 33

## RESULT 7

BH902184

LOCUS  
BH902184 57 bp DNA linear GSS  
SALK\_091427.17.20.x Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_091427.17.20.x;  
survey sequence.

ACCESSION  
BH902184.1 GI:22713065

VERSION  
GSS.

KEYWORDS  
SOURCE  
Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr

Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
rosids; eurosids II; Brassicales; Brassicaceae; Arabido

REFERENCE  
1 (bases 1 to 57)

O.J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 nab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 P., Zimmerman, J., and Ecker, J.R.  
 Sequence-Indexed Library of Insertion Mutations in the  
 dopsis Genome  
 blished (2001)  
 ict: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGnAL)  
 Salk Institute for Biological Studies  
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 : ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 . This sequence lies within an annotated exon of At3g23970.  
 : TDNA tagged.

Location/Qualifiers  
 1. .57  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_091427.17.20.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

73.3%; Score 13.2; DB 28; Length 57;  
 ilarity 83.3%; Pred. No. 8.3e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTTTGCC 18  
 |||||  
 TATTGGGATGATGTC 25

0275 25 bp DNA linear GSS 26-NOV-2002  
 114881.40.40.x Arabidopsis thaliana TDNA insertion lines  
 dopsis thaliana genomic clone SALK\_114881.40.40.x, genomic  
 y sequence.

0275  
 0275.1 GI:25472978

dopsis thaliana (thale cress)  
 idopsis thaliana  
 cyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicot;  
 as; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 25)  
 so, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 nab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 a, P., Zimmerman, J., and Ecker, J.R.  
 uence-Indexed Library of Insertion Mutations in the  
 idopsis Genome  
 blished (2001)  
 act: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGnAL)  
 Salk Institute for Biological Studies  
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 1: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 . This sequence lies within 300 bases of the 5' end of  
 44370.  
 : TDNA tagged.

FEATURES  
 source  
 Location/Qualifiers  
 1. .25  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_114881.40.40.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /notes="PCR was performed on Arabidopsis thaliana  
 each of which contains one or more TDNA insert:  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN  
 Query Match 72.2%; Score 13; DB 28; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTCATTGGGAATT 13  
 |||||  
 Db 13 CTCATTGGGAATT 25

RESULT 9  
 BZ380283 59 bp DNA linear GSS  
 SALK\_114889.22.40.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_114889.22.40.x,  
 survey sequence.

ACCESSION  
 BZ380283  
 BZ380283.1 GI:25472995  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 59)  
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P  
 Shinn, P., Zimmerman, J., and Ecker, J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bor  
 TDNA. This sequence lies within 300 bases of the 5' end  
 At2g44370  
 Class: TDNA tagged.

FEATURES  
 source  
 Location/Qualifiers  
 1. .59  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_114889.22.40.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /notes="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

```

72.2%; Score 13; DB 28; Length 59;
ilarity 100.0%; Pred. No. 1e+05;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CATTGGGAATT 13
|||||
CATTGGGAATT 59

4722 57 bp DNA linear GSS 15-DEC-2003
idopsis thaliana T-DNA flanking sequence GK-682C08-023963,
mic survey sequence.
4722.1 GI:39927217

idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
Weisshaar,B.
eline for automated high-throughput generation of FSTs
nking sequence tags) from Arabidopsis thaliana T-DNA
ushed lines
ublished
(bases 1 to 57)
f., Strizhov,N., Rosso,M. and Weisshaar,B.
ct Submission
itted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer
htungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
s sequence is recovered from the left border of the T-DNA. It
icates an insertion close to or within gene Atlg79000. The
ences are generated at the MPI for Plant Breeding Research in
context of the GABI-kat project. GABI-Kat is part of the German
it Genomics program designated 'GABI'. Information on line
lability can be found at:
p://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. 57
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-682C08-023963"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

71.1%; Score 12.8; DB 29; Length 57;
milarity 87.5%; Pred. No. 1.3e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TATTGGGAATTTGCC 18
|||||
TATTGAAATTTTGGC 53

```

```

RESULT 11
AZ477130 58 bp DNA linear GSS
LOCUS
DEFINITION
1M0296021F Mouse 10kb plasmid UUGC1M library Mus musculus
clone UUGC1M0296021 F, genomic survey sequence.
ACCESSION
AZ477130
VERSION
AZ477130.1 GI:10635333
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
1 (bases 1 to 58)
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,I
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads fr
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0296 Row: 0 Column: 21
Seq primer: CTTTGAACACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 58.
Location/Qualifiers
1. 58
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0296021"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resist
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA f
musculus C57BL/6J (male) was obtained from th
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares
was hydrodynamically sheared by repeated passa
0.005 inch orifice at constant velocity. The s
was blunt end-repaired with T4 DNA polymerase
polynucleotide kinase. Adaptor oligonucleotide
ligated to the blunt ends in high molar excess
adaptor DNA was purified and size-selected f
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from
of pMD42 (gi|4732114|gb|AF129072.1), a copy-nu
inducible derivative of plasmid R1. The vector
with adaptors complementary to the insert adap
purified. The sheared, adaptor mouse DNA was
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Strata
and selected for ampicillin resistance."

Query Match 71.1%; Score 12.8; DB 28; Length 58;
Best Local Similarity 87.5%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCATTGGGAATTTGCC 17
|||||
DB 25 TGAGTTGGAATTTGCC 40

```

775 58 bp DNA linear GSS 03-SEP-2002  
phila melanogaster DNA, clone:NP6401-5-1, flanking P(GaWB)  
poson insertion, genomic survey sequence.

775.1 GI:22764775

phila melanogaster (fruit fly)

phila melanogaster  
yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
era; Endopterygota; Diptera; Brachycera; Muscomorpha;  
roidea; Drosophilidae; Drosophila.

hi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H.,  
i,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R.,  
a,T., Yoshihara,M. and Goto,S.  
a database compiling expression patterns and molecular  
ions of a collection of Gal4 enhancer traps  
his (2002) In press  
ases 1 to 58)

hi,S.

t Submission  
tted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for  
limental Biology, Laboratory for Morphogenetic Singaling;  
-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan  
ail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,  
91-78-301-3183)

clone was isolated from genomic DNA flanking an insertion of  
p element vector P(GaWB) of a Drosophila strain.

Location/Qualifiers

```
1..58
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP6401"
/db_xref="taxon:7227"
/chromosome="2"
/map="50D1"
/clone="NP6401-5-1"
/note="flanking P(GaWB) transposon insertion"
```

71.1%; Score 12.8; DB 29; Length 58;  
ilarity 87.5%; Pred. No. 1.3e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CATTGGGAATTTTG 16

|||||

CATTTTGGATTTTG 15

1979 59 bp DNA linear GSS 09-OCT-2003  
idopsis thaliana T-DNA flanking sequence GK-682C08-023112,  
mic survey sequence.

1979.1 GI:37618401

idopsis thaliana (thale cress)

idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Siedler,H.  
Weisshaar,B.

ipeline for automated high-throughput generation of FSTs  
inking sequence tags) from Arabidopsis thaliana T-DNA

nsformed lines

ublished

AUTHORS  
TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Wei  
A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 59)

Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.

Direct Submission

Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829,  
This sequence is recovered from the left border of the T-  
indicates an insertion close to or within gene Atlg79000  
sequences are generated at the MPI for Plant Breeding Re:  
the context of the GABI-Kat project. GABI-Kat is part of  
Plant Genomics program designated 'GABI'. Information on  
availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1..59

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-682C08-023112"

/clone\_lib="Arabidopsis thaliana T-DNA insertion;  
/note="PCR was performed on DNA from Arabidopsis  
plants (T1) which were transformed with the T-DNA  
vector pAC161. The lines contain one or more T-  
insertions. The DNA fragment(s) resulting from  
were directly sequenced to determine the genomic  
flanking the insertion. Sequences displaying si-  
milarity to the A. thaliana nuclear genome se-  
processed for submission. T-DNA derived sequenc  
removed"

ORIGIN

Query Match 71.1%; Score 12.8; DB 29; Length 59;  
Best Local Similarity 87.5%; Pred. No. 1.3e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CATTGGGAATTTTGGC 18

|||||

Db 40 CATTACAAATTTTGGC 55

RESULT 14  
AL758081 60 bp DNA linear GSS  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence GK-155F02-0  
genomic survey sequence.

AL758081

AL758081

AL758081.1 GI:21496429

GSS.

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabido

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institi



ntungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 states an insertion within the locus defined by clone t31e10.  
 sequences are generated at the MPI for Plant Breeding Research  
 he context of the GABI-Kat project. GABI-Kat is part of the  
 an Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. 50

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-155F02-013141"

/note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

71.1%; Score 12.8; DB 29; Length 60;

ilarity 87.5%; Pred. No. 1.3e+05; Length 60; Indels 0; Gaps 0;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CATTTGGAATTTG 16

|||||

'CTTTGCAATTTG 57

7315 45 bp mRNA linear EST 31-JUL-1998

7315 Schizosaccharomyces pombe late log phase cDNA

izosaccharomyces pombe cDNA clone spc01747, mRNA sequence.

7315

7315.1 GI:3343773

izosaccharomyces pombe (fission yeast)

izosaccharomyces pombe

ryota; Fungi; Ascomycota; Schizosaccharomycetes;

izosaccharomycetales; Schizosaccharomycetaceae;

izosaccharomycetes.

(bases 1 to 45)

lmyo.M. and Mita, K.

atification of expressed sequence tags of Schizosaccharomyces

de

ublished (1998)

act: Mitsuoki Morimyo

me Research Group

ional Institute of Radiological Sciences

, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

il: morimyo@nirs.go.jp

Location/Qualifiers

1. 45

/organism="Schizosaccharomyces pombe"

/mol\_type="mRNA"

/strain="972"

/db\_xref="taxon:4896"

/clone="spc01747"

/sex="n minus"

/note="lib="Schizosaccharomyces pombe late log phase cDNA"  
 /clone="vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA  
 sequences was not always from 5' to 3'. The cDNA data of  
 Schizosaccharomyces pombe are available for searching on

the World Wide Web. (URL, <http://www.nirs.go.jp>)

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 45;

Best Local Similarity 92.9%; Pred. No. 1.9e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 2 TCATTGGAATTTT 15

|||||

Db 28 TCATTGGAATTTT 15

RESULT 16

AUI03941/c

LOCUS

DEFINITION AUI03941 Sugano Homo sapiens cDNA library Homo sapiens c

HEP17626, mRNA sequence.

ACCESSION

AUI03941

VERSION

AUI03941.1 GI:13553462

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Se  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Ok  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S., Ok  
 Diverse transcriptional initiation revealed by fine, lar  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A.  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gen  
 149-156 (1997).

FEATURES

source

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEP17626"

/clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 50;

Best Local Similarity 92.9%; Pred. No. 1.9e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 5 TTTTGGAAATTTGCC 18

|||||

Db 30 TTTTGGAAATTTGCC 17

RESULT 17

CC85817

LOCUS

DEFINITION

CC85817 30 bp DNA linear GSS  
 SALK\_147877.15.70.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_147877.15.70.x,  
 survey sequence.

ACCESSION

CC85817

VERSION

CC85817.1 GI:33362173

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudi

```

Class: TDNA tagged.
FEATURES
    source
        1..34
            /location/Qualifiers
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="SALK_078369.50.70.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion"
            /note="PCR was performed on Arabidopsis thalian
            each of which contains one or more TDNA insert
            elements. The resultant fragment for each line
            directly sequenced to determine the genomic seq
            the site of insertion. Details of the protocol
            be found at http://signal.salk.edu/tdna_protoc

```

**SOURCE**  
**ORGANISM** Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 37)  
**REFERENCE**  
**AUTHORS** Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
**TITLE** A sequence-indexed library of Insertion Mutations in the  
 Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bor  
 TDNA. This sequence lies within an annotated exon of At3:  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..37  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_098616"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

**ORIGIN**  
 Query Match 67.8%; Score 12.2; DB 28; Length 37;  
 Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGAAATTTCG 17  
 ||||| ||||| ||||| |||||  
 Db 9 CTCATATGGAGTTTGGC 25

**RESULT 22**  
**LOCUS** BZ355646  
**DEFINITION** SALK\_127150.32.95.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_127150.32.95.x,  
 survey sequence.  
**ACCESSION** BZ355646  
**VERSION** BZ355646.1 GI:24946805  
**KEYWORDS** GSS  
**SOURCE** Arabidopsis thaliana (thale cress)  
**ORGANISM** Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 40)  
**REFERENCE**  
**AUTHORS** Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
**TITLE** A sequence-indexed library of Insertion Mutations in the  
 Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752

858 558 6379

: ecker@salk.edu

is single pass sequence recovered from the left border of

:: TDNA tagged.

Location/Qualifiers

1. .40

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_127150.32.95.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

Query Match 67.8%; Score 12.2; DB 28; Length 40;

Best Local Similarity 82.4%; Pred. No. 2.4e+05;

Matches 0; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAAATTTGC 17

||||| ||||| |||||

CTATGGGACTTTGGC 25

3201

086477.45.50.x Arabidopsis thaliana TDNA insertion lines

[opsis thaliana genomic clone SALK\_086477.45.50.x, genomic

y sequence.

3201

3201.1 GI:21704791

dopsis thaliana (thale cress)

.dopsis thaliana

yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

natophyta; Magnoliophyta; eudicotyledons; core eudicots;

is; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

ases 1 to 41)

so J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

l, P., Zimmerman, J., and Ecker, J.R.

pence-Indexed Library of Insertion Mutations in the

dopsis Genome

ublished (2001)

ct: Joseph R. Ecker

Institute Genomic Analysis Laboratory (IGNAL)

Salk Institute for Biological Studies

) N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

l: ecker@salk.edu

is single pass sequence recovered from the left border of

. This sequence lies within an annotated exon of At3g33056.

s: TDNA tagged.

Location/Qualifiers

1. .41

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_086477.45.50.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

## ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 41;

Best Local Similarity 82.4%; Pred. No. 2.4e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGC 17

||||| ||||| |||||

Db 5 CTCATATGGACTTTGC 21

RESULT 24

CC887116

LOCUS

DEFINITION

SALK\_149581.42.50.x Arabidopsis thaliana TDNA insertion ]

Arabidopsis thaliana genomic clone SALK\_149581.42.50.x, s

survey sequence.

CC887116

CC887116.1 GI:33363472

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac

Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

rosids; eurosids II; Brassicales; Brassicaceae; Arabidop

1 (bases 1 to 41)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P

Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (IGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bor

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .41

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_149581.42.50.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion

/note="PCR was performed on Arabidopsis thalian

each of which contains one or more TDNA insert

elements. The resultant fragment for each line

directly sequenced to determine the genomic seq

the site of insertion. Details of the protocol

be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

## ORIGIN

Query Match 67.8%; Score 12.2; DB 29; Length 41;

Best Local Similarity 82.4%; Pred. No. 2.4e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGC 17

||||| ||||| |||||

Db 10 CTCATATGGACTTTGC 26

RESULT 25

AU012201/c

LOCUS

DEFINITION

AU012201 Schizosaccharomyces pombe late log phase EST

AU012201 42 bp mRNA linear EST

zosaaccharomyces pombe cDNA clone spc06480, mRNA sequence.

```

2201      1 GI:3357110
2201.1    GI:3357110

zosaaccharomyces pombe (fission yeast)
zosaaccharomyces pombe
cyota; Fungi; Ascomycota; Schizosaccharomycetes;
zosaaccharomycetales; Schizosaccharomycetaceae;
zosaaccharomyces.
cases 1 to 42)
nyo, M. and Mita, K.
tification of expressed sequence tags of Schizosaccharomyces
published (1998)
act: Mitsuoki Morimyo
ne Research Group
onal Institute of Radiological Sciences
Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
l: morimyo@nirs.go.jp.
Location/Qualifiers
1..42
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc06480"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
67.8%; Score 12.2; DB 9; Length 42;
ilarity 82.4%; Pred. NO. 2.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CATTTGGAATTTC 17
|||||
'CATTTGAATTTC 8

14071      42 bp      DNA      linear      GSS 20-OCT-2003
162C05.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
rey sequence.
14071
14071.1    GI:37776563

mays
mays
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
e; Panicoideae; Andropogoneae; Zea.
(bases 1 to 42)
ot, V.
ze genomic sequences found using engineered RescueMu transposon
ublished (2001)
tact: Walbot V
artment of Biological Sciences
nford University
California Ave, Palo Alto, CA 94304, USA
: 650 723 2227
: 650 725 8221
il: walbot@stanford.edu
sible ligation site of ends cut by 2 different endonucleases.
erse complemented post-ligation sequence from source sequence.
te: 1119162 column: 1
ss: transposon-tagged.

```

# FEATURES

source

```

Location/Qualifiers
1..42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered
pBluescript backbone); Site 1: BamHI; Site 2: B
RescueMu is a 4.9 kb, modified maize Mu transpo
designed to allow plasmid rescue from total gen
Mu elements insert preferentially into transcri
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the link
'RescueMu.' Grid AA was grown at UC San Diego i
was extracted from leaf strips, double digested
BamHI and BglII, and ligated to form circular p
DH10B cells were transformed and then screened
plates with ampicillin."

```

## ORIGIN

```

Query Match      67.8%; Score 12.2; DB 29; Length 42;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

```

```

OY      1 CTCATTGGAAATTTC 17
        |||||
DB      10 CTCATTGAATTTC 26

```

## RESULT 27

```

BZ765054      43 bp      DNA      linear      GSS
BZ765054
LOCUS      SALK_128153.35.60.n Arabidopsis thaliana TDNA insertion
DEFINITION      Arabidopsis thaliana genomic clone SALK_128153.35.60.n,
survey sequence.
ACCESSION      BZ765054.1 GI:28937607
VERSION      BZ765054
KEYWORDS      GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi
1 (bases 1 to 43)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., I
Shinn, P., Zimmerman, J. and Ecker, J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bo:
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_128153.35.60.n"
/clone_lib="Arabidopsis thaliana TDNA insertion"
/note="PCR was performed on Arabidopsis thalia

```

'CATTTGGAATTTGC 17  
||| ||| ||| ||| |||  
'CATATGGACTTTGGC 32

1

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P  
Shinn, P., Zimmerman, J. and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)  
at: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 558 6379  
1: ecker@salk.edu  
is single pass sequence recovered from the left border of

s: TDNA tagged.  
Location/Qualifiers  
1. 47  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="SALK\_130130.43.05.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)."

67.8%; Score 12.2; DB 28; Length 47;  
Similarity 82.4%; Pred. No. 2.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTCG 17  
CTATAGGACTTTGGC 32

11466 48 bp DNA linear GSS 02-APR-2002  
\_060006.39.50.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_060006.39.50.x, genomic  
rey sequence.

11466 GI:19885359

idopsis thaliana (thale cress)  
idopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
(bases 1 to 48)  
onso,J.M., Leisae,T.J., Barajas,P., Chen,H., Cheuk,R.,  
cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predniss,L.,  
an,P., Zimmerman,J. and Ecker,J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)

act: Joseph R. Ecker  
k Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 558 6379  
1: ecker@salk.edu  
is single pass sequence recovered from the left border of

A.

ss: TDNA tagged.  
Location/Qualifiers  
1. 48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_060006.39.50.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion  
/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA inser  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

Query Match 67.8%; Score 12.2; DB 28; Length 48;  
Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTCG 17  
|||||  
DB 17 CTCATATGGACTTTGGC 33  
|||||

RESULT 32  
BZ765295 48 bp DNA linear GSS  
LOCUS SALK\_129795.21.75.x Arabidopsis thaliana TDNA insertion  
DEFINITION Arabidopsis thaliana genomic clone SALK\_129795.21.75.x,  
survey sequence.

ACCESSION BZ765295

VERSION BZ765295.1 GI:28937848

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi

REFERENCE 1 (bases 1 to 48)

AUTHORS Alonso,J.M., Leisae,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., i  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)

JOURNAL

COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bo  
TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1. 48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_129795.21.75.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion  
/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA inser  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 48;  
Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTCG 17

|||||  
 ATATGGACTTTGGC 45

392 50 bp DNA linear GSS 02-APR-2002  
 056948.49.55.x Arabidopsis thaliana TDNA insertion lines  
 dopsis thaliana genomic clone SALK\_056948.49.55.x, genomic  
 y sequence.  
 392  
 392.1 GI:19883490

dopsis thaliana (thale cress)

yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 s; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 50)

O.J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 nab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 P., Zimmerman, J., and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the  
 dopsis Genome

lished (2001)

ct: Joseph R. Ecker

Institute Genomic Analysis Laboratory (SIGNAL)

alk Institute for Biological Studies

N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

eker@salk.edu

is single pass sequence recovered from the left border of

TDNA tagged.

Location/Qualifiers

1. .50

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_056948.49.55.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

67.8%; Score 12.2; DB 28; Length 50;

ilarity 82.4%; Pred. No. 2.4e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGTGGAATTTGC 17

|||||

CATATGGACTTTGGC 35

6964 51 bp DNA linear GSS 07-JAN-2003

097916.43.45.x Arabidopsis thaliana TDNA insertion lines

idopsis thaliana genomic clone SALK\_097916.43.45.x, genomic

ey sequence.

6964

6964.1 GI:27537676

idopsis thaliana (thale cress)

idopsis thaliana

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

matophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidops  
 1 (bases 1 to 51)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P  
 Shinn, P., Zimmerman, J., and Ecker, J.R.

A sequence-indexed library of insertion mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bord

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .51

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_097916.43.45.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion

/note="PCR was performed on Arabidopsis thaliana

each of which contains one or more TDNA inserti

elements. The resultant fragment for each line

directly sequenced to determine the genomic seq

the site of insertion. Details of the protocols

be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

# ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 51;

Best Local Similarity 82.4%; Pred. No. 2.4e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGTGGAATTTGC 17

|||||

Db 20 CTCATATGGACITTTGCG 36

RESULT 35

BZ766946

LOCUS

DEFINITION

BZ766946 51 bp DNA linear GSS

SALK\_138093.30.10.n Arabidopsis thaliana TDNA insertion

Arabidopsis thaliana genomic clone SALK\_138093.30.10.n,

survey sequence.

ACCESSION BZ766946

VERSION BZ766946.1 GI:28939499

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

rosids; eurosids II; Brassicales; Brassicaceae; Arabidop

1 (bases 1 to 51)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P

Shinn, P., Zimmerman, J., and Ecker, J.R.

A sequence-indexed library of insertion mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bor

TDNA.



s: TDNA tagged.  
 Location/Qualifiers  
 1..51  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_138093.30.10.n"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

67.8%; Score 12.2; DB 28; Length 51;  
 ilarity 82.4%; Pred. NO. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CATTTGGAATTTGTC 17  
 |||||  
 'CATATGGACTTTGCC 48

5493 52 bp DNA linear GSS 05-AUG-2002  
 0398653 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_098653, genomic survey sequence.  
 5493  
 5493.1 GI:22101391

idopsis thaliana (thale cress)  
 idopsis thaliana  
 yryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 (bases 1 to 52)  
 iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 in,P., Zimmerman,J. and Ecker,J.R.  
 sequence-indexed library of insertion mutations in the  
 idopsis Genome  
 ublished (2001)  
 act: Joseph R. Ecker  
 c Institute Genomic Analysis Laboratory (SIGAL)  
 Salk Institute for Biological Studies  
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 : 858 453 4100 x1752  
 : 858 558 6379  
 l: ecker@salk.edu  
 s is single pass sequence recovered from the left border of  
 a. This sequence lies within an annotated exon of At3g3056.  
 ss: TDNA tagged.  
 Location/Qualifiers  
 1..52  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_098653"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

67.8%; Score 12.2; DB 28; Length 52;

Best Local Similarity 82.4%; Pred. NO. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTTGGAAATTTGTC 17  
 |||||  
 Db 21 CTCATATGGACTTTGCC 37

RESULT 37  
 CF048724 54 bp mRNA linear EST  
 LOCUS QCU26f05.yg QCL Zea mays cDNA clone QCU26f05, mRNA sequ  
 ACCESSION CF048724  
 VERSION CF048724.1 GI:32943905  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 54)  
 Genoplante.  
 Genoplante, a major partnership french program in plant  
 Unpublished (2003)  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the  
 plant genomics programme 'Genoplante' (<http://www.genopl>)  
 and <http://genoplante-info.inbio.gen.fr>.  
 Location/Qualifiers  
 1..54  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="F2"  
 /db\_xref="taxon:4577"  
 /clone="QCU26f05"  
 /tissue type="apex"  
 /clone\_lib="QCL"

Query Match 67.8%; Score 12.2; DB 14; Length 54;  
 Best Local Similarity 82.4%; Pred. NO. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTTGGAATTTGCC 18  
 |||||  
 Db 12 TCATTTCGATTTTCCC 28

RESULT 38  
 CF053832 54 bp mRNA linear EST  
 LOCUS QCN2ic11.yg QCN Zea mays cDNA clone QCN2ic11, mRNA sequ  
 ACCESSION CF053832  
 VERSION CF053832.1 GI:33093838  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 54)  
 Genoplante.  
 Genoplante, a major partnership french program in plant  
 Unpublished (2003)  
 Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10

sequence has been generated in the framework of the french genomics programme 'genoplante' (<http://www.genoplante.com>)  
<http://genoplante-info.inbio.gen.fr>.

Location/Qualifiers  
 1..54  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P2"  
 /db\_xref="taxon:4577"  
 /clone="QC21c11"  
 /tissue\_type="apex"  
 /clone\_lib="QC21"  
 67.8%; Score 12.2; DB 14; Length 54;  
 larity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TTTCGAAATTTGGC 18  
 |||||  
 TTTCGATTTTCCC 28  
 961  
 139587.40.90.x Arabidopsis thaliana TDNA insertion lines  
 dopsis thaliana genomic clone SALK\_139587.40.90.x, genomic  
 y sequence.  
 961  
 961.1 GI:28940903  
 dopsis thaliana (thale cress)  
 dopsis thaliana  
 yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 is; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 55)  
 o.J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 nab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 i,P., Zimmerman,J. and Ecker,J.R.  
 uence-Indexed Library of Insertion Mutations in the  
 dopsis Genome  
 lished (2001)  
 ct: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (Signal)  
 alk Institute for Biological Studies  
 ) N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 s: TDNA tagged.  
 Location/Qualifiers  
 1..55  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_139587.40.90.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 67.8%; Score 12.2; DB 28; Length 55;  
 ilarity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTCATTTGGAATTTGC 17  
 |||||  
 Db 24 CTCATATGGACTTTGC 40  
 RESULT 40  
 BZ352570  
 LOCUS  
 DEFINITION  
 SALK\_081150.33.65.x Arabidopsis thaliana TDNA insertion 1  
 Arabidopsis thaliana genomic clone SALK\_081150.33.65.x, 9  
 survey sequence.  
 ACCESSION  
 BZ352570  
 VERSION  
 BZ352570.1 GI:24943432  
 SOURCE  
 Arabidopsis thaliana (thale cress)  
 ORGANISM  
 Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicc  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidops  
 1 (bases 1 to 56)  
 AUTHORS  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P;  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (Signal)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bord  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..56  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_081150.33.65.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 each of which contains one or more TDNA inserti  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)  
 ORIGIN  
 Query Match 67.8%; Score 12.2; DB 28; Length 56;  
 Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTTGGAATTTGC 17  
 |||||  
 Db 25 CTCATATGGACTTTGC 41  
 RESULT 41  
 AU007849  
 LOCUS  
 DEFINITION  
 AU007849 Schizosaccharomyces pombe late log phase cDNA  
 Schizosaccharomyces pombe cDNA clone spc02572, mRNA sequ  
 ACCESSION  
 AU007849  
 VERSION  
 AU007849.1 GI:3344307  
 KEYWORDS  
 EST.  
 SOURCE  
 Schizosaccharomyces pombe (fission yeast)  
 ORGANISM  
 Schizosaccharomyces pombe  
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

zooaccharomycetales; Schizosaccharomycetaceae;  
 bases 1 to 58)  
 myo.M. and Mita.K.  
 ification of expressed sequence tags of Schizosaccharomycetes  
 ublished (1998)  
 act: Mitsuoki Morimyo  
 me Research Group  
 onal Institute of Radiological Sciences  
 Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
 l: morimyo@nirs.go.jp.  
 Location/Qualifiers  
 1. 58  
 /organism="Schizosaccharomycetes pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc02572"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomycetes pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomycetes pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA  
 sequences was not always from 5' to 3'. The cDNA data of  
 Schizosaccharomycetes pombe are available for searching on  
 the World Wide Web. (URL, <http://www.nirs.go.jp>)"

67.8%; Score 12.2; DB 9; Length 58;  
 ilarity 82.4%; Pred. No. 2.3e+05;  
 Conservative 0; Mismatches 3; Indels 0;

TCATTGGCAATTTCG 17  
 |||||  
 TCATTGAATATTGC 26

8039 58 bp mRNA linear EST 31-JUL-1998  
 8039 Schizosaccharomycetes pombe late log phase cDNA  
 .zooaccharomycetes pombe cDNA clone spc02795, mRNA sequence.  
 8039  
 8039.1 GI:3344497  
 .zooaccharomycetes pombe (fission yeast)  
 .zooaccharomycetes pombe  
 ryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 .zooaccharomycetales; Schizosaccharomycetaceae;  
 .zooaccharomycetes.  
 (bases 1 to 58)  
 myo.M. and Mita.K.  
 ification of expressed sequence tags of Schizosaccharomycetes  
 ublished (1998)  
 -act: Mitsuoki Morimyo  
 me Research Group  
 ional Institute of Radiological Sciences  
 Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
 l: morimyo@nirs.go.jp.  
 Location/Qualifiers  
 1. 58  
 /organism="Schizosaccharomycetes pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc02795"  
 /sex="h minus"  
 /clone\_lib="Schizosaccharomycetes pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of  
 Schizosaccharomycetes pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA

## ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 58;  
 Best Local Similarity 82.4%; Pred. No. 2.3e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTCG 17  
 |||||  
 DB 42 CTCATTGAATATTGC 26

## RESULT 43

BZ769782 58 bp DNA linear GSS  
 LOCUS BZ769782  
 DEFINITION SALK\_142715.38.60.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_142715.38.60.x,  
 survey sequence.

ACCESSION BZ769782  
 VERSION BZ769782.1 GI:28943466  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (Chale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 58)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., I  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome

## AUTHORS

Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752

## TITLE

Arabidopsis Genome

## JOURNAL

Unpublished (2001)

## COMMENT

This is single pass sequence recovered from the left bo  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 58  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_142715.38.60.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protocol](http://signal.salk.edu/tdna_protocol)

## FEATURES

source

## ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 58;  
 Best Local Similarity 82.4%; Pred. No. 2.3e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTCG 17  
 |||||  
 DB 25 CTCATATGGCAATTTCG 41

## RESULT 44

BZ765982 59 bp DNA linear GSS  
 LOCUS BZ765982

09:38:23 2004

us-10-090-326-16.max.rst

136100.47.80.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_136100.47.80.x, genomic  
ey sequence.  
5982  
5982.1 GI:28938535  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 59)  
so,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
n,P., Zimmerman,J. and Ecker,J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)  
act: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (SIGnAL)  
Salk Institute for Biological Studies  
O.N. Torrey Pines Road, La Jolla, CA 92037, USA  
958 453 4100 x1752  
858 558 6379  
l: ecker@salk.edu  
is single pass sequence recovered from the left border of  
s: TDNA tagged.  
Location/Qualifiers  
l. 59  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_136100.47.80.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
67.8%; Score 12.2; DB 28; Length 59;  
ilarity 82.4%; Pred. No. 2.3e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CATTTGGATTTCG 17  
CATATGGACTTGGC 44  
1034  
1034.1 GI:19884457  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 60)  
so,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
n,P., Zimmerman,J. and Ecker,J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome

JOURNAL  
COMMENT  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left bor  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
l. 60  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_058410.43.20.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion  
/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA insert  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)  
Query Match 67.8%; Score 12.2; DB 28; Length 60;  
Best Local Similarity 82.4%; Pred. No. 2.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
Qy 1 CTCATTTGGATTTCG 17  
|||||  
Db 28 CTCATATGGACTTGGC 44  
Search completed: February 29, 2004, 11:21:24  
Job time : 1391.17 secs



09:38:23 2004

us-10-090-326-17.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

Local search, using sw model

February 29, 2004, 08:42:24 ; Search time 530.753 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

TS-10-090-326-17

cgagtgaagatccctt 17

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: gb.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pln.\*

35: em.htg.rtd.\*

36: em.htg.mam.\*

37: em.htg.vrt.\*

38: em.sy.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being p  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	13.4	78.8	20	6	AR315288	AR315288
C 2	12.4	72.9	17	6	BD197525	BD197525
C 3	12.4	72.9	17	6	BD197526	BD197526
C 4	12.4	72.9	32	6	I24919	I24919 Se
C 5	12.4	72.9	41	6	AX518499	AX518499
C 6	12.2	71.8	17	6	AX215216	AX215216
C 7	12.2	71.8	24	6	AX443791	AX443791
C 8	12.2	71.8	25	6	AX447772	AX447772
C 9	12.2	71.8	25	6	AX467554	AX467554
C 10	12.2	71.8	36	6	AR285893	AR285893
C 11	12.2	71.8	36	6	AX815952	AX815952
C 12	12.2	71.8	37	6	AR397883	AR397883
C 13	12.2	71.8	38	6	AR286827	AR286827
C 14	12.2	71.8	38	6	AR286885	AR286885
C 15	12.2	71.8	38	6	AR286931	AR286931
C 16	12.2	71.8	38	6	AR286960	AR286960
C 17	12.2	71.8	38	6	AR398817	AR398817
C 18	12.2	71.8	38	6	AR398875	AR398875
C 19	12.2	71.8	38	6	AR398921	AR398921
C 20	12.2	71.8	38	6	AR398950	AR398950
C 21	12.2	71.8	38	6	AX220484	AX220484
C 22	12.2	71.8	38	6	AX228757	AX228757
C 23	12.2	71.8	38	6	AX273935	AX273935
C 24	12.2	71.8	38	6	AX425294	AX425294
C 25	12.2	71.8	38	6	AX463628	AX463628
C 26	12.2	71.8	40	6	AX805954	AX805954
C 27	12.2	71.8	46	6	AR126440	AR126440
C 28	12	70.6	17	6	AX759214	AX759214
C 29	12	70.6	17	6	AX762760	AX762760
C 30	12	70.6	26	6	AX753432	AX753432
C 31	12	70.6	31	6	E59836	E59836 Me
C 32	12	70.6	31	6	AR340181	AR340181
C 33	12	70.6	38	6	AX135624	AX135624
C 34	12	70.6	43	6	I71937	I71937 Se
C 35	11.8	69.4	17	6	AX216871	AX216871
C 36	11.8	69.4	20	6	AX296625	AX296625
C 37	11.8	69.4	20	6	AX537893	AX537893
C 38	11.8	69.4	24	6	AX291992	AX291992
C 39	11.8	69.4	27	6	A57409	A57409 Se
C 40	11.8	69.4	27	6	AR131454	AR131454
C 41	11.8	69.4	33	6	BD273188	BD273188
C 42	11.8	69.4	33	6	AR381516	AR381516
C 43	11.8	69.4	33	6	AX474382	AX474382
C 44	11.8	69.4	33	6	BD073213	BD073213
C 45	11.8	69.4	33	6	BD181899	BD181899
C 46	11.8	69.4	35	11	C75890	C75890 H
C 47	11.8	69.4	46	6	A01315	A01315 H.
C 48	11.8	69.4	46	6	A01316	A01316 H.
C 49	11.8	69.4	50	6	AR210368	AR210368
C 50	11.8	69.4	52	6	AR356147	AR356147
C 51	11.8	69.4	57	6	BD074138	BD074138
C 52	11.4	67.1	17	6	I37628	I37628 Se
C 53	11.4	67.1	17	6	I94478	I94478 Se
C 54	11.4	67.1	17	6	AX217232	AX217232
C 55	11.4	67.1	17	6	AX217233	AX217233
C 56	11.4	67.1	17	6	BD197527	BD197527
C 57	11.4	67.1	20	6	AR312818	AR312818
C 58	11.4	67.1	20	6	AR314161	AR314161
C 59	11.4	67.1	20	6	AR315815	AR315815
C 60	11.4	67.1	21	6	AR263717	AR263717
C 61	11.4	67.1	21	6	AX282174	AX282174
C 62	11.4	67.1	21	6	AX282283	AX282283
C 63	11.4	67.1	21	6	AX322934	AX322934
C 64	11.4	67.1	22	6	AX454914	AX454914
C 65	11.4	67.1	23	6	AX211678	AX211678

67.1	26	6	AR122725	AR122725 Sequence	139	11.2	65.9	38	6	AR399019	AR399019
67.1	29	6	BD270473	BD270473 Synthetic	140	11.2	65.9	38	6	AR399043	AR399043
67.1	29	6	AX039225	AX039225 Sequence	141	11.2	65.9	38	6	AR399071	AR399071
67.1	29	6	AX039306	AX039306 Sequence	142	11.2	65.9	38	6	AR399080	AR399080
67.1	29	6	AX039515	AX039515 Sequence	143	11.2	65.9	38	6	AX220488	AX220488
67.1	29	6	BD103468	BD103468 Methods a	144	11.2	65.9	38	6	AX220521	AX220521
67.1	30	6	AX698766	AX698766 Sequence	145	11.2	65.9	38	6	AX223173	AX223173
67.1	33	6	BD266668	BD266668 Death dom	146	11.2	65.9	38	6	AX273941	AX273941
67.1	33	6	AR183734	AR183734 Sequence	147	11.2	65.9	38	6	AX273987	AX273987
67.1	33	6	AR235742	AR235742 Sequence	148	11.2	65.9	38	6	AX274016	AX274016
67.1	33	6	BD056815	BD056815 Death dom	149	11.2	65.9	38	6	AX25318	AX25318
67.1	35	6	BD247628	BD247628 A method	150	11.2	65.9	38	6	AX425438	AX425438
67.1	35	6	AR345097	AR345097 Sequence	151	11.2	65.9	38	6	AX425447	AX425447
67.1	36	6	I74525	I74525 Sequence 29	152	11.2	65.9	39	6	AR018945	AR018945
67.1	37	6	AX481790	AX481790 Sequence	153	11.2	65.9	39	6	AR066573	AR066573
67.1	40	6	E13253	E13253 Oligonucleo	154	11.2	65.9	39	6	I72290	I72290
67.1	41	6	AR161440	AR161440 Sequence	155	11.2	65.9	39	6	I76857	I76857
67.1	41	6	I81456	I81456 Sequence 15	156	11.2	65.9	42	6	AX614944	AX614944
67.1	42	6	AR161439	AR161439 Sequence	157	11.2	65.9	43	6	AX6303	AX6303
67.1	42	6	I81455	I81455 Sequence 14	158	11.2	65.9	43	6	AX6307	AX6307
67.1	42	6	AR263729	AR263729 Sequence	159	11.2	65.9	43	6	AR0184	AR0184
67.1	42	6	AX282186	AX282186 Sequence	160	11.2	65.9	43	6	AR0188	AR0188
67.1	42	6	AX282295	AX282295 Sequence	161	11.2	65.9	47	6	AR2317	AR2317
67.1	42	6	AX322294	AX322294 Sequence	162	11.2	65.9	51	6	AR404988	AR404988
67.1	45	6	I45552	I45552 Sequence 1	163	11.2	65.9	51	6	AX158926	AX158926
67.1	45	6	I45561	I45561 Sequence 10	164	11.2	65.9	51	6	AX441334	AX441334
67.1	47	6	AR288849	AR288849 Sequence	165	11.2	65.9	51	6	BD171635	BD171635
67.1	47	6	AR292007	AR292007 Sequence	166	11.2	65.9	54	6	AX776474	AX776474
65.9	20	6	AR297233	AR297233 Sequence	167	11.2	65.9	55	6	AX485766	AX485766
65.9	20	6	AR312449	AR312449 Sequence	168	11.2	65.9	56	9	HUMTCRVJ22	HUMTCRVJ22
65.9	20	6	AX297421	AX297421 Sequence	169	11.2	65.9	58	4	AF330204	AF330204
65.9	20	6	BD102630	BD102630 L-Glutama	170	11.2	65.9	60	6	AR118197	AR118197
65.9	22	6	I46707	I46707 Sequence 68	171	11.2	65.9	60	6	AR337357	AR337357
65.9	22	6	I46708	I46708 Sequence 68	172	11.2	65.9	60	6	AR372205	AR372205
65.9	22	6	I46710	I46710 Sequence 68	173	11.2	65.9	60	6	BD130717	BD130717
65.9	22	6	I46711	I46711 Sequence 69	174	11	64.7	15	6	AR180491	AR180491
65.9	24	6	I07719	I07719 Sequence 24	175	11	64.7	17	6	AX649518	AX649518
65.9	24	6	AX232788	AX232788 Sequence	176	11	64.7	17	6	AX649519	AX649519
65.9	26	6	A23966	A23966 Vacuolar AT	177	11	64.7	17	6	AX649520	AX649520
65.9	28	6	AX252348	AX252348 Sequence	178	11	64.7	17	6	AX649521	AX649521
65.9	30	6	A97150	A97150 Sequence 6	179	11	64.7	17	6	AX649522	AX649522
65.9	30	6	I29845	I29845 Sequence 31	180	11	64.7	17	6	AX649523	AX649523
65.9	30	6	AX792853	AX792853 Sequence	181	11	64.7	17	6	AX649524	AX649524
65.9	31	6	AR018946	AR018946 Sequence	182	11	64.7	17	6	AX725133	AX725133
65.9	31	6	AR066574	AR066574 Sequence	183	11	64.7	17	6	AX726680	AX726680
65.9	31	6	I72291	I72291 Sequence 74	184	11	64.7	17	6	AX761621	AX761621
65.9	31	6	I76858	I76858 Sequence 74	185	11	64.7	17	6	BD168809	BD168809
65.9	33	6	AX611962	AX611962 Sequence	186	11	64.7	17	6	BD178165	BD178165
65.9	36	6	A29215	A29215 Oligonucleo	187	11	64.7	20	6	AR315439	AR315439
65.9	37	6	E36454	E36454 DNA polymer	188	11	64.7	21	6	AX033430	AX033430
65.9	37	6	I13355	I13355 Sequence 12	189	11	64.7	21	6	BD088182	BD088182
65.9	37	6	AR286801	AR286801 Sequence	190	11	64.7	21	12	AB069005	AB069005
65.9	38	6	AR286806	AR286806 Sequence	191	11	64.7	25	6	AX651022	AX651022
65.9	38	6	AR286846	AR286846 Sequence	192	11	64.7	25	6	AX651023	AX651023
65.9	38	6	AR286864	AR286864 Sequence	193	11	64.7	25	6	AX651024	AX651024
65.9	38	6	AR286900	AR286900 Sequence	194	11	64.7	25	6	AX651025	AX651025
65.9	38	6	AR286903	AR286903 Sequence	195	11	64.7	25	6	AX651026	AX651026
65.9	38	6	AR286905	AR286905 Sequence	196	11	64.7	25	6	AX651027	AX651027
65.9	38	6	AR286929	AR286929 Sequence	197	11	64.7	25	6	AX651028	AX651028
65.9	38	6	AR287020	AR287020 Sequence	198	11	64.7	25	6	AX651029	AX651029
65.9	38	6	AR287029	AR287029 Sequence	199	11	64.7	25	6	AX651030	AX651030
65.9	38	6	AR287053	AR287053 Sequence	200	11	64.7	25	6	AX651031	AX651031
65.9	38	6	AR287081	AR287081 Sequence	201	11	64.7	25	6	AX651032	AX651032
65.9	38	6	AR287090	AR287090 Sequence	202	11	64.7	25	6	AX651033	AX651033
65.9	38	6	AR398791	AR398791 Sequence	203	11	64.7	25	6	AX651034	AX651034
65.9	38	6	AR398796	AR398796 Sequence	204	11	64.7	25	6	AX651035	AX651035
65.9	38	6	AR398836	AR398836 Sequence	205	11	64.7	25	6	AX651036	AX651036
65.9	38	6	AR398854	AR398854 Sequence	206	11	64.7	28	6	AR170364	AR170364
65.9	38	6	AR398890	AR398890 Sequence	207	11	64.7	28	6	BD233814	BD233814
65.9	38	6	AR398893	AR398893 Sequence	208	11	64.7	28	6	BD237164	BD237164
65.9	38	6	AR398895	AR398895 Sequence	209	11	64.7	28	6	I19818	I19818
65.9	38	6	AR398919	AR398919 Sequence	210	11	64.7	28	6	I19819	I19819
65.9	38	6	AR399010	AR399010 Sequence	211	11	64.7	28	6	I19869	I19869

64.7	28	6	I19870	I19870 Sequence 10	285	10.8	63.5	33	6	AR126131	AR126131
64.7	28	6	I20278	I20278 Sequence 48	c 286	10.8	63.5	33	6	AX062294	AX062294
64.7	28	6	I20279	I20279 Sequence 49	287	10.8	63.5	34	6	AX283668	AX283668
64.7	28	6	I20329	I20329 Sequence 99	c 288	10.8	63.5	38	6	A23776	A23776 C
64.7	28	6	I20330	I20330 Sequence 10	289	10.8	63.5	38	6	A41604	A41604 S
64.7	28	6	AR199695	AR199695 Sequence	290	10.8	63.5	38	6	A95666	A95666 S
64.7	28	6	AR221340	AR221340 Sequence	291	10.8	63.5	38	6	A95708	A95708 S
64.7	28	6	BD075106	BD075106 MAGE-3 pe	292	10.8	63.5	38	6	A95750	A95750 S
64.7	33	6	A69040	A69040 Sequence 28	293	10.8	63.5	38	6	A95792	A95792 S
64.7	33	6	AR193490	AR193490 Sequence	294	10.8	63.5	38	6	AR116283	AR116283
64.7	33	6	BD006117	BD006117 Feline po	c 295	10.8	63.5	38	6	I26306	I26306 S
64.7	41	6	AX517090	AX517090 Sequence	c 296	10.8	63.5	38	6	I47762	I47762 S
64.7	41	6	AX519619	AX519619 Sequence	c 297	10.8	63.5	38	6	I64634	I64634 S
64.7	42	6	BD266496	BD266496 Universal	298	10.8	63.5	38	6	147762	147762
64.7	48	6	AX426329	AX426329 Sequence	299	10.8	63.5	39	6	AX053634	AX053634
64.7	50	6	AR032527	AR032527 Sequence	300	10.8	63.5	40	6	AR053634	AR053634
64.7	50	6	I29267	I29267 Sequence 13	301	10.8	63.5	40	6	AR258569	AR258569
64.7	50	6	I90941	I90941 Sequence 13	302	10.8	63.5	41	6	AX514068	AX514068
64.7	50	6	AR209191	AR209191 Sequence	c 303	10.8	63.5	41	6	AX514189	AX514189
64.7	50	6	I82053	I82053 Sequence 3	c 304	10.8	63.5	41	6	AX519048	AX519048
64.7	17	6	AR191860	AR191860 Sequence	c 305	10.8	63.5	41	6	AX520222	AX520222
64.7	17	6	AR325755	AR325755 Sequence	306	10.8	63.5	42	6	BD209218	BD209218
64.7	18	6	E32527	E32527 Scavenger r	c 307	10.8	63.5	43	6	AR035251	AR035251
64.7	20	6	AR085483	AR085483 Sequence	c 308	10.8	63.5	43	6	AR035252	AR035252
64.7	20	6	E40657	E40657 Antihuman F	c 309	10.8	63.5	43	6	AR107121	AR107121
64.7	20	6	AR281890	AR281890 Sequence	c 310	10.8	63.5	43	6	AR107122	AR107122
64.7	20	6	AR312525	AR312525 Sequence	c 311	10.8	63.5	43	6	AR112712	AR112712
64.7	20	6	AR315443	AR315443 Sequence	c 312	10.8	63.5	43	6	AR112713	AR112713
64.7	20	6	AR315544	AR315544 Sequence	c 313	10.8	63.5	43	6	AR169883	AR169883
64.7	20	6	AR427881	AR427881 Sequence	c 314	10.8	63.5	43	6	I73533	I73533 S
64.7	20	6	AX018881	AX018881 Sequence	c 315	10.8	63.5	43	6	I73534	I73534 S
64.7	20	6	AX018896	AX018896 Sequence	c 316	10.8	63.5	45	6	A40305	A40305 S
64.7	20	6	AX018913	AX018913 Sequence	c 317	10.8	63.5	45	6	A84478	A84478 S
64.7	20	6	AX018928	AX018928 Sequence	c 318	10.8	63.5	45	6	A95463	A95463 S
64.7	20	6	AX019042	AX019042 Sequence	c 319	10.8	63.5	45	6	AR144895	AR144895
64.7	20	6	AX117394	AX117394 Sequence	c 320	10.8	63.5	45	6	AR177526	AR177526
64.7	20	6	AX295460	AX295460 Sequence	c 321	10.8	63.5	45	6	BD267924	BD267924
64.7	20	6	AX329282	AX329282 Sequence	c 322	10.8	63.5	45	6	AR279936	AR279936
64.7	20	6	AX394375	AX394375 Sequence	c 323	10.8	63.5	45	6	AR361783	AR361783
64.7	20	6	AX590794	AX590794 Sequence	c 324	10.8	63.5	45	6	AX010327	AX010327
64.7	20	6	AX741290	AX741290 Sequence	c 325	10.8	63.5	45	6	AX329066	AX329066
64.7	20	6	BD091320	BD091320 Dull1 cod	c 326	10.8	63.5	45	6	AX427377	AX427377
64.7	20	6	BD170190	BD170190 Method of	c 327	10.8	63.5	45	6	BD082558	BD082558
64.7	21	6	AX094962	AX094962 Sequence	c 328	10.8	63.5	45	6	BD124117	BD124117
64.7	21	6	BD134579	BD134579 Method fo	c 329	10.8	63.5	45	6	BD177969	BD177969
64.7	22	6	AR207707	AR207707 Sequence	c 330	10.8	63.5	46	6	E63262	E63262 Co
64.7	22	6	AR265033	AR265033 Sequence	331	10.8	63.5	46	6	AX612094	AX612094
64.7	22	6	AX696164	AX696164 Sequence	332	10.8	63.5	46	6	AX612095	AX612095
64.7	23	6	BD094035	BD094035 A novel p	333	10.8	63.5	46	6	AX612096	AX612096
64.7	24	6	A49391	A49391 Sequence 9	334	10.8	63.5	46	6	AX612097	AX612097
64.7	24	6	A65736	A65736 Sequence 17	335	10.8	63.5	46	6	AX612099	AX612099
64.7	24	6	AR176297	AR176297 Sequence	336	10.8	63.5	46	6	AX614571	AX614571
64.7	25	6	AX290827	AX290827 Sequence	c 337	10.8	63.5	46	6	BD133457	BD133457
64.7	25	6	AR170299	AR170299 Sequence	c 338	10.8	63.5	46	6	BD133468	BD133468
64.7	25	6	E51073	E51073 Novel Esche	339	10.8	63.5	47	6	AR288782	AR288782
64.7	25	6	AX007127	AX007127 Sequence	c 340	10.8	63.5	47	6	AX194947	AX194947
64.7	25	6	AX521586	AX521586 Sequence	c 341	10.8	63.5	47	6	AX302472	AX302472
64.7	29	6	AR146958	AR146958 Sequence	c 342	10.8	63.5	48	6	AR007502	AR007502
64.7	29	6	I24909	I24909 Sequence 50	343	10.8	63.5	48	6	AX614572	AX614572
64.7	29	6	AR222155	AR222155 Sequence	344	10.8	63.5	50	6	AX199566	AX199566
64.7	30	6	I35737	I35737 Sequence 1	345	10.8	63.5	50	6	AX485734	AX485734
64.7	30	6	I95599	I95599 Sequence 1	346	10.8	63.5	50	6	AX697162	AX697162
64.7	30	6	AR211352	AR211352 Sequence	c 347	10.8	63.5	50	6	AX923414	AX923414
64.7	30	6	AR430800	AR430800 Sequence	c 348	10.8	63.5	51	6	E14328	E14328 P
64.7	30	6	AX235827	AX235827 Sequence	349	10.8	63.5	51	6	AX116621	AX116621
64.7	30	6	AX791760	AX791760 Sequence	c 350	10.8	63.5	51	6	AX157031	AX157031
64.7	30	6	AX793046	AX793046 Sequence	c 351	10.8	63.5	51	6	AX157032	AX157032
64.7	30	6	BD016830	BD016830 Novel cyt	c 352	10.8	63.5	51	6	AX157033	AX157033
64.7	30	6	BD161108	BD161108 N-Acetyl	c 353	10.8	63.5	51	6	AX199084	AX199084
64.7	31	6	AR022300	AR022300 Sequence	354	10.8	63.5	51	6	AX199565	AX199565
64.7	31	6	AX615155	AX615155 Sequence	c 355	10.8	63.5	51	6	AX204077	AX204077
64.7	31	6	AX754987	AX754987 Sequence	c 356	10.8	63.5	51	6	AX612493	AX612493
64.7	32	6	A10251	A10251 Oligonucleo	357	10.8	63.5	54	6	A01255	A01255 Nu



63.5	54	6	A01256	A01256 (reverse co	431	10.6	62.4	38	6	AR287084	AR287084
63.5	54	6	A01268	A01268 Nucleotide	432	10.6	62.4	38	6	AR287105	AR287105
63.5	54	6	A01269	A01269 (reverse co	433	10.6	62.4	38	6	AR398582	AR398582
63.5	54	6	A13102	A13102 Nucleotide	434	10.6	62.4	38	6	AR398693	AR398693
63.5	54	6	A13103	A13103 Nucleotide	435	10.6	62.4	38	6	AR398713	AR398713
63.5	54	6	A18344	A18344 BIN19 polyI	436	10.6	62.4	38	6	AR398730	AR398730
63.5	55	6	A18345	A18345 Primer DNA	437	10.6	62.4	38	6	AR398806	AR398806
63.5	55	6	AR365150	AR365150 Sequence	438	10.6	62.4	38	6	AR398811	AR398811
63.5	55	6	AX521528	AX521528 Sequence	439	10.6	62.4	38	6	AR398822	AR398822
63.5	55	11	AX296254	AX296254 Arabidops	440	10.6	62.4	38	6	AR398826	AR398826
63.5	58	10	AF357503	AF357503 Mus muscu	441	10.6	62.4	38	6	AR398874	AR398874
63.5	60	6	A33490	A33490 Synthetic p	442	10.6	62.4	38	6	AR398903	AR398903
63.5	60	6	AR118183	AR118183 Sequence	443	10.6	62.4	38	6	AR398909	AR398909
63.5	60	6	BD232441	BD232441 Antibodie	444	10.6	62.4	38	6	AR398974	AR398974
63.5	60	6	I42386	I42386 Sequence 15	445	10.6	62.4	38	6	AR399024	AR399024
63.5	60	6	AR337343	AR337343 Sequence	446	10.6	62.4	38	6	AR399029	AR399029
63.5	60	6	AR372191	AR372191 Sequence	447	10.6	62.4	38	6	AR399045	AR399045
63.5	60	6	AX010631	AX010631 Sequence	448	10.6	62.4	38	6	AR399074	AR399074
63.5	60	6	AX657142	AX657142 Sequence	449	10.6	62.4	38	6	AR399095	AR399095
63.5	60	6	BD130703	BD130703 High-affi	450	10.6	62.4	38	6	AX220166	AX220166
63.5	60	6	BD134501	BD134501 Lipopolys	451	10.6	62.4	38	6	AX220225	AX220225
63.5	60	12	SYNLTKSD	MI3108 Mouse I cel	452	10.6	62.4	38	6	AX220302	AX220302
62.4	18	6	I66349	I66349 Sequence 8	453	10.6	62.4	38	6	AX220335	AX220335
62.4	19	6	AR298314	AR298314 Sequence	454	10.6	62.4	38	6	AX220379	AX220379
62.4	20	6	AR016139	AR016139 Sequence	455	10.6	62.4	38	6	AX220392	AX220392
62.4	20	6	AR019137	AR019137 Sequence	456	10.6	62.4	38	6	AX220395	AX220395
62.4	20	6	E14591	E14591 PCR primer	457	10.6	62.4	38	6	AX220414	AX220414
62.4	20	6	AR350258	AR350258 Sequence	458	10.6	62.4	38	6	AX220420	AX220420
62.4	21	6	AX096571	AX096571 Sequence	459	10.6	62.4	38	6	AX220454	AX220454
62.4	21	6	AX153989	AX153989 Sequence	460	10.6	62.4	38	6	AX220455	AX220455
62.4	22	6	AR211944	AR211944 Sequence	461	10.6	62.4	38	6	AX220507	AX220507
62.4	22	6	AX244545	AX244545 Sequence	462	10.6	62.4	38	6	AX220512	AX220512
62.4	23	6	BD078733	BD078733 B type DN	463	10.6	62.4	38	6	AX223075	AX223075
62.4	23	6	BD170322	BD170322 Novel pol	464	10.6	62.4	38	6	AX223086	AX223086
62.4	24	6	A48486	A48486 Sequence 7	465	10.6	62.4	38	6	AX223101	AX223101
62.4	24	6	AX206737	AX206737 Sequence	466	10.6	62.4	38	6	AX223156	AX223156
62.4	24	6	AX166709	AX166709 Sequence	467	10.6	62.4	38	6	AX228654	AX228654
62.4	25	6	AX241132	AX241132 Sequence	468	10.6	62.4	38	6	AX228673	AX228673
62.4	25	6	AX486739	AX486739 Sequence	469	10.6	62.4	38	6	AX228712	AX228712
62.4	27	6	I04705	I04705 sequence 29	470	10.6	62.4	38	6	AX228713	AX228713
62.4	28	6	BD176660	BD176660 Promoter.	471	10.6	62.4	38	6	AX228778	AX228778
62.4	31	6	AR211939	AR211939 Sequence	472	10.6	62.4	38	6	AX273921	AX273921
62.4	31	6	AX248207	AX248207 Sequence	473	10.6	62.4	38	6	AX273924	AX273924
62.4	33	6	AR169342	AR169342 Sequence	474	10.6	62.4	38	6	AX273973	AX273973
62.4	33	6	I66358	I66358 Sequence 17	475	10.6	62.4	38	6	AX274017	AX274017
62.4	34	6	AR242786	AR242786 Sequence	476	10.6	62.4	38	6	AX425201	AX425201
62.4	34	6	AR261523	AR261523 Sequence	477	10.6	62.4	38	6	AX425213	AX425213
62.4	34	6	AR285929	AR285929 Sequence	478	10.6	62.4	38	6	AX425220	AX425220
62.4	35	6	AR000139	AR000139 Sequence	479	10.6	62.4	38	6	AX425300	AX425300
62.4	35	6	I66253	I66253 Sequence 5	480	10.6	62.4	38	6	AX425321	AX425321
62.4	35	6	AR397919	AR397919 Sequence	481	10.6	62.4	38	6	AX425324	AX425324
62.4	35	11	C75907	C75907 Homo sapien	482	10.6	62.4	38	6	AX425376	AX425376
62.4	36	6	AR033955	AR033955 Sequence	483	10.6	62.4	38	6	AX425388	AX425388
62.4	36	6	AR175088	AR175088 Sequence	484	10.6	62.4	38	6	AX425429	AX425429
62.4	36	6	AR285904	AR285904 Sequence	485	10.6	62.4	38	6	AX425433	AX425433
62.4	36	6	AX032536	AX032536 Sequence	486	10.6	62.4	38	6	BD012178	BD012178
62.4	37	6	AR397894	AR397894 Sequence	487	10.6	62.4	40	6	AR3621 St	AR3621 St
62.4	37	6	AX581915	AX581915 Sequence	488	10.6	62.4	40	6	BD166453	BD166453
62.4	38	6	AR286532	AR286532 Sequence	489	10.6	62.4	41	6	AX514811	AX514811
62.4	38	6	AR286703	AR286703 Sequence	490	10.6	62.4	41	6	AX517169	AX517169
62.4	38	6	AR286723	AR286723 Sequence	491	10.6	62.4	44	6	I75987 St	I75987 St
62.4	38	6	AR286740	AR286740 Sequence	492	10.6	62.4	47	6	BD124134	BD124134
62.4	38	6	AR286816	AR286816 Sequence	493	10.6	62.4	48	6	AX391335	AX391335
62.4	38	6	AR286821	AR286821 Sequence	494	10.6	62.4	50	6	AX164969	AX164969
62.4	38	6	AR286832	AR286832 Sequence	495	10.6	62.4	50	6	AX277229	AX277229
62.4	38	6	AR286836	AR286836 Sequence	496	10.6	62.4	51	6	AX000112	AX000112
62.4	38	6	AR286884	AR286884 Sequence	497	10.6	62.4	51	6	AX000229	AX000229
62.4	38	6	AR286913	AR286913 Sequence	498	10.6	62.4	51	6	AX158452	AX158452
62.4	38	6	AR286919	AR286919 Sequence	499	10.6	62.4	51	6	AX159567	AX159567
62.4	38	6	AR286984	AR286984 Sequence	500	10.6	62.4	51	6	AX280272	AX280272
62.4	38	6	AR287034	AR287034 Sequence	501	10.6	62.4	51	6	BD271119	BD271119
62.4	38	6	AR287039	AR287039 Sequence	502	10.6	62.4	54	6	BD271125	BD271125
62.4	38	6	AR287055	AR287055 Sequence	503	10.6	62.4	54	6	BD271125	BD271125

09:38:23 2004

us-10-090-326-17.max.rge

62.4	54	6	AX000113	Sequence	C 577	10.4	61.2	24	6	AX444730	AX444730
62.4	54	6	AX000230	Sequence	578	10.4	61.2	24	6	AX922624	AX922624
62.4	54	9	AF305521	Homo sapi	579	10.4	61.2	24	6	BD017385	BD017385
62.4	57	6	E30631	Antibody an	580	10.4	61.2	25	6	A97532	A97532
62.4	57	6	E31240	Device for	581	10.4	61.2	25	6	AR239182	AR239182
62.4	59	6	AR031481	Sequence	C 582	10.4	61.2	25	6	AR350155	AR350155
62.4	59	6	AR031481	Sequence	583	10.4	61.2	25	6	AX278984	AX278984
62.4	59	6	AR031481	Sequence	584	10.4	61.2	25	6	AX281070	AX281070
62.4	59	6	AR374547	Sequence	C 585	10.4	61.2	25	6	AX322634	AX322634
62.4	59	6	AR374547	Sequence	586	10.4	61.2	25	6	AX609392	AX609392
62.4	60	6	AR031473	Sequence	C 587	10.4	61.2	25	6	AX683285	AX683285
62.4	60	6	AR031473	Sequence	C 588	10.4	61.2	26	6	BD170718	BD170718
62.4	60	6	AR374539	Sequence	C 589	10.4	61.2	27	6	AR002481	AR002481
62.4	60	6	AR374539	Sequence	590	10.4	61.2	27	6	AX455011	AX455011
61.2	12	6	AR121279	Sequence	591	10.4	61.2	27	6	AX742862	AX742862
61.2	12	6	AR139766	Sequence	C 592	10.4	61.2	28	9	S80742	S80742
61.2	12	6	AR165225	Sequence	C 593	10.4	61.2	29	6	AR135344	AR135344
61.2	12	6	BD231392	Isolated	C 594	10.4	61.2	29	6	I46773	I46773
61.2	12	6	I13332	Sequence 6	595	10.4	61.2	29	6	I95021	I95021
61.2	12	6	I19025	Sequence 6	C 596	10.4	61.2	30	6	AR086689	AR086689
61.2	12	6	AR201396	Sequence	C 597	10.4	61.2	30	6	AX766127	AX766127
61.2	12	6	AR208444	Sequence	C 598	10.4	61.2	31	6	AX248154	AX248154
61.2	12	6	AR225779	Sequence	599	10.4	61.2	31	6	AX248439	AX248439
61.2	12	6	AR230328	Sequence	C 600	10.4	61.2	31	6	AX440501	AX440501
61.2	12	6	AR243310	Sequence	C 601	10.4	61.2	31	6	BD016882	BD016882
61.2	12	6	AR264185	Sequence	C 602	10.4	61.2	32	6	AR000590	AR000590
61.2	12	6	AR279228	Sequence	C 603	10.4	61.2	32	6	AR174604	AR174604
61.2	12	6	AR310023	Sequence	C 604	10.4	61.2	32	6	AR174613	AR174613
61.2	12	6	AR339823	Sequence	C 605	10.4	61.2	32	6	AR174615	AR174615
61.2	12	6	AR350435	Sequence	C 606	10.4	61.2	32	6	BD248997	BD248997
61.2	12	6	AX023542	Sequence	C 607	10.4	61.2	32	6	BD249006	BD249006
61.2	12	6	AX301752	Sequence	C 608	10.4	61.2	32	6	BD249008	BD249008
61.2	12	6	AX347896	Sequence	C 609	10.4	61.2	32	6	BD208903	BD208903
61.2	12	6	AX348103	Sequence	C 610	10.4	61.2	32	6	AR374096	AR374096
61.2	12	6	AX384672	Sequence	C 611	10.4	61.2	32	6	AR374105	AR374105
61.2	12	6	AX459952	Sequence	C 612	10.4	61.2	32	6	AR374107	AR374107
61.2	12	6	AX470044	Sequence	C 613	10.4	61.2	33	6	A31501	A31501
61.2	12	6	BD016444	Gene deri	C 614	10.4	61.2	33	6	AR004756	AR004756
61.2	12	6	BD080840	Aschma-re	C 615	10.4	61.2	33	6	AR085171	AR085171
61.2	12	6	BD082008	Aschma as	C 616	10.4	61.2	33	6	BD235483	BD235483
61.2	12	6	BD086212	Transcrip	C 617	10.4	61.2	33	6	E12453	E12453
61.2	12	6	BD106871	Isolated	C 618	10.4	61.2	33	6	AR256883	AR256883
61.2	12	6	BD195210	Method fo	C 619	10.4	61.2	33	6	AX085550	AX085550
61.2	12	6	BD223679	Leptin-me	C 620	10.4	61.2	33	6	BD062058	BD062058
61.2	17	6	I37629	Sequence 64	C 621	10.4	61.2	34	6	AR218090	AR218090
61.2	17	6	I94479	Sequence 64	C 622	10.4	61.2	35	6	AR016271	AR016271
61.2	17	6	AR192089	Sequence	C 623	10.4	61.2	35	6	AR016273	AR016273
61.2	17	6	AR192090	Sequence	C 624	10.4	61.2	35	6	AX084255	AX084255
61.2	17	6	AR325971	Sequence	C 625	10.4	61.2	36	6	A65536	A65536
61.2	17	6	AR325972	Sequence	C 626	10.4	61.2	36	6	AX407218	AX407218
61.2	17	6	AX217231	Sequence	C 627	10.4	61.2	36	6	AX755153	AX755153
61.2	17	6	AX419971	Sequence	C 628	10.4	61.2	36	6	AX755164	AX755164
61.2	17	6	AX736810	Sequence	C 629	10.4	61.2	37	6	BD161877	BD161877
61.2	17	6	AX760374	Sequence	C 630	10.4	61.2	38	6	AR000588	AR000588
61.2	17	6	BD197528	Method an	C 631	10.4	61.2	38	6	AR208901	AR208901
61.2	18	6	AR110042	Sequence	C 632	10.4	61.2	38	6	AX244434	AX244434
61.2	18	6	AX029247	Sequence	C 633	10.4	61.2	40	6	E37760	E37760
61.2	18	6	BD008906	High leve	C 634	10.4	61.2	41	6	AX514878	AX514878
61.2	18	12	AB069423	Synthetic	C 635	10.4	61.2	41	6	AX517020	AX517020
61.2	19	6	AX202442	Sequence	C 636	10.4	61.2	41	6	AX519531	AX519531
61.2	20	6	I79517	Sequence 8	C 637	10.4	61.2	41	6	AX520176	AX520176
61.2	20	6	AR313886	Sequence	C 638	10.4	61.2	41	6	AX520177	AX520177
61.2	20	6	AX453690	Sequence	C 639	10.4	61.2	42	6	A76875	A76875
61.2	20	6	BD128225	Primer fo	C 640	10.4	61.2	44	3	CCA427066	CCA427066
61.2	20	11	DOGDCN1B	I77441 Canis fami	C 641	10.4	61.2	44	3	CCA427078	CCA427078
61.2	22	6	AX106989	Sequence 6	C 642	10.4	61.2	45	9	HSBIA1G1B	HSBIA1G1B
61.2	23	6	I13182	Sequence 6	C 643	10.4	61.2	46	6	AX612098	AX612098
61.2	23	6	BD012531	Inhibitor	C 644	10.4	61.2	47	6	AR288486	AR288486
61.2	23	6	BD017007	Detection	C 645	10.4	61.2	47	6	AR289580	AR289580
61.2	24	6	AR070885	Sequence	C 646	10.4	61.2	47	6	AR291043	AR291043
61.2	24	6	AR088622	Sequence	C 647	10.4	61.2	48	6	A13267	A13267
61.2	24	6	AR122727	Sequence	C 648	10.4	61.2	48	6	I09475	I09475
61.2	24	6	E11770	Synthetic o	C 649	10.4	61.2	49	6	A13268	A13268
61.2	24	6	AR429447	Sequence							

61.2	49	6	I09476	723	10.2	60.0	24	6	AX443815	AX443811
61.2	49	6	AR239838	724	10.2	60.0	25	6	AR069348	AR069348
61.2	49	6	AX279640	725	10.2	60.0	25	6	164565	164565
61.2	50	6	A13269	726	10.2	60.0	25	6	AX259784	AX259784
61.2	50	6	I09477	727	10.2	60.0	25	6	AX34981	AX34981
61.2	51	6	AX165529	728	10.2	60.0	25	6	AX354438	AX354438
61.2	51	6	AX165586	729	10.2	60.0	25	6	AX447739	AX447739
61.2	51	9	HSDCRV08	730	10.2	60.0	25	6	AX447796	AX447796
61.2	51	10	AF005611	731	10.2	60.0	25	6	AX650588	AX650588
61.2	53	6	A14920	732	10.2	60.0	25	6	AX650589	AX650589
61.2	53	6	A14921	733	10.2	60.0	25	6	AX650590	AX650590
61.2	57	6	AR075442	734	10.2	60.0	25	6	AX650591	AX650591
61.2	57	6	AR174607	735	10.2	60.0	25	6	AX650592	AX650592
61.2	57	6	BD249000	736	10.2	60.0	25	6	AX650593	AX650593
61.2	57	6	AR374099	737	10.2	60.0	25	6	AX650594	AX650594
61.2	57	6	AX277164	738	10.2	60.0	25	6	AX650595	AX650595
61.2	57	9	AF234185	739	10.2	60.0	25	6	AX650596	AX650596
61.2	60	6	E22195	740	10.2	60.0	25	6	AX650597	AX650597
61.2	60	6	E35599	741	10.2	60.0	25	6	AX650598	AX650598
61.2	17	6	152069	742	10.2	60.0	26	6	AR199674	AR199674
60.0	17	6	AX215217	743	10.2	60.0	27	6	AR429675	AR429675
60.0	17	6	AX649084	744	10.2	60.0	27	6	AX236776	AX236776
60.0	17	6	AX649085	745	10.2	60.0	27	6	AX236778	AX236778
60.0	17	6	AX649086	746	10.2	60.0	27	6	AX458033	AX458033
60.0	18	6	BD104990	747	10.2	60.0	27	6	BD171716	BD171716
60.0	18	6	BD176748	748	10.2	60.0	28	6	AR060524	AR060524
60.0	19	6	AR292703	749	10.2	60.0	28	6	E30200	E30200
60.0	19	6	AX398090	750	10.2	60.0	28	6	AR262748	AR262748
60.0	19	6	BD089801	751	10.2	60.0	28	6	AX015595	AX015595
60.0	19	12	AB068728	752	10.2	60.0	28	6	AX592213	AX592213
60.0	20	6	E40117	753	10.2	60.0	28	6	AX592216	AX592216
60.0	20	6	AR313841	754	10.2	60.0	28	6	AX592222	AX592222
60.0	20	6	AR338211	755	10.2	60.0	28	6	AX592225	AX592225
60.0	20	6	AR338212	756	10.2	60.0	28	6	BD097676	BD097676
60.0	20	6	AX233302	757	10.2	60.0	28	6	BD141269	BD141269
60.0	20	6	AX234152	758	10.2	60.0	28	6	BD194450	BD194450
60.0	20	6	AX323432	759	10.2	60.0	29	6	AR153322	AR153322
60.0	20	6	AX662830	760	10.2	60.0	29	6	BD259963	BD259963
60.0	20	6	AX805100	761	10.2	60.0	29	6	BD260976	BD260976
60.0	21	6	A51697	762	10.2	60.0	29	6	AX045390	AX045390
60.0	21	6	A65479	7						

60.0	37	6	AR397903	Sequence	869	10.2	60.0	38	6	AX223129	AX223129
60.0	37	6	AR397912	Sequence	870	10.2	60.0	38	6	AX228749	AX228749
60.0	37	6	AX057241	Sequence	871	10.2	60.0	38	6	AX273927	AX273927
60.0	37	6	BD136678	Method of	872	10.2	60.0	38	6	AX273942	AX273942
60.0	37	6	BD205260	Crystall	873	10.2	60.0	38	6	AX273947	AX273947
60.0	38	6	AR286776	Sequence	874	10.2	60.0	38	6	AX273977	AX273977
60.0	38	6	AR286777	Sequence	875	10.2	60.0	38	6	AX273991	AX273991
60.0	38	6	AR286779	Sequence	876	10.2	60.0	38	6	AX273992	AX273992
60.0	38	6	AR286783	Sequence	877	10.2	60.0	38	6	AX273997	AX273997
60.0	38	6	AR286786	Sequence	878	10.2	60.0	38	6	AX274008	AX274008
60.0	38	6	AR286793	Sequence	879	10.2	60.0	38	6	AX425285	AX425285
60.0	38	6	AR286826	Sequence	880	10.2	60.0	38	6	AX425326	AX425326
60.0	38	6	AR286861	Sequence	881	10.2	60.0	38	6	AX425341	AX425341
60.0	38	6	AR286886	Sequence	882	10.2	60.0	38	6	AX425393	AX425393
60.0	38	6	AR286889	Sequence	883	10.2	60.0	38	6	AX425396	AX425396
60.0	38	6	AR286890	Sequence	884	10.2	60.0	38	6	AX425404	AX425404
60.0	38	6	AR286899	Sequence	885	10.2	60.0	38	6	AX425446	AX425446
60.0	38	6	AR286904	Sequence	886	10.2	60.0	38	6	AX425452	AX425452
60.0	38	6	AR286909	Sequence	887	10.2	60.0	38	6	AX425553	AX425553
60.0	38	6	AR286942	Sequence	888	10.2	60.0	39	6	AR162118	AR162118
60.0	38	6	AR286969	Sequence	889	10.2	60.0	39	6	AR162124	AR162124
60.0	38	6	AR286970	Sequence	890	10.2	60.0	39	6	AR162130	AR162130
60.0	38	6	AR286976	Sequence	891	10.2	60.0	39	6	E28332	E28332 Pr
60.0	38	6	AR286985	Sequence	892	10.2	60.0	39	6	E28338	E28338 Pr
60.0	38	6	AR286989	Sequence	893	10.2	60.0	39	6	E28344	E28344 Pr
60.0	38	6	AR287000	Sequence	894	10.2	60.0	40	6	AR012107	AR012107
60.0	38	6	AR287012	Sequence	895	10.2	60.0	40	6	AR014546	AR014546
60.0	38	6	AR287021	Sequence	896	10.2	60.0	40	6	AR034275	AR034275
60.0	38	6	AR287022	Sequence	897	10.2	60.0	40	6	AX338656	AX338656
60.0	38	6	AR287037	Sequence	898	10.2	60.0	40	6	Z69828 M	Z69828 M
60.0	38	6	AR287056	Sequence	899	10.2	60.0	41	6	BD250835	BD250835
60.0	38	6	AR287059	Sequence	900	10.2	60.0	41	6	BD250836	BD250836
60.0	38	6	AR287067	Sequence	901	10.2	60.0	41	6	AX515258	AX515258
60.0	38	6	AR287071	Sequence	902	10.2	60.0	41	6	AX515960	AX515960
60.0	38	6	AR287095	Sequence	903	10.2	60.0	41	6	AX517755	AX517755
60.0	38	6	AR398766	Sequence	904	10.2	60.0	41	6	AX518711	AX518711
60.0	38	6	AR398767	Sequence	905	10.2	60.0	42	6	A68014	A68014 Se
60.0	38	6	AR398769	Sequence	906	10.2	60.0	42	6	AR163115	AR163115
60.0	38	6	AR398773	Sequence	907	10.2	60.0	42	6	AX202202	AX202202
60.0	38	6	AR398776	Sequence	908	10.2	60.0	42	6	BD209155	BD209155
60.0	38	6	AR398816	Sequence	909	10.2	60.0	43	6	AR107037	AR107037
60.0	38	6	AR398851	Sequence	910	10.2	60.0	43	6	AX180641	AX180641
60.0	38	6	AR398876	Sequence	911	10.2	60.0	44	6	AX180429	AX180429
60.0	38	6	AR398879	Sequence	912	10.2	60.0	45	6	AR032344	AR032344
60.0	38	6	AR398880	Sequence	913	10.2	60.0	45	6	AR162121	AR162121
60.0	38	6	AR398889	Sequence	914	10.2	60.0	45	6	AR162127	AR162127
60.0	38	6	AR398894	Sequence	915	10.2	60.0	45	6	AR162133	AR162133
60.0	38	6	AR398899	Sequence	916	10.2	60.0	45	6	E28335	E28335 Pr
60.0	38	6	AR398932	Sequence	917	10.2	60.0	45	6	E28341	E28341 Pr
60.0	38	6	AR398959	Sequence	918	10.2	60.0	45	6	E28347	E28347 Pr
60.0	38	6	AR398959	Sequence	919	10.2	60.0	45	6	I21548	I21548 Se
60.0	38	6	AR398960	Sequence	920	10.2	60.0	45	6	AX611815	AX611815
60.0	38	6	AR398966	Sequence	921	10.2	60.0	45	6	AX611816	AX611816
60.0	38	6	AR398975	Sequence	922	10.2	60.0	45	6	BD188252	BD188252
60.0	38	6	AR398979	Sequence	923	10.2	60.0	47	6	AR289556	AR289556
60.0	38	6	AR398990	Sequence	924	10.2	60.0	47	6	AR289678	AR289678
60.0	38	6	AR399002	Sequence	925	10.2	60.0	48	6	AX452012	AX452012
60.0	38	6	AR399011	Sequence	926	10.2	60.0	48	6	AX538801	AX538801
60.0	38	6	AR399012	Sequence	927	10.2	60.0	49	6	AX662182	AX662182
60.0	38	6	AR399027	Sequence	928	10.2	60.0	49	6	AX662184	AX662184
60.0	38	6	AR399046	Sequence	929	10.2	60.0	50	6	AR226508	AR226508
60.0	38	6	AR399049	Sequence	930	10.2	60.0	51	6	A62596	A62596 Se
60.0	38	6	AR399057	Sequence	931	10.2	60.0	51	6	AR019023	AR019023
60.0	38	6	AR399061	Sequence	932	10.2	60.0	51	6	AR130423	AR130423
60.0	38	6	AR399085	Sequence	933	10.2	60.0	51	6	AR204093	AR204093
60.0	38	6	AX220266	Sequence	934	10.2	60.0	51	6	AR227834	AR227834
60.0	38	6	AX220303	Sequence	935	10.2	60.0	51	6	AR355946	AR355946
60.0	38	6	AX220451	Sequence	936	10.2	60.0	51	6	AX118349	AX118349
60.0	38	6	AX220503	Sequence	937	10.2	60.0	51	6	AX158872	AX158872
60.0	38	6	AX223081	Sequence	938	10.2	60.0	51	6	AX159372	AX159372
60.0	38	6	AX223084	Sequence	939	10.2	60.0	51	6	AX160095	AX160095
60.0	38	6	AX223088	Sequence	940	10.2	60.0	51	6	AX160096	AX160096
60.0	38	6	AX223113	Sequence	941	10.2	60.0	51	6	AX161411	AX161411

## ALIGNMENTS

linear PAT 12-JUN-2003

AX15563	Sequence
AB074048	Sequence
AB077009	Lipocalin
AB071169	Attenuate
AB43634	Sequence 24
AB195445	Two compo
I30876	Sequence 10
I34926	Sequence 10
I21546	Sequence 93
AE223431	Sequence
AR021177	Sequence
I60553	Sequence 30
I60558	Sequence 35
AB04142	Sequence
AB03568	Sequence
AB039301	Sequence
AX917070	Sequence
AB052603	Sequence
A08376	Oligomucilo
E22175	Yeast capab
AX37933	Sequence
W27097	H.sapiens {
X72108	H.sapiens {
AX133481	Sequence
AX133033	Sequence
I57710	Sequence 24
B0207214	Enzymatic
AX29434	Sequence
AX139384	Sequence
I37630	Sequence 64
I94480	Sequence 64
A649517	Sequence
AX649525	Sequence
X722801	Sequence
AX724784	Sequence
AX729050	Sequence
X737111	Sequence
AX734669	Sequence
AX736694	Sequence
AX736876	Sequence
AX759445	Sequence
AX759411	Sequence
AX760239	Sequence
AX762431	Sequence
AX45778	Sequence 16
AR076027	Sequence
AR085592	Sequence
AR092798	Sequence
AR092800	Sequence
AR261513	Sequence
AR261889	Sequence
AX192388	Sequence
AX128808	Sequence
AX128609	Sequence
AR084342	Sequence
AR085567	Sequence
AX162350	Sequence
AR320499	Sequence

```

Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Griffiths,R., Horseth,S.K., Zagursky,R.J., Metcalf,B.J.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5825 06-MAY-2003;
FEATURES
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 78.8%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY
1 CGAGTGAAGATCCCC 15
Db
17 CGAATGAAGATCCCC 3

RESULT 2
BD197525/c
LOCUS
DEFINITION Method and reagent for treating diseases or conditions c
BD197525 molecule participating in vasculogenic response.
ACCESSION BD197525
VERSION BD197525.1 GI:33007295
KEYWORDS JP 2002509721-A/551.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Carnathini; Hominidae; Hom
1 (bases 1 to 17)
Pavco,P.A., Roberts,B., Jarvis,T., Coeshott,C. and Mcswi
Method and reagent for treating diseases or conditions c
molecule participating in vasculogenic response
Patent: JP 2002509721-A 551 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/551
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIR
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7086,A61K31/7125,A61K48/00,A61P3/10,A61
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C1
C12N5/00
CC Method and reagent for treating diseases or condi
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source i..17
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

FEATURES
source

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY
3 AGTGAAGATCCCCCT 16
Db
17 AGTGAAGATCCCCCT 4

```

526 17 bp RNA linear PAT 17-JUL-2003  
 and reagent for treating diseases or conditions concerning  
 rule participating in vasculogenic response.  
 526 1 GI:33007296  
 02509721-A/552.  
 sapiens (human)  
 sapiens  
 yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 ilia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ases 1 to 17)  
 J.F.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.  
 and reagent for treating diseases or conditions concerning  
 rule participating in vasculogenic response  
 it: JP 2002509721-A 552 02-APR-2002;  
 YME PHARMACEUTICALS INC  
 Homo sapiens (human)  
 JP 2002509721-A/552  
 02-APR-2002  
 24-MAR-1999 JP 2000541291  
 27-MAR-1998 US 60/079678  
 PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,  
 JAMES A MCSWIGGEN  
 5/09,A61K31/7088,A61K31/7125,A61K48/00,A61P2/10,A61P17/06, PC  
 29/00,  
 A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC  
 IN5/00  
 Method and reagent for treating diseases or conditions CC  
 concerning molecule  
 participating in vasculogenic response  
 key Location/Qualifiers  
 source 1..17  
 /organism="Homo sapiens (human)".  
 Location/Qualifiers  
 1..17  
 /organism="Homo sapiens"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:9606"  
 72.9%; Score 12.4; DB 6; Length 17;  
 larity 92.9%; Pred. No. 1.2e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 GAAGATCCCT 16  
 |||||  
 GAAGATACCT 2  
 9 32 bp DNA linear PAT 07-OCT-1996  
 nce 70 from patent US 5547669.  
 9.1 GI:1604789  
 sapiens (human)  
 sapiens  
 1 to 32)  
 s,B.L., Morgenstern,J.P., Bond,J.F., Garman,R.D.,  
 stein,J.L., Kuo,M.-C. and Morville,M.  
 biant peptides comprising T cell epitopes of the cat  
 'gen, Fel d 1  
 it: US 5547669-A 70 20-AUG-1996;  
 Location/Qualifiers  
 1..32  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 72.9%; Score 12.4; DB 6; Length 17;  
 larity 92.9%; Pred. No. 1.2e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 GAAGATCCCT 16  
 |||||  
 GAAGATACCT 2

Query Match 72.9%; Score 12.4; DB 6; Length 32;  
 Best Local Similarity 92.9%; Pred. No. 1.1e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 2 GAGTGAAGATCCCT 15  
 Db 14 GAGTGAAGATCCCT 1  
 RESULT 5  
 AX518499/c  
 LOCUS AX518499 41 bp DNA linear PAT  
 DEFINITION Sequence 4697 from Patent WO02052044.  
 ACCESSION AX518499  
 VERSION AX518499.1 GI:233568156  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1  
 REFERENCE Nakamura,Y., Sekine,A., Iida,A. and Saito,S.  
 AUTHORS Detection of genetic polymorphisms  
 TITLE Patent: WO 02052044-A 4697 04-JUL-2002;  
 JOURNAL Riken (JP)  
 FEATURES Location/Qualifiers  
 source 1..41  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 ORIGIN  
 Query Match 72.9%; Score 12.4; DB 6; Length 41;  
 Best Local Similarity 92.9%; Pred. No. 1e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 2 GAGTGAAGATCCCT 15  
 Db 39 GAGTGAAGATCCCT 26  
 RESULT 6  
 AX215216/c  
 LOCUS AX215216 17 bp RNA linear PAT  
 DEFINITION Sequence 658 from Patent WO0159103.  
 ACCESSION AX215216  
 VERSION AX215216.1 GI:15525259  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 1  
 REFERENCE Blatt,L., Mcswiggen,J. and Chowrira,B.M.  
 AUTHORS Method and reagent for the modulation and diagnosis of cc  
 TITLE nogo gene expression  
 JOURNAL Patent: WO 0159103-A 658 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)  
 Mcswiggen, James (US); Chowrira, Bharat M. (US)  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"  
 ORIGIN  
 Query Match 71.8%; Score 12.2; DB 6; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CGAGTGAAGATCCCTT 17  
 |||||

```
GAATGAAATATCCCTT 1
13791       24 bp      DNA      linear      PAT 03-JUL-2002
ence 246 from Patent WO0216649.
13791
13791.1 GI:21691069
thetic construct
thetic construct
thetic sequences.
erson,K.
es and decoder oligonucleotides
nt: WO 0216649-A 246 28-FEB-2002;
mina, Inc. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
71.8%; Score 12.2; DB 6; Length 24;
ilarity 82.4%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
AGTGAAGATCCCTT 17
|||||
3CGTGAAGACCCCAT 17
7772       25 bp      DNA      linear      PAT 03-JUL-2002
ence 4227 from Patent WO0216649.
7772
7772.1 GI:21696671
thetic construct
thetic construct
thetic sequences.
erson,K.
es and decoder oligonucleotides
nt: WO 0216649-A 4227 28-FEB-2002;
mina, Inc. (US)
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
71.8%; Score 12.2; DB 6; Length 25;
ilarity 82.4%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
AGTGAAGATCCCTT 17
|||||
3CGTGAAGACCCCAT 18
7554       25 bp      DNA      linear      PAT 16-JUL-2002
ence 1 from Patent WO0214547.
7554
7554.1 GI:21900749
```

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
1  
REFERENCE Fuchs,S., Ilani,T. and Perl,O.  
AUTHORS Method for the diagnosis and follow up of schizophrenia  
TITLE mental and neurodegenerative disorders  
JOURNAL Patent: WO 0214547-A 1 21-FEB-2002;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)  
FEATURES Location/Qualifiers  
source  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 71.8%; Score 12.2; DB 6; Length 25;  
Best Local Similarity 82.4%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
|||||  
DB 25 CGAGTGAAGATCCCTT 9  
RESULT 10  
AR285893 36 bp RNA linear PAT  
LOCUS Sequence 265 from patent US 6528640.  
DEFINITION AR285893  
ACCESSION AR285893  
VERSION AR285893.1 GI:29723487  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE Synthetic ribonucleic acids with RNase activity  
JOURNAL Patent: US 6528640-A 265 04-MAR-2003;  
FEATURES Location/Qualifiers  
source  
1..36  
/organism="unknown"  
/mol\_type="unassigned RNA"  
ORIGIN  
Query Match 71.8%; Score 12.2; DB 6; Length 36;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
|||||  
DB 17 CGAGTGAAGATCCCTT 33  
RESULT 11  
AX815952 36 bp DNA linear PAT  
LOCUS Sequence 25 from Patent WO03066842.  
DEFINITION AX815952  
ACCESSION AX815952  
VERSION AX815952.1 GI:39646609  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
1  
REFERENCE Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. and Paster  
AUTHORS Method for producing recombinant proteins in micro-orga  
TITLE Patent: WO 03066842-A 25 14-AUG-2003;  
JOURNAL Trommsdorff GmbH & Co.KG Arzneimittel (DE)

```
Location/Qualifiers
1..36
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

71.8%; Score 12.2; DB 6; Length 36;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTCAGATCCCTT 17
|||||
AGAAAGAGCCCTT 24

7883 37 bp RNA linear PAT 18-DEC-2003
ence 264 from patent US 6617438.
7883
7883.1 GI:40135233

OWN.
own.
assified.
bases 1 to 37)
elman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
lic-Adamic,J., Sweedler,D. and Zinnen,S.
ribonucleotides with enzymatic activity
nt: US 6617438-A 264 09-SEP-2003;
Location/Qualifiers
1..37
/organism="unknown"
/mol_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 37;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTCAGATCCCTT 17
|||||
AGTCAAGGTCCTT 33

6827 38 bp RNA linear PAT 10-APR-2003
ence 1199 from patent US 6528640.
6827
6827.1 GI:29724423

OWN.
own.
assified.
bases 1 to 38)
elman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
lic-Adamic,J., Sweedler,D. and Zinnen,S.
hetic ribonucleic acids with RNase activity
nt: US 6528640-A 1199 04-MAR-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 38;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

IAGTCAGATCCCTT 17
|||||

Location/Qualifiers
1..36
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

71.8%; Score 12.2; DB 6; Length 36;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTCAGATCCCTT 17
|||||
AGAAAGAGCCCTT 24

7883 37 bp RNA linear PAT 18-DEC-2003
ence 264 from patent US 6617438.
7883
7883.1 GI:40135233

OWN.
own.
assified.
bases 1 to 37)
elman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
lic-Adamic,J., Sweedler,D. and Zinnen,S.
ribonucleotides with enzymatic activity
nt: US 6617438-A 264 09-SEP-2003;
Location/Qualifiers
1..37
/organism="unknown"
/mol_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 37;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTCAGATCCCTT 17
|||||
AGTCAAGGTCCTT 33

6827 38 bp RNA linear PAT 10-APR-2003
ence 1199 from patent US 6528640.
6827
6827.1 GI:29724423

OWN.
own.
assified.
bases 1 to 38)
elman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
lic-Adamic,J., Sweedler,D. and Zinnen,S.
hetic ribonucleic acids with RNase activity
nt: US 6528640-A 1199 04-MAR-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 38;
ilarity 82.4%; Pred. No. 1.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

IAGTCAGATCCCTT 17
|||||

Db 18 CGAGTCAAGGTCCTT 34

RESULT 14
AR286885 38 bp RNA linear PAT
LOCUS
DEFINITION Sequence 1257 from patent US 6528640.
ACCESSION AR286885
VERSION AR286885.1 GI:29724481
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 1257 04-MAR-2003;
FEATURES
source
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 71.8%; Score 12.2; DB 6; Length 38;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
|||||
18 CGAGTCAAGGTCCTT 34

Db 18 CGAGTCAAGGTCCTT 34

RESULT 15
AR286931 38 bp RNA linear PAT
LOCUS
DEFINITION Sequence 1303 from patent US 6528640.
ACCESSION AR286931
VERSION AR286931.1 GI:29724527
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 1303 04-MAR-2003;
FEATURES
source
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 71.8%; Score 12.2; DB 6; Length 38;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
|||||
18 CGAGTCAAGGTCCTT 34

Db 18 CGAGTCAAGGTCCTT 34

RESULT 16
AR286960 38 bp RNA linear PAT
LOCUS
DEFINITION Sequence 1332 from patent US 6528640.
ACCESSION AR286960
VERSION AR286960.1 GI:29724556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 1332 04-MAR-2003;
FEATURES
source
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 71.8%; Score 12.2; DB 6; Length 38;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
|||||
18 CGAGTCAAGGTCCTT 34

Db 18 CGAGTCAAGGTCCTT 34

RESULT 16
AR286960 38 bp RNA linear PAT
LOCUS
DEFINITION Sequence 1332 from patent US 6528640.
ACCESSION AR286960
VERSION AR286960.1 GI:29724556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 1332 04-MAR-2003;
FEATURES
source
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 71.8%; Score 12.2; DB 6; Length 38;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
|||||
18 CGAGTCAAGGTCCTT 34

Db 18 CGAGTCAAGGTCCTT 34
```



(bases 1 to 38)  
gelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
ulic-Adamic,J., Sweedler,D. and Zinnen,S.  
thetic ribonucleic acids with RNase activity  
ent: US 6528640-A 1332 04-MAR-2003;  
Location/Qualifiers  
1..38  
/organism="unknown"  
/mol\_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GAGTGAAGATCCCTT 17  
|||||  
SAGTCAAGGTCTCCTT 34

98817 38 bp RNA linear PAT 18-DEC-2003  
ence 1198 from patent US 6617438.

98817 38 bp RNA linear PAT 18-DEC-2003  
98817.1 GI:40136970

nown.  
lassified.  
(bases 1 to 38)  
gelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
ulic-Adamic,J., Sweedler,D. and Zinnen,S.  
goribonucleotides with enzymatic activity  
ent: US 6617438-A 1198 09-SEP-2003;  
Location/Qualifiers  
1..38  
/organism="unknown"  
/mol\_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GAGTGAAGATCCCTT 17  
|||||  
GAGTCAAGGTCTCCTT 34

98875 38 bp RNA linear PAT 18-DEC-2003  
ence 1256 from patent US 6617438.

98875 38 bp RNA linear PAT 18-DEC-2003  
98875.1 GI:40137078

nown.  
lassified.  
(bases 1 to 38)  
gelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
ulic-Adamic,J., Sweedler,D. and Zinnen,S.  
goribonucleotides with enzymatic activity  
ent: US 6617438-A 1256 09-SEP-2003;  
Location/Qualifiers  
1..38  
/organism="unknown"  
/mol\_type="unassigned RNA"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. No. 1.4e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCTCCTT 34

RESULT 19  
AR398921 38 bp RNA linear PAT  
LOCUS  
DEFINITION  
Sequence 1302 from patent US 6617438.  
ACCESSION  
AR398921  
VERSION  
AR398921.1 GI:40137165  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 38)  
AUTHORS  
Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE  
Oligoribonucleotides with enzymatic activity  
JOURNAL  
Patent: US 6617438-A 1302 09-SEP-2003;  
FEATURES  
Location/Qualifiers  
1..38  
source  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 38;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCTCCTT 34

RESULT 20

AR398950 38 bp RNA linear PAT  
LOCUS  
DEFINITION  
Sequence 1331 from patent US 6617438.  
ACCESSION  
AR398950  
VERSION  
AR398950.1 GI:40137217  
KEYWORDS  
SOURCE  
Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 38)  
AUTHORS  
Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
TITLE  
Oligoribonucleotides with enzymatic activity  
JOURNAL  
Patent: US 6617438-A 1331 09-SEP-2003;  
FEATURES  
Location/Qualifiers  
1..38  
source  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 38;  
Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCTCCTT 34

RESULT 21

AX220484 38 bp RNA linear PAT  
LOCUS  
DEFINITION  
Sequence 5926 from Patent WO0159103.  
ACCESSION  
AX220484  
VERSION  
AX220484.1 GI:15548208

helic construct  
helic construct  
ficial sequences.

t.L., Mcswiggen,J. and Chowrira,B.M.  
od and reagent for the modulation and diagnosis of cd20 and  
gene expression  
nt: WO 0159103-A 5926 16-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
iggen, James (US) ; Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .38

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. NO. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0;

AGTGAGATCCCTT 17  
|||||  
AGTCAAGGTCCTT 34

8757 38 bp RNA linear PAT 10-SEP-2001  
ence 2129 from Patent WO0157206.

8757.1 GI:15557898

helic construct  
helic construct  
ficial sequences.

aeY,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.  
od and reagent for the inhibition of checkpoint kinase-1 (chk  
nzyme  
nt: WO 0157206-A 2129 09-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)  
Location/Qualifiers  
1. .38

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. NO. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0;

AGTGAGATCCCTT 17  
|||||  
AGTCAAGGTCCTT 34

3935 38 bp RNA linear PAT 29-OCT-2001  
ence 1504 from Patent WO0162911.

3935.1 GI:16546672

helic construct  
helic construct  
ficial sequences.

is,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and  
S.J.H.

TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 1504 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITE

FEATURES  
Location/Qualifiers  
1. .38

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 38;  
Best Local Similarity 82.4%; Pred. NO. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCCTT 34

RESULT 24  
AX425294  
LOCUS AX425294 38 bp RNA linear PAT  
DEFINITION Sequence 3630 from Patent WO0188124.  
ACCESSION AX425294  
VERSION AX425294.1 GI:21528676

KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE

AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,  
Randi,A.M.  
TITLE Method and reagent for the inhibition of erg  
JOURNAL Patent: WO 0188124-A 3630 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITE

FEATURES  
Location/Qualifiers  
1. .38

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 38;  
Best Local Similarity 82.4%; Pred. NO. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCCTT 34

RESULT 25

AX463628

LOCUS AX463628 38 bp DNA linear PAT  
DEFINITION Sequence 7 from Patent WO0250290.  
ACCESSION AX463628  
VERSION AX463628.1 GI:21886388

KEYWORDS  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

REFERENCE  
AUTHORS Nagai,N., Laroche,Y. and Collen,D.J.  
TITLE A yeast expression vector and a method of making a recom  
protein by expression in a yeast cell  
JOURNAL Patent: WO 0250290-A 7 27-JUN-2002;  
THROMB X NV (BE)

FEATURES  
Location/Qualifiers  
1. .38

/organism="Homo sapiens"

1 09:38:23 2004

us-10-090-326-17.max.rge

/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3AGTGAAGATCCCTT 17  
|||||  
3AGAAAAGAGCCCTT 28

35954 40 bp DNA linear PAT 25-NOV-2003  
ence 9 from Patent WO03060159.

35954  
35954.1 GI:38522865

thetic construct  
thetic construct  
ificial sequences.

i, K. and Holck, A.

ods of nucleic acid amplification  
nt: WO 03060159-A 9 24-JUL-2003;

ORSK, Norwegian Food Research Institute (NO)

Location/Qualifiers

1..40

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

71.8%; Score 12.2; DB 6; Length 40;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3AGTGAAGATCCCTT 17  
|||||  
3AGCGAAGATCTCTT 36

6440 46 bp DNA linear PAT 16-MAY-2001  
ence 67 from patent US 6180341.

6440  
6440.1 GI:14113033

own.

assified.

(bases 1 to 46)

son, B.L., Georgiou, G. and Burks, E.A.

itro scanning saturation mutagenesis of proteins

nt: US 6180341-A 67 30-JAN-2001;

Location/Qualifiers

1..46

/organism="unknown"

/mol\_type="unassigned DNA"

71.8%; Score 12.2; DB 6; Length 46;  
ilarity 82.4%; Pred. No. 1.3e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3AGTGAAGATCCCTT 17  
|||||  
3GGTGAATGATCCCAT 19

RESULT 28  
AX759214/c

LOCUS AX759214 17 bp DNA linear PAT  
DEFINITION Sequence 2535 from Patent WO03040369.

ACCESSION AX759214

VERSION AX759214.1 GI:32253830

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reve;

apoptosis and/or viral resistance phenomena and their u;

medicines

JOURNAL Patent: WO 03040369-A 2535 15-MAY-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATC 12

|||||

Db 12 CGAGTGAAGATC 1

RESULT 29  
AX762760/c

LOCUS AX762760 17 bp DNA linear PAT  
DEFINITION Sequence 6081 from Patent WO03040369.

ACCESSION AX762760

VERSION AX762760.1 GI:32257376

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE  
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.  
TITLE Sequences involved in tumoral suppression, tumoral reve;

apoptosis and/or viral resistance phenomena and their u;

medicines

JOURNAL Patent: WO 03040369-A 6081 15-MAY-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATC 12

|||||

Db 12 CGAGTGAAGATC 1

RESULT 30  
AX753432

LOCUS AX753432 26 bp DNA linear PAT  
DEFINITION Sequence 20 from Patent WO03037362.

3432  
3432.1 GI:32166193  
helic construct  
helic construct  
ficial sequences.  
ernagel,A., Eulenberger,K., Broemner,G., Ciossek,T., Rudolph,B.,  
lph,D., Belgore,F. and Jaekel,S.  
kinase homologous proteins involved in the regulation of energy  
ostasis and organelle metabolism  
nt: WO 03037362-A 20 08-MAY-2003;  
logen Aktiengesellschaft fuer entwicklungsbiologische Forschung  
Location/Qualifiers  
1. .26  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Human Mnk2b forward primer"  
70.6%; Score 12; DB 6; Length 26;  
ilarity 100.0%; Pred. No. 1.9e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
GTGAAGATCC 13  
|||||  
GTGAAGATCC 23  
36  
36.1 GI:18622672  
000312586-A/2.  
helic construct  
helic construct  
ficial sequences.  
ases 1 to 31)  
jima,H. and Nagasawa,A.  
od for imparting herbicide tolerance  
nt: JP 2000312586-A 2 14-NOV-2000;  
TOMO CHEM CO LTD  
Artificial Sequence  
JP 2000312586-A/2  
14-NOV-2000  
28-APR-1999 JP 1999121955  
HIROKI NAKAJIMA,AKITO NAGASAWA  
C12N15/09,A01H5/00,C12N5/10,C12N9/88//A01N63/00,C12N15/00, PC  
N5/00  
Key Location/Qualifiers  
source 1. .31  
/organism="Artificial Sequence".  
Location/Qualifiers  
1. .31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
70.6%; Score 12; DB 6; Length 31;  
ilarity 100.0%; Pred. No. 1.9e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
AGTGAAGATC 12  
|||||  
AGTGAAGATC 12

RESULT 32  
AR340181/c  
LOCUS AR340181 31 bp DNA linear PAT  
DEFINITION Sequence 2 from patent US 6570070.  
ACCESSION AR340181  
VERSION AR340181.1 GI:33731581  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Nakajima,H. and Nagasawa,A.  
TITLE Production of plants either transformed with the protopc  
IX binding subunit of a magnesium chelataase or a ferroch  
having increased herbicide resistance  
JOURNAL Patent: US 6570070-A 2 27-MAY-2003;  
FEATURES  
source Location/Qualifiers  
1. .31  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 70.6%; Score 12; DB 6; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
QY 1 CGAGTGAAGATC 12  
|||||  
Db 23 CGAGTGAAGATC 12  
RESULT 33  
AX135624/c  
LOCUS AX135624 38 bp DNA linear PAT  
DEFINITION Sequence 2 from Patent WO0132896.  
ACCESSION AX135624  
VERSION AX135624.1 GI:14271894  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Alexandrov,K. and Grun,M.  
TITLE Protein expression systems for non-pathogenic kinetoplas  
JOURNAL Patent: WO 0132896-A 2 10-MAY-2001;  
Jena Bioscience GmbH (DE)  
FEATURES Location/Qualifiers  
source 1. .38  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
ORIGIN  
Query Match 70.6%; Score 12; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
QY 1 CGAGTGAAGATC 12  
|||||  
Db 25 CGAGTGAAGATC 14  
RESULT 34  
I71937  
LOCUS I71937 43 bp DNA linear PAT  
DEFINITION Sequence 3 from patent US 5683870.  
ACCESSION I71937  
VERSION I71937.1 GI:3008076  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

classified.  
(bases 1 to 43)  
Bond, P. and Endozo, A.  
leic acid probes to Chlamydia pneumoniae  
ant: US 5683870-A 3 04-NOV-1997;  
Location/Qualifiers  
1. .43  
/organism="unknown"  
/mol\_type="unassigned DNA"

70.6%; Score 12; DB 6; Length 43;  
nilarity 100.0%; Pred. No. 1.8e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCTT 17  
|||||  
AGATCCCTT 25

6871 17 bp RNA linear PAT 07-SEP-2001  
ence 2313 from Patent WO0159103.

6871.1 GI:15526932

thetic construct  
thetic construct  
ificial sequences.

t, L., Mcswiggen, J. and Chowrira, B.M.  
od and reagent for the modulation and diagnosis of cd20 and  
gene expression  
ant: WO 0159103-A 2313 16-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
wigen, James (US); Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .17

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

69.4%; Score 11.8; DB 6; Length 17;  
nilarity 86.7%; Pred. No. 2.7e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAGATCCCTT 17  
|||||  
TGAGATCCCTT 3

6625 20 bp DNA linear PAT 21-NOV-2001  
ence 8387 from Patent WO0179548.

6625.1 GI:17058314

thetic construct  
thetic construct  
ificial sequences.

any, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.  
od of designing addressable array for detection of nucleic acid  
ence differences using ligase detection reaction  
ant: WO 0179548-A 8387 25-OCT-2001;  
WELL RESEARCH FOUNDATION, INC. (US)  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 GAGTGAAGATCCCTT 16  
|||||

Db 5 GAGTAAGAGCCCTT 19  
|||||

# RESULT 37

AX537893/c 20 bp DNA linear PAT  
LOCUS Sequence 44 from Patent WO02072822.  
DEFINITION AX537893  
ACCESSION AX537893  
VERSION AX537893.1 GI:25270001  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

# REFERENCE

1  
AUTHORS Hadano, S., Ikeda, J. E. and Hayden, M. R.  
TITLE Als2 gene and amyotrophic lateral sclerosis type 2  
JOURNAL Patent: WO 02072822-A 44 19-SEP-2002;  
The University of British Columbia (CA); Japan Science  
Technology Corporation (JP)  
FEATURES  
Location/Qualifiers  
1. .20

# source

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="synthesized oligonucleotide"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCTT 17  
|||||

Db 16 AATGAAGATCCCTT 2  
|||||

# RESULT 38

AX291992 24 bp DNA linear PAT  
LOCUS Sequence 3754 from Patent WO0179548.  
DEFINITION AX291992  
ACCESSION AX291992  
VERSION AX291992.1 GI:17053675  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

# REFERENCE

1  
AUTHORS Barany, F., Zirvi, M., Gerry, N. P., Favis, R. and Kliman, R.  
TITLE Method of designing addressable array for detection of  
sequence differences using ligase detection reaction  
JOURNAL Patent: WO 0179548-A 3754 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
FEATURES  
Location/Qualifiers  
1. .24

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;  
Best Local Similarity 86.7%; Pred. No. 2.5e+05;

```

Conservative 0; Mismatches 2; Indels 0; Gaps 0;
GTGAAGATCCCT 16
|||||
GTAAGAGCCCT 23

09
  27 bp      DNA      linear      PAT 03-MAR-1998
ence 17 from Patent EP0739988.
09
09.1 GI:3713285
onella jordanis
onella jordanis
eria; Proteobacteria; Gammaproteobacteria; Legionellales;
onellaceae; Legionella.

rich, B., Robinson, P.D., Tiecke, F. and Rolfs, A.D.
od for genus and species specific identification of Legionella
nt: EP 0739988-A 17 30-OCT-1996;
RINGER MANNHEIM GMBH (DE)
r publication DE 19515891 961031.
  Location/Qualifiers
    1..27
      /organism="Legionella jordanis"
      /mol_type="unassigned DNA"
      /db_xref="taxon:456"

    69.4%; Score 11.8; DB 6; Length 27;
    ilarity 86.7%; Pred. No. 2.5e+05;
    Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16
|||||
ATGAATATCCCT 19

1454
ence 17 from patent US 6194145.
1454
1454.1 GI:14120357
OWN.
assified.
bases 1 to 27)
rich, B., Robinson, P.-N., Tiecke, F. and Rolfs, A.
s and species-specific identification of Legionella
nt: US 6194145-A 17 27-FEB-2001;
  Location/Qualifiers
    1..27
      /organism="unknown"
      /mol_type="unassigned DNA"

    69.4%; Score 11.8; DB 6; Length 27;
    ilarity 86.7%; Pred. No. 2.5e+05;
    Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16
|||||
ATGAATATCCCT 19

3188
ods for making proteins containing free cysteine residues.
  33 bp      DNA      linear      PAT 17-JUL-2003

```

---

```

ACCESSION BD273188
VERSION BD273188.1 GI:33082956
KEYWORDS JP 2002534119-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cox, G.N., Doherty, D.H. and Rosendahl, M.S.
TITLE Methods for making proteins containing free cysteine res
JOURNAL Patent: JP 2002534119-A 4 15-OCT-2002;
COMMENT BOLDER BIOTECHNOLOGY INC
OS Artificial Sequence
PN JP 2002534119-A/4
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593732
PR 14-JAN-1999 US 60/116041
PI GEORGE N COX, DANIEL H DOHERTY, MARY S ROSENDAHL, PC
C12N15/09, A61K38/04, A61K38/21, A61K38/22, A61K38/27, A61K47
A61P5/02,
PC A61P7/06, A61P43/00, A61P43/00, C07K14/47, C07K14/505, C
PC C07K14/575,
PC C12P21/02, C12P21/02, C12P21/19, (C12P21/02, C12P21/91), C12
A61K37/36,
PC A61K37/24, A61K37/66, A61K37/43
CC artificial sequence
FH Key Location/Qualifiers
FT misc feature (1)..(20).
FEATURES
  source
    1..33
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 33;
Best Local Similarity 86.7%; Pred. No. 2.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15
  |||||
Db 16 CTAGTGAGGATCCCC 2

RESULT 42
AR381516/c
LOCUS AR381516 33 bp DNA linear PAT
DEFINITION Sequence 25 from patent US 6608183.
ACCESSION AR381516
VERSION AR381516.1 GI:40089609
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cox, G.N. III.
TITLE Derivatives of growth hormone and related proteins
JOURNAL Patent: US 6608183-A 25 19-AUG-2003;
FEATURES
  source
    1..33
      /organism="unknown"
      /mol_type="genomic DNA"

ORIGIN
Query Match 69.4%; Score 11.8; DB 6; Length 33;
Best Local Similarity 86.7%; Pred. No. 2.4e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15
  |||||
Db 16 CTAGTGAGGATCCCC 2

```

74382 33 bp DNA linear PAT 12-AUG-2002  
 ence 6 from Patent EP1223220.  
 74382  
 74382.1 GI:22213988

thetic construct  
 hetic construct  
 icial sequences.  
 ab.H., Glieder,A., Kratky,C., Dreveny,I., Poehlauer,P.,  
 anc.W., Mayrhofer,H., Wirth,I., Neuhofer,R. and Bona,R.  
 ss coding for hydroxynitrile lyase, recombinant proteins with  
 :oxynitrile lyase activity and their use  
 nt: EP 1223220-A 6 17-JUL-2002;  
 Fine Chemicals Austria Nfg GmbH & Co KG (AT)  
 Location/Qualifiers  
 1. .33  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Primer"

69.4%; Score 11.8; DB 6; Length 33;  
 ilarity 86.7%; Pred.No.2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 GTGAGATCCCTT 17  
 |||||  
 TACAGATCCCTT 16

73213 33 bp DNA linear PAT 27-AUG-2002  
 th hormone and related protein derivative.

73213  
 73213.1 GI:22618816  
 :hetic construct  
 :hetic construct  
 :ficial sequences.  
 (bases 1 to 33)  
 G.N.C.  
 th hormone and related protein derivative  
 nt: JP 2001510033-A 2 31-JUL-2001;  
 DER BIOTECHNOLOGY INC  
 Artificial Sequence  
 JP 2001510033-A/2  
 31-JUL-2001  
 13-JUL-1998 JP 200503109  
 14-JUL-1997 US 60/052516  
 GEORGE N COX III

15/09,C07K14/475,C07K14/505,C07K14/52,C07K14/53,C07K14/535, PC  
 K14/54,  
 C07K14/55,C07K14/555,C07K14/56,C07K14/565,C07K14/57,C12N15/00  
 Description of Artificial Sequence:PCR Primer FH Key  
 Location/Qualifiers  
 source 1. .33  
 /organism='Artificial Sequence'.  
 Location/Qualifiers  
 1. .33  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

69.4%; Score 11.8; DB 6; Length 33;  
 ilarity 86.7%; Pred.No.2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGAGTGAAGATCCCC 15  
 |||||  
 Db 16 CTAGTGAGATCCCC 2

## RESULT 45

BD181899/c

LOCUS

DEFINITION

Novel gene containing DNA sequence encoding hydroxynitr  
 recombinant protein originating in the gene and having

hydroxynitrile lyase activity and utilization thereof.

BD181899

BD181899.1 GI:30792817

JP 2002330791-A/6.

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 33)

AUTHORS

Schwab,H., Greeder,A., Kratky,C., Drefeny,I., Bon,R., P  
 Scharnke,W., Milfofar,H., Viruto,I. and Noyhoffar,R.

TITLE

Novel gene containing DNA sequence encoding hydroxynitr  
 recombinant protein originating in the gene and having

hydroxynitrile lyase activity and utilization thereof

JOURNAL

Patent: JP 2002330791-A 6 19-NOV-2002;

COMMENT

DSM FINE CHEMICALS AUSTRIA NFG GMBH AND CO KG  
 OS Artificial Sequence  
 PN JP 2002330791-A/6  
 PD 19-NOV-2002  
 PF 11-JAN-2002 JP 2002005090  
 PR 16-JAN-2001 AT A60/2001.03-APR-2001 AT A523;  
 HELMUT SCHWAB,ANTON GREEDER,CHRISTOPH KRATKY,INGREET DRI  
 RUDOLPH BONA,  
 PI PETER PEHRAWEL,WOLFGANG SCHARNKE,HERBERT  
 MILFOFAR,ILMA VIRUTO,  
 PC C12N15/09,C07K19/00,C12N9/04,C12N9/88,C12P13/00,CL:  
 Description of the artificial sequence: primer FH Key  
 Location/Qualifiers  
 FT source 1. .33  
 /organism='Artificial Sequence'.

## FEATURES

source

1. .33

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

## ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 33;  
 Best Local Similarity 86.7%; Pred.No.2.4e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCTT 17

|||||

Db 30 AGAGAAGATCCTT 16

|||||

Search completed: February 29, 2004, 09:43:40

Job time : 542.753 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 07:46:14 ; Search time 145.052 Seconds  
(without alignments)  
497.986 Million cell updates/sec

US-10-090-326-17

1 cgagtgagatccctt 17

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
100.0	17	6	ABQ82551	Abq82551 Glucuroni
100.0	22	6	ABQ82538	Abq82538 Beta-gluc
100.0	22	9	ADD68259	Add68259 PCR prime
90.6	50	2	AAQ12740	Aaq12740 UidA-2 pr
78.8	20	2	AXX96499	Axx96499 PCR prime
78.8	25	8	ACK21696	Ack21696 Human mic
78.8	32	6	ABA05396	Aba05396 Human IL-
78.8	33	6	AAL45621	Aal45621 T lymphoc
78.8	41	6	ABA94071	Aba94071 Human oes
78.8	41	6	AAL45624	Aal45624 T lymphoc
78.8	41	6	AAL45623	Aal45623 T lymphoc
78.8	41	6	ABA94074	Aba94074 Human oes
78.8	41	6	ABA94073	Aba94073 Human oes
75.3	25	8	ACI66631	ACI66631 Human mic
75.3	25	8	ACI114844	ACI114844 Human mic
75.3	25	8	ACI60413	ACI60413 Human mic
75.3	25	8	ACI30900	ACI30900 Human mic
75.3	25	8	ACK09897	ACK09897 Human mic
75.3	29	4	AAL65129	Aal65129 PCR prime
75.3	50	6	ABZ00943	Abz00943 Human leu
75.3	60	6	ABN59114	Abn59114 Human spl
72.9	17	2	AAAL7325	Aaal7325 Aryl hydr
72.9	17	2	AAAL7326	Aaal7326 Aryl hydr

12.4	12.4	72.9	29	3	AAA99103	Aaa99103
12.4	12.4	72.9	32	2	AAQ41588	Aaq41588
12.4	12.4	72.9	32	3	AAZ89659	Aaz89659
12.4	12.4	72.9	32	3	AAC60150	Aac60150
12.4	12.4	72.9	32	3	AAA07479	Aaa07479
12.4	12.4	72.9	32	3	AAA12286	Aaa12286
12.4	12.4	72.9	41	6	ABZ47913	Abz47913
12.4	12.4	72.9	41	6	ABL54116	AbL54116
12.4	12.4	72.9	17	4	ABK00658	Abk00658
12.4	12.4	71.8	17	4	ABK00691	Abk00691
12.4	12.4	71.8	24	2	AAZ30691	Aaz30691
12.4	12.4	71.8	24	2	ABQ00239	Abq00239
12.4	12.4	71.8	24	6	ABQ04478	Abq04478
12.4	12.4	71.8	24	6	ABQ10765	Abq10765
12.4	12.4	71.8	24	6	ABQ10806	Abq10806
12.4	12.4	71.8	24	6	ABQ04519	Abq04519
12.4	12.4	71.8	25	6	AAD27955	Aad27955
12.4	12.4	71.8	25	6	ABQ12342	Abq12342
12.4	12.4	71.8	25	6	ABQ12301	Abq12301
12.4	12.4	71.8	25	8	ACI15438	ACI15438
12.4	12.4	71.8	25	8	ACK09806	ACK09806
12.4	12.4	71.8	25	8	AAH96915	Aah96915
12.4	12.4	71.8	38	4	ABK05926	Abk05926
12.4	12.4	71.8	38	4	ABL47871	AbL47871
12.4	12.4	71.8	38	6	ABN89462	Abn89462
12.4	12.4	71.8	38	6	ABK20983	Abk20983
12.4	12.4	71.8	46	4	AAF73142	Aaf73142
12.4	12.4	71.8	50	6	ABA97764	AbA97764
12.4	12.4	71.8	50	6	ADB42212	Adb42212
12.4	12.4	71.8	17	9	ADB42212	Adb42212
12.4	12.4	71.8	17	9	ADB45758	Adb45758
12.4	12.4	71.8	17	9	ACI13905	ACI13905
12.4	12.4	71.8	25	8	ACK22725	ACK22725
12.4	12.4	71.8	25	8	ACC57605	ACC57605
12.4	12.4	71.8	30	3	AAZ42403	Aaz42403
12.4	12.4	71.8	31	3	AAZ45268	Aaz45268
12.4	12.4	71.8	38	5	AAH24333	Aah24333
12.4	12.4	71.8	43	2	AAQ44465	Aaq44465
12.4	12.4	71.8	17	4	ABK02313	ABK02313
12.4	12.4	71.8	20	6	ABI96667	Abi96667
12.4	12.4	71.8	20	6	ABQ82286	Abq82286
12.4	12.4	71.8	20	9	ADE71382	Ade71382
12.4	12.4	71.8	20	9	ADE71377	Ade71377
12.4	12.4	71.8	23	2	AAQ34295	Aaq34295
12.4	12.4	71.8	24	6	ABI89905	ABi89905
12.4	12.4	71.8	24	6	ABI89904	ABi89904
12.4	12.4	71.8	25	8	ACI52164	ACi52164
12.4	12.4	71.8	25	8	ACI68983	ACi68983
12.4	12.4	71.8	25	8	ACK21697	ACK21697
12.4	12.4	71.8	25	8	ACI52792	ACi52792
12.4	12.4	71.8	25	8	ACH61998	ACH61998
12.4	12.4	71.8	27	2	AAT48267	Aat48267
12.4	12.4	71.8	28	5	AAH73870	Aah73870
12.4	12.4	71.8	31	2	AAH38717	Aah38717
12.4	12.4	71.8	33	2	AAZ21961	Aaz21961
12.4	12.4	71.8	33	3	AAZ74773	Aaz74773
12.4	12.4	71.8	33	6	AAF88765	Aaf88765
12.4	12.4	71.8	50	2	AAZ76532	Aaz76532
12.4	12.4	71.8	50	4	AAZ27796	Aaz27796
12.4	12.4	71.8	50	6	ABZ05688	Abz05688
12.4	12.4	71.8	50	6	ADB17673	Adb17673
12.4	12.4	71.8	51	4	AAZ27149	Aaz27149
12.4	12.4	71.8	51	4	AAZ27387	Aaz27387
12.4	12.4	71.8	52	2	AAV76576	Aav76576
12.4	12.4	71.8	53	3	AAA47183	Aaa47183
12.4	12.4	71.8	57	2	AAZ27832	Aaz27832
12.4	12.4	71.8	60	6	ABN35808	Abn35808
12.4	12.4	71.8	60	6	ABN42825	Abn42825
12.4	12.4	71.8	17	2	AAZ64009	Aaz64009
12.4	12.4	71.8	17	2	AAAL7327	Aaal7327
12.4	12.4	71.8	17	4	ABK02675	Abk02675
12.4	12.4	71.8	17	4	ABK02674	Abk02674
12.4	12.4	71.8	20	2	AAZ05109	Aaz05109
12.4	12.4	71.8	20	2	AAZ97026	Aaz97026
12.4	12.4	71.8	20	2	AAZ94029	Aaz94029



67.1	20	2	AAx95372	AAx95372 PCR prime	170	11.2	65.9	20	6	AAI69369	AAI69369
67.1	21	3	AAA30533	AAA30533 C. tropic	171	11.2	65.9	20	6	ABI97463	ABI97463
67.1	21	6	ABX31852	ABX31852 Candida t	172	11.2	65.9	20	7	ABZ69288	ABZ69288
67.1	21	8	ADA73994	ADA73994 PCR prime	173	11.2	65.9	20	7	ACC70535	ACC70535
67.1	21	9	ADC45047	ADC45047 Yeast CYP	c 174	11.2	65.9	22	2	AAQ25485	AAQ25485
67.1	21	9	ADC45617	ADC45617 Yeast CYP	c 175	11.2	65.9	22	2	AAQ47482	AAQ47482
67.1	21	9	ADE52128	ADE52128 C. tropic	c 176	11.2	65.9	22	2	AAQ47481	AAQ47481
67.1	21	10	ADE64292	ADE64292 C. tropic	c 177	11.2	65.9	22	2	AAQ47478	AAQ47478
67.1	22	6	ABX33518	ABX33518 Human nov	c 178	11.2	65.9	22	2	AAT59005	AAT59005
67.1	23	4	AAV51668	AAV51668 Zea mays	c 179	11.2	65.9	22	9	ADC42663	ADC42663
67.1	23	4	AAH26387	AAH26387 Arabidops	180	11.2	65.9	24	1	AAZ48745	AAZ48745
67.1	25	7	ABZ84293	ABZ84293 Toxicology	181	11.2	65.9	24	2	AAQ03988	AAQ03988
67.1	25	8	ACI08297	ACI08297 Human mic	182	11.2	65.9	24	6	ABI91496	ABI91496
67.1	25	8	ACI24037	ACI24037 Human mic	c 183	11.2	65.9	24	6	ABI91497	ABI91497
67.1	25	8	ACI96759	ACI96759 Human mic	184	11.2	65.9	25	8	ACI60412	ACI60412
67.1	25	8	ACK06719	ACK06719 Human mic	185	11.2	65.9	25	8	ACI52542	ACI52542
67.1	25	8	ACI84796	ACI84796 Human mic	186	11.2	65.9	25	8	ACI14845	ACI14845
67.1	25	8	ACT72482	ACT72482 Human mic	187	11.2	65.9	25	8	ACK27387	ACK27387
67.1	25	8	ACK02959	ACK02959 Human mic	188	11.2	65.9	25	8	ACI60528	ACI60528
67.1	25	8	ACI81958	ACI81958 Human mic	189	11.2	65.9	25	8	ACI60529	ACI60529
67.1	25	8	ACH64513	ACH64513 DNA tagge	c 190	11.2	65.9	25	8	ACI86997	ACI86997
67.1	26	2	AAV41896	AAV41896 Nucleotid	191	11.2	65.9	25	8	ACK27386	ACK27386
67.1	28	3	AA90486	AA90486 Human GM-	192	11.2	65.9	25	8	ACI30901	ACI30901
67.1	29	3	AA97475	AA97475 Human cyt	c 193	11.2	65.9	25	8	ACK09896	ACK09896
67.1	29	3	AC66470	AC66470 Chimaeric	194	11.2	65.9	25	8	ACI66630	ACI66630
67.1	29	3	AC62388	AC62388 PCR prime	c 195	11.2	65.9	25	8	ACH56625	ACH56625
67.1	29	4	AA65402	AA65402 Oligonucl	196	11.2	65.9	26	2	AAQ35448	AAQ35448
67.1	29	6	ABA92587	ABA92587 His-tagge	c 197	11.2	65.9	28	5	AAZ89563	AAZ89563
67.1	30	7	ABQ82808	ABQ82808 Human Akt	198	11.2	65.9	28	5	AAI71525	AAI71525
67.1	30	7	ABV76894	ABV76894 PCR prime	199	11.2	65.9	29	2	AAH28381	AAH28381
67.1	30	7	ABQ82821	ABQ82821 Human Akt	c 200	11.2	65.9	29	5	AAH79354	AAH79354
67.1	30	7	AAO0527	AAO0527 Human Akt	201	11.2	65.9	30	2	AAQ31229	AAQ31229
67.1	30	7	AAO00725	AAO00725 IL-1 anti	202	11.2	65.9	30	2	AAT58617	AAT58617
67.1	30	9	ADD96166	ADD96166 Human Akt	203	11.2	65.9	30	5	AAF73600	AAF73600
67.1	30	9	ADD96162	ADD96162 Human Akt	204	11.2	65.9	30	6	ABX69090	ABX69090
67.1	30	9	ADE06650	ADE06650 Primer #1	205	11.2	65.9	33	2	AAQ63125	AAQ63125
67.1	30	9	ADE15864	ADE15864 Primer #1	206	11.2	65.9	33	3	AAZ92394	AAZ92394
67.1	33	2	AAV49532	AAV49532 Human DR4	207	11.2	65.9	34	3	AAZ92392	AAZ92392
67.1	33	3	AAO02220	AAO02220 Human Dea	208	11.2	65.9	34	7	ACD66090	ACD66090
67.1	33	6	ABL54272	ABL54272 Human kid	209	11.2	65.9	36	7	ACD66014	ACD66014
67.1	35	3	AA70370	AA70370 3' oligon	210	11.2	65.9	36	7	AAZ55016	AAZ55016
67.1	36	2	AA717651	AA717651 ATP kinas	211	11.2	65.9	37	2	AAQ79551	AAQ79551
67.1	37	6	ABQ74340	ABQ74340 Truncated	212	11.2	65.9	37	2	AAT42364	AAT42364
67.1	40	2	AAV781196	AAV781196 Micro gen	213	11.2	65.9	37	6	AAZ42543	AAZ42543
67.1	41	2	AAV51139	AAV51139 Maize pol	214	11.2	65.9	37	8	ACH00385	ACH00385
67.1	41	2	AAV03900	AAV03900 Primer MP	215	11.2	65.9	38	4	ABK05930	ABK05930
67.1	41	4	AAH46990	AAH46990 PCR mutag	216	11.2	65.9	38	4	ABK08615	ABK08615
67.1	42	2	AAV47887	AAV47887 Maize pol	217	11.2	65.9	38	4	ABK05963	ABK05963
67.1	42	2	AAV03899	AAV03899 Primer MP	218	11.2	65.9	38	4	ABL47952	ABL47952
67.1	42	3	AA30545	AA30545 C. tropic	219	11.2	65.9	38	4	ABL47877	ABL47877
67.1	42	4	AAH46989	AAH46989 PCR mutag	220	11.2	65.9	38	4	ABL47923	ABL47923
67.1	42	6	ABK31864	ABK31864 Candida t	221	11.2	65.9	38	6	ABK21136	ABK21136
67.1	42	9	ADC45059	ADC45059 Yeast CYP	222	11.2	65.9	38	6	ABK21007	ABK21007
67.1	42	9	ADC45629	ADC45629 Yeast CYP	223	11.2	65.9	38	6	ABK21127	ABK21127
67.1	42	9	ADE52140	ADE52140 C. tropic	224	11.2	65.9	38	7	ACD54078	ACD54078
67.1	42	10	ADE64304	ADE64304 C. tropic	225	11.2	65.9	38	7	ACD53781	ACD53781
67.1	45	2	AA77766	AA77766 Human Fce	226	11.2	65.9	38	7	ACD53867	ACD53867
67.1	47	3	AAZ66237	AAZ66237 Human map	227	11.2	65.9	38	7	ACD54081	ACD54081
67.1	47	3	AAZ69386	AAZ69386 Human map	228	11.2	65.9	41	6	ABZ48126	ABZ48126
67.1	47	7	ACA61137	ACA61137 VEE virus	229	11.2	65.9	41	6	AA519996	AA519996
67.1	50	6	ABZ02370	ABZ02370 Human leu	c 230	11.2	65.9	42	6	ABK50960	ABK50960
67.1	50	7	ACA61138	ACA61138 Vector en	231	11.2	65.9	43	2	AAT03423	AAT03423
67.1	51	4	AAZ26839	AAZ26839 Human SNP	232	11.2	65.9	43	2	AAT03419	AAT03419
67.1	51	6	AAZ30141	AAZ30141 Human pit	233	11.2	65.9	44	2	AAT31178	AAT31178
67.1	51	6	AAZ30535	AAZ30535 Human PTT	c 234	11.2	65.9	45	2	AAV04792	AAV04792
67.1	58	5	ABV12543	ABV12543 Human pro	c 235	11.2	65.9	45	2	AAV31047	AAV31047
67.1	60	6	ABN48834	ABN48834 Human spl	c 236	11.2	65.9	45	3	AAV71611	AAV71611
67.1	60	6	ABN38174	ABN38174 Human spl	237	11.2	65.9	46	3	AAV71610	AAV71610
67.1	60	6	ABN35972	ABN35972 Human spl	238	11.2	65.9	46	3	AAZ48234	AAZ48234
67.1	60	6	ABN59571	ABN59571 Human spl	c 239	11.2	65.9	47	2	AAV04796	AAV04796
67.1	60	6	ABN43569	ABN43569 Human spl	c 240	11.2	65.9	47	2	AAV31051	AAV31051
65.9	20	2	AAZ93660	AAZ93660 PCR prime	241	11.2	65.9	47	2	AAZ05441	AAZ05441
65.9	20	3	AAZ74612	AAZ74612 Human bia	242	11.2	65.9	50	4	AAZ29316	AAZ29316



63.5	25	8	ACH55721	Ach55721 DNA seque	462	10.8	63.5	47	3	AAZ65874	Aaz65874
63.5	25	8	ACH55596	Ach55596 DNA targe	C 463	10.8	63.5	47	4	Aah88577	Aah88577
63.5	25	8	ACH53411	Ach53411 DNA targe	C 464	10.8	63.5	47	6	AAQ23733	Aad23733
63.5	25	8	ACH61594	Ach61594 DNA targe	C 465	10.8	63.5	48	2	AAQ12494	Aaq12494
63.5	26	6	ABQ96692	Abq96692 KIAA 0858	466	10.8	63.5	48	2	AAV29088	Aav29088
63.5	27	6	AAx80874	Aax80874 Oligonuc	467	10.8	63.5	50	3	AAAF37167	Aaf37167
63.5	27	6	ABA92330	Aba92330 Human neu	468	10.8	63.5	50	4	AAAF54365	Aaf54365
63.5	28	2	AAQ34762	Aaq34762 PCR prime	469	10.8	63.5	50	4	Aah89715	Aah89715
63.5	28	2	AAQ41583	Aaq41583 XYZ const	470	10.8	63.5	50	6	ABZ28951	Abz28951
63.5	29	3	AAV26135	Aav26135 IBRV gD g	471	10.8	63.5	50	6	ABX03302	Abx03302
63.5	29	3	AAZ88654	Aaz88654 Human TRF	472	10.8	63.5	50	6	ABZ05971	Abz05971
63.5	29	3	AAAC60145	Aac60145 cDNA #3.	473	10.8	63.5	50	6	ACD68402	AcD68402
63.5	29	3	AAAL07474	Aaal07474 Oligonuc	474	10.8	63.5	50	8	ACH04504	Ach04504
63.5	29	3	AAAL2281	Aaal2281 Primer us	475	10.8	63.5	50	8	ACD68048	AcD68048
63.5	29	4	AAF73430	Aaf73430 Grand fir	476	10.8	63.5	50	9	ADCL18099	Adcl18099
63.5	29	6	ABA05907	Aba05907 Human RTN	477	10.8	63.5	50	9	ADD70745	Add70745
63.5	29	6	ABA01904	Aba01904 Human Cha	478	10.8	63.5	50	9	ADD39822	AdD39822
63.5	29	9	ADD41419	Add41419 Murine G+	479	10.8	63.5	50	9	ADD70268	AdD70268
63.5	30	1	AAAN91929	Aaan91929 Variable	480	10.8	63.5	50	9	ADD38389	AdD38389
63.5	30	2	AAQ22380	Aaq22380 Alpha-car	481	10.8	63.5	50	9	ADD39345	AdD39345
63.5	30	3	AAAC88016	Aac88016 Human CLA	482	10.8	63.5	50	9	ADD38868	AdD38868
63.5	30	3	AAAC55309	Aac55309 Activatio	483	10.8	63.5	50	9	ADD39345	AdD39345
63.5	30	3	AAA49125	Aaa49125 P4M1AS pr	484	10.8	63.5	50	9	ADD40299	AdD40299
63.5	30	4	AAAD17808	Aad17808 Zea mays	485	10.8	63.5	50	9	ADE50520	AdE50520
63.5	30	6	ABX67997	Abx67997 Novel Hel	486	10.8	63.5	50	9	ADE20132	AdE20132
63.5	30	6	ABX69283	Abx69283 Novel Hel	487	10.8	63.5	50	9	ADE50043	AdE50043
63.5	30	6	ABK89309	Abk89309 N-acetyl g	488	10.8	63.5	50	9	ADG93362	AdG93362
63.5	30	6	ABK84938	Abk84938 Cadherin-	489	10.8	63.5	51	2	ADE21601	AdE21601
63.5	30	6	ABK84958	Abk84958 Cadherin-	490	10.8	63.5	51	2	AAQ24985	Aaq24985
63.5	30	7	ABX77184	Abx77184 Mouse ser	491	10.8	63.5	51	2	AAV19306	Aav19306
63.5	30	9	ADE25894	Ade25894 GalNac-tr	492	10.8	63.5	51	4	AAI73420	Aai73420
63.5	31	2	AAQ90543	Aaq90543 Human SII	493	10.8	63.5	51	4	AAI73418	Aai73418
63.5	31	2	AAQ60010	Aat60010 RNA polym	494	10.8	63.5	51	4	AAH89233	Aah89233
63.5	31	7	ABZ75115	Abz75115 Cole1 ori	495	10.8	63.5	51	4	AAH89233	Aah89233
63.5	33	2	AAZ06811	Aaz06811 Maize met	496	10.8	63.5	51	4	AAH89714	Aah89714
63.5	33	5	AAAF63968	Aaf63968 Human TRF	497	10.8	63.5	51	4	AAH89448	Aah89448
63.5	34	6	ABA01513	Aba01513 TyLM2 PCR	498	10.8	63.5	51	4	AAH79568	Aah79568
63.5	36	2	AAAT47524	Aat47524 Human hep	499	10.8	63.5	53	7	ACC80814	Acc80814
63.5	36	8	ACA61590	Aca61590 Human hep	500	10.8	63.5	54	1	AAH71173	Aah71173
63.5	38	2	AAQ28045	Aaq28045 Primer CA	501	10.8	63.5	55	6	ABK70409	Abk70409
63.5	39	6	ABS61136	Abs61136 Human pol	502	10.8	63.5	60	2	AAZ19575	Aaz19575
63.5	40	2	AAV69456	Aav69456 plasmid p	503	10.8	63.5	60	2	AAZ25695	Aaz25695
63.5	40	6	AAAX88880	Aax88880 circular	504	10.8	63.5	60	3	AAZ34765	Aaz34765
63.5	41	2	AAAT36338	Aat36338 Oligonuc	505	10.8	63.5	60	6	ABN37568	Abn37568
63.5	41	4	AAH75954	Aah75954 Primer ML	506	10.8	63.5	60	6	ABN48987	Abn48987
63.5	41	6	ABL54117	AbL54117 Arrestin	507	10.8	63.5	60	6	ABN41483	Abn41483
63.5	41	6	ABK50367	Abk50367 Embryonic	508	10.8	63.5	60	7	ABN46458	Abn46458
63.5	41	6	ABV73446	Abv73446 Novel pol	509	10.8	63.5	60	7	ADA89026	Ada89026
63.5	42	3	AAZ64640	Aaz64640 Hairpin r	510	10.6	62.4	60	8	ABT43554	Abt43554
63.5	43	2	AAQ20830	Aaq20830 Primer PC	511	10.6	62.4	13	5	ABC05503	Abc05503
63.5	43	2	AAQ20831	Aaq20831 Primer PC	512	10.6	62.4	13	5	ABC05502	Abc05502
63.5	43	2	AAQ55335	Aaq55335 ICAM-1 pr	513	10.6	62.4	18	2	AAV01067	Aav01067
63.5	43	2	AAQ55334	Aaq55334 ICAM-1 pr	514	10.6	62.4	18	2	AAV12357	Aav12357
63.5	43	2	AAV03175	Aav03175 PCR prime	515	10.6	62.4	19	3	AAZ75693	Aaz75693
63.5	43	2	AAV03176	Aav03176 PCR prime	516	10.6	62.4	20	7	AAAT68325	Aaat68325
63.5	43	2	AAV40177	Aav40177 DNA seque	517	10.6	62.4	21	3	AAAC35394	Aaac35394
63.5	43	2	AAQ04202	Aaq04202 Truncated	518	10.6	62.4	22	5	AAH62117	Aah62117
63.5	43	3	AAQ04203	Aaq04203 Truncated	519	10.6	62.4	22	5	AAH49299	Aah49299
63.5	43	3	AAA07187	Aaa07187 PCR prime	520	10.6	62.4	23	4	AAI70050	Aai70050
63.5	43	3	AAA07188	Aaa07188 PCR prime	521	10.6	62.4	23	6	ABL99937	AbL99937
63.5	43	3	AAAB8946	Aaab8946 PCR prime	522	10.6	62.4	24	2	AAAT16974	Aaat16974
63.5	43	3	AAAB8945	Aaab8945 PCR prime	523	10.6	62.4	24	4	AAAS06829	Aaas06829
63.5	45	2	AAQ74805	Aaq74805 Cannabino	524	10.6	62.4	25	3	AAAS35478	Aaas35478
63.5	45	2	AAV71056	Aav71056 Primer Rh	525	10.6	62.4	25	6	ABZ29888	Abz29888
63.5	45	3	AAZ06983	Aaz06983 GABA B re	526	10.6	62.4	25	8	ABZ29887	Abz29887
63.5	45	3	AAZ46393	Aaz46393 IL-6 rece	527	10.6	62.4	25	8	ACI09567	AcI09567
63.5	45	4	AAAD04061	Aaad04061 R. sphaer	528	10.6	62.4	25	8	ACI99970	AcI99970
63.5	46	2	AAAS9756	Aas9756 Primer P1	529	10.6	62.4	25	8	ACK30923	AcK30923
63.5	46	3	AAAS4262	Aas4262 PCR prime	530	10.6	62.4	25	8	ACK09807	AcK09807
63.5	46	6	ABL41019	AbL41019 Human fib	531	10.6	62.4	25	8	ACI71492	AcI71492
63.5	47	3	AAZ666170	Aaz666170 Human map	532	10.6	62.4	25	8	ACI39340	AcI39340
					533	10.6	62.4	25	8	ACI15439	AcI15439
					534	10.6	62.4	25	8	ACI11362	AcI11362

62.4	25	8	ACI08001	Human mic	608	10.6	62.4	38	6	ABK21077	Abk21077
62.4	25	8	ACI30817	Human mic	609	10.6	62.4	38	6	ABK30890	Abk30890
62.4	25	8	ACI45908	Human mic	610	10.6	62.4	38	7	ACD54053	AcD54053
62.4	25	8	ACK15855	Human mic	611	10.6	62.4	38	7	ACD53974	AcD53974
62.4	25	8	ACI09566	Human mic	612	10.6	62.4	38	7	ACD54069	AcD54069
62.4	25	8	ACI06917	Human mic	613	10.6	62.4	38	7	ACD53888	AcD53888
62.4	25	8	ACK14137	Human mic	614	10.6	62.4	38	7	ACD53707	AcD53707
62.4	25	8	ACK02617	Human mic	615	10.6	62.4	38	7	ACD54002	AcD54002
62.4	25	8	ACI08930	Human mic	616	10.6	62.4	39	6	ABS61164	AbS61164
62.4	25	8	ACI181976	Human mic	617	10.6	62.4	40	6	ABS53840	AbS53840
62.4	25	8	ACI06156	Human mic	618	10.6	62.4	47	2	AZ06997	Az06997
62.4	25	8	ACI69675	Human mic	619	10.6	62.4	47	3	AZ06997	Az06997
62.4	25	8	ACK6328	Human mic	620	10.6	62.4	48	4	AAC93125	AaC93125
62.4	25	8	ACH62969	DNA targe	621	10.6	62.4	50	1	AAN91670	AaN91670
62.4	25	8	ACH64693	DNA targe	622	10.6	62.4	50	4	AAL33780	AaL33780
62.4	27	2	AAX60980	HIV-1 gag	623	10.6	62.4	50	4	AAL20738	AaL20738
62.4	28	6	ABQ82519	Pyroliido	624	10.6	62.4	50	5	ABL00173	AbL00173
62.4	29	3	AA99345	PCR prime	625	10.6	62.4	50	6	ABZ03886	AbZ03886
62.4	30	2	AAV64585	Tobacco C	626	10.6	62.4	50	6	ABZ02293	AbZ02293
62.4	30	4	AAI69870	Bovine la	627	10.6	62.4	50	7	ABX79093	AbX79093
62.4	31	2	AAQ90108	VCAM-1 ex	628	10.6	62.4	51	4	AAL28634	AaL28634
62.4	33	2	AAV58706	Nucleotid	629	10.6	62.4	51	4	AAL33431	AaL33431
62.4	34	2	AZ32615	TeTr (tet	630	10.6	62.4	51	4	AAI74839	AaI74839
62.4	34	3	AA63507	PCR prime	631	10.6	62.4	51	4	AAI75954	AaI75954
62.4	34	6	AD26978	Left SOR	632	10.6	62.4	51	4	AAS59923	AaS59923
62.4	34	7	ACD65956	Anti-HCV	633	10.6	62.4	54	2	AZ06429	Az06429
62.4	34	7	ACD66088	Anti-HCV	634	10.6	62.4	54	2	AZ06429	Az06429
62.4	35	2	AAQ79589	Primer to	635	10.6	62.4	54	2	AZ06429	Az06429
62.4	35	9	ADC08969	PCR prime	636	10.6	62.4	57	3	AZ44220	Az44220
62.4	36	2	AAQ22009	Subtilisi	637	10.6	62.4	57	3	AZ58678	Az58678
62.4	36	2	AAI34758	PCR prime	638	10.6	62.4	59	2	AAI16859	AaI16859
62.4	36	2	AAI86982	Primer us	639	10.6	62.4	59	2	AAI16859	AaI16859
62.4	36	7	ACA60735	Mouse MHC	640	10.6	62.4	60	2	AAQ34076	AaQ34076
62.4	36	7	ACD65957	Anti-HCV	641	10.6	62.4	60	2	AAI16851	AaI16851
62.4	36	7	ACD66079	Anti-HCV	642	10.6	62.4	60	2	AAI16851	AaI16851
62.4	37	6	ABQ83137	Human HGP	643	10.6	62.4	60	6	ABN39843	AbN39843
62.4	37	6	ABK53582	Human CLC	644	10.6	62.4	60	6	ABN48722	AbN48722
62.4	37	7	ACA08168	Necrosis	645	10.6	62.4	60	6	ABN36428	AbN36428
62.4	38	4	AAH96871	Human Chk	646	10.6	62.4	60	6	ABN47773	AbN47773
62.4	38	4	AAH96936	Human Chk	647	10.6	62.4	60	8	ACC83844	AcC83844
62.4	38	4	AAH96831	Human Chk	648	10.4	61.2	12	2	AAQ65643	AaQ65643
62.4	38	4	AAH96870	Human Chk	649	10.4	61.2	12	2	AAI00035	AaI00035
62.4	38	4	AAH96812	Human Chk	650	10.4	61.2	12	2	AAI13200	AaI13200
62.4	38	4	ABK05862	Human NOG	651	10.4	61.2	12	2	AAV27829	AaV27829
62.4	38	4	ABK05954	Human NOG	652	10.4	61.2	12	2	AAV58766	AaV58766
62.4	38	4	ABK05608	Human NOG	653	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05667	Human NOG	654	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05667	Human NOG	655	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05667	Human NOG	656	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05834	Human NOG	657	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05897	Human NOG	658	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05828	Human NOG	659	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05744	Human NOG	660	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05837	Human NOG	661	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05949	Human NOG	662	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05821	Human NOG	663	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05856	Human NOG	664	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05851	Human NOG	665	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05843	Human NOG	666	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05777	Human NOG	667	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABK05896	Human NOG	668	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABL47909	Human GRI	669	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABL47860	Human GRI	670	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABL47857	Human GRI	671	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	4	ABL47953	Human GRI	672	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABL41275	Staphyloc	673	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK21118	Human ERG	674	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK21122	Human ERG	675	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK20902	Human ERG	676	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK21010	Human ERG	677	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK21065	Human ERG	678	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK20909	Human ERG	679	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK20989	Human ERG	680	10.4	61.2	12	2	AAI1385	AaI1385
62.4	38	6	ABK21013	Human ERG	680	10.4	61.2	12	2	AAI1385	AaI1385



61.2	33	4	AAH74189	AaH74189 s1 RNA bi	C 900	10.4	61.2	60	6	ABN37235	Abn37235
61.2	33	4	AAH49782	AaH49782 Human gam	901	10.4	61.2	60	6	ABN38490	Abn38490
61.2	33	6	ABK12617	AbK12617 NR1 in ver	C 902	10.4	61.2	60	6	ABN42436	Abn42436
61.2	33	6	ABA96887	Aba96887 Retinal b	C 903	10.4	61.2	60	6	ABN41914	Abn41914
61.2	33	6	AAI54040	Aai54040 Human EF-	904	10.4	61.2	60	6	ABN58871	Abn58871
61.2	33	6	ABK88397	AbK88397 Human clu	C 905	10.4	61.2	60	6	ABN37537	Abn37537
61.2	33	6	ABZ20665	AbZ20665 Human G p	906	10.4	61.2	60	6	ABN38700	Abn38700
61.2	33	6	ABQ76776	AbQ76776 Human bin	907	10.4	61.2	60	6	ABN38450	Abn38450
61.2	33	6	ACC47533	Acc47533 Human L-a	908	10.4	61.2	60	6	ABN49945	Abn49945
61.2	33	6	ABA93682	Aba93682 Human zin	C 909	10.4	61.2	60	6	ABN41445	Abn41445
61.2	33	6	ABV77388	AbV77388 DNA bindi	910	10.4	61.2	60	6	ABN50405	Abn50405
61.2	33	6	AAI42073	Aai42073 Human apo	911	10.4	61.2	60	6	ABN49956	Abn49956
61.2	33	6	ABL56255	AbL56255 Ribosomal	912	10.4	61.2	60	6	ABN36109	Abn36109
61.2	33	6	AAI99781	Aai99781 Human nuc	913	10.4	61.2	60	6	ABN38242	Abn38242
61.2	33	6	ABA96635	Aba96635 Human adh	C 914	10.4	61.2	60	6	ABN41094	Abn41094
61.2	33	7	ABX12246	AbX12246 Human lys	915	10.4	61.2	60	6	ABN49600	Abn49600
61.2	34	2	AAZ23458	Aaz23458 Plant Dre	916	10.2	60.0	15	4	AAF52071	Aaf52071
61.2	34	4	AAI65144	Aai65144 Neurogene	C 917	10.2	60.0	17	4	ABK00659	Abk00659
61.2	34	5	AAH75521	Aah75521 Human hun	918	10.2	60.0	17	6	ABN10489	Abn10489
61.2	35	2	AAV31138	Aav31138 C-Jun ami	919	10.2	60.0	17	6	ABN10490	Abn10490
61.2	35	2	AAV31140	Aav31140 Fos amino	920	10.2	60.0	17	6	ABN10491	Abn10491
61.2	35	4	AAF74463	Aaf74463 Human PRO	C 921	10.2	60.0	17	7	ACD50674	Acd50674
61.2	36	2	AAQ74213	Aaq74213 Influenza	922	10.2	60.0	17	7	ACD61500	Acd61500
61.2	36	2	AAQ74230	Aaq74230 Influenza	C 923	10.2	60.0	17	7	ACD54536	Acd54536
61.2	36	2	AAI90211	Aai90211 DP-1 PCR	C 924	10.2	60.0	17	7	ACD64416	Acd64416
61.2	36	6	AAAD35820	Aad35820 Human MIS	C 925	10.2	60.0	17	8	ACF05206	Acf05206
61.2	36	7	ACC69897	Acc69897 HIV-1 pla	C 926	10.2	60.0	17	9	ADC04439	Adc04439
61.2	36	7	ACC69886	Acc69886 HIV-1 pla	C 927	10.2	60.0	17	9	ADC04437	Adc04437
61.2	37	6	ABK87815	AbK87815 Human Kai	C 928	10.2	60.0	17	9	ADC04438	Adc04438
61.2	38	2	AAI29811	Aai29811 Sense pri	929	10.2	60.0	18	6	ABV72903	Abv72903
61.2	38	2	AAI45848	Aai45848 Hepatitis	930	10.2	60.0	18	6	ABL31605	AbL31605
61.2	38	4	AAF82375	Aaf82375 Rabies vi	931	10.2	60.0	19	3	AAZ70082	Aaz70082
61.2	38	4	AAF82383	Aaf82383 Rabies vi	C 932	10.2	60.0	19	6	ABL45001	AbL45001
61.2	40	3	AAC61030	Aac61030 Protease	933	10.2	60.0	19	6	ABL45001	AbL45001
61.2	40	7	ABX76598	AbX76598 M. avium	C 934	10.2	60.0	19	9	ADD00605	Add00605
61.2	41	6	ABA05171	Aba05171 Human gam	C 935	10.2	60.0	19	9	ADD00606	Add00606
61.2	41	6	ABA05170	Aba05170 Human gam	936	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ46434	AbZ46434 Human ald	937	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ44292	AbZ44292 Human ATP	C 938	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ46504	AbZ46504 Human ALD	939	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ49034	AbZ49034 Human ALD	C 940	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ48946	AbZ48946 Human ald	C 941	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	8	ACC42076	Acc42076 Human SCN	942	10.2	60.0	20	3	AAA08053	Aaa08053
61.2	47	3	AAZ67299	Aaz67299 Human map	943	10.2	60.0	20	4	AAH25872	Aah25872
61.2	47	3	AAZ66968	Aaz66968 Human map	944	10.2	60.0	20	6	AAH25872	Aah25872
61.2	47	3	AAZ66843	Aaz66843 Human map	C 945	10.2	60.0	20	6	AAH25872	Aah25872
61.2	48	1	AAH82108	Aah82108 Part of r	C 946	10.2	60.0	20	6	AAH25872	Aah25872
61.2	48	1	AAH91668	Aah91668 Cloning s	947	10.2	60.0	20	6	AAH25872	Aah25872
61.2	48	2	AAH28522	Aah28522 WO 990919	948	10.2	60.0	20	6	AAH25872	Aah25872
61.2	49	1	AAH82109	Aah82109 Part of r	C 949	10.2	60.0	20	6	AAH25872	Aah25872
61.2	49	1	AAH91669	Aah91669 Cloning s	C 950	10.2	60.0	20	7	ABZ89261	Abz89261
61.2	49	5	ABA10683	Aba10683 Tail adap	C 951	10.2	60.0	20	7	ABZ89261	Abz89261
61.2	50	1	AAH82110	Aah82110 Part of r	C 952	10.2	60.0	20	7	ABZ89261	Abz89261
61.2	50	4	AAH33543	Aah33543 Human SNP	C 953	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	4	AAH86408	Aah86408 Human pro	C 954	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	6	ABZ01340	AbZ01340 Human leu	C 955	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	6	ABZ04848	AbZ04848 Human leu	C 956	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	50	6	ABZ06154	AbZ06154 Human leu	C 957	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	50	6	ABZ02443	AbZ02443 Human leu	C 958	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	4	AAH31922	Aah31922 Human SNP	959	10.2	60.0	21	2	AAV05819	Aav05819
61.2	51	4	AAH33266	Aah33266 Human SNP	960	10.2	60.0	21	2	AAV05819	Aav05819
61.2	51	4	AAH33400	Aah33400 Human SNP	C 961	10.2	60.0	21	2	AAV05819	Aav05819
61.2	51	4	AAH33441	Aah33441 Human SNP	C 962	10.2	60.0	21	2	AAV05819	Aav05819
61.2	51	5	ABL00733	AbL00733 Human ami	963	10.2	60.0	21	3	AAZ76372	Aaz76372
61.2	51	5	ABL00790	AbL00790 Human ami	964	10.2	60.0	21	3	AAZ76372	Aaz76372
61.2	51	6	ABD44422	Abd44422 FMDV DNA	C 965	10.2	60.0	21	5	AAF74397	Aaf74397
61.2	53	1	AAH97169	Aah97169 Clair-BamH	966	10.2	60.0	21	7	ABZ21588	Abz21588
61.2	57	3	AAH75586	Aah75586 PCR prime	C 967	10.2	60.0	21	9	ADCS6979	Adc6979
61.2	57	4	AAH32991	Aah32991 DNA encod	968	10.2	60.0	21	9	ADCS6979	Adc6979
61.2	57	6	AAH20697	Aah20697 Human zal	969	10.2	60.0	22	2	AAQ82691	Aaq82691
61.2	58	9	AAH59860	Aah59860 Bacillus	970	10.2	60.0	22	2	AAQ82691	Aaq82691
61.2	60	2	AAH15730	Aah15730 PCR prime	971	10.2	60.0	22	2	AAV13071	Aav13071
61.2	60	3	AAH29382	Aah29382 Holliday	972	10.2	60.0	22	2	AAV13069	Aav13069

60.0 22 3 AAZ43166  
 60.0 24 2 AAT91333  
 60.0 24 3 AAZ54548  
 60.0 24 3 AAZ54540  
 60.0 24 4 AAZ32563  
 60.0 24 4 AAS09674  
 60.0 24 6 ABQ04543  
 60.0 24 6 ABQ04543  
 60.0 24 6 ABQ10691  
 60.0 24 6 ABQ10830  
 60.0 24 6 ABQ00206  
 60.0 24 6 ABQ04445  
 60.0 24 6 ABQ10732  
 60.0 24 6 ABQ10871  
 60.0 24 6 ABQ04502  
 60.0 24 6 ABQ00263  
 60.0 24 6 ABQ04404  
 60.0 24 6 ABK13817  
 60.0 24 6 AB185885  
 60.0 24 6 AB183258  
 60.0 24 6 AB185884  
 60.0 24 6 AB183259  
 60.0 24 6 AB184958  
 60.0 24 6 AB192525  
 60.0 24 6 AB184959  
 60.0 24 6 AB192524  
 60.0 24 9 ADC71555  
 60.0 25 4 AAI65599

Aaz43166 PCR prime  
 Aat91333 Bacillus  
 Aaz54548 Neisseria  
 Aaz54540 Neisseria  
 Aat32563 Energy tr  
 Aas09674 Oat Beta  
 Abk33443 Human TNF  
 Abq04543 Oligonucl  
 Abq10691 Oligonucl  
 Abq10830 Oligonucl  
 Abq00206 Oligonucl  
 Abq04445 Oligonucl  
 Abq10732 Oligonucl  
 Abq10871 Oligonucl  
 Abq04502 Oligonucl  
 Abq00263 Oligonucl  
 Abq04404 Oligonucl  
 Abk13817 RT-PCR pr  
 Ab185885 Capture o  
 Ab183258 Capture o  
 Ab185884 Capture o  
 Ab183259 Capture o  
 Ab184958 Capture o  
 Ab192525 Capture o  
 Ab184959 Capture o  
 Ab192524 Capture o  
 Ade71555 Human NOV  
 Aai65599 Primer fo

## ALIGNMENTS

andard; DNA; 17 BP.

; (first entry)

use PCR primer SEQ ID NO:17.

oma; oesophagus; malignancy; PCR primer; ss.

S.

-Al.

; 2002WO-US006504.

; 2001US-0273277P.

V PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

32795/79.

CR method for detecting malignancies, e.g. adenocarcinoma of  
 us comprises conducting a PCR amplification on a DNA sample in  
 ion mixture.

ge 40; 141pp; English.

invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 ducted in first and second amplification stages, each with one  
 cycles comprising denaturing, annealing and elongating steps  
 longating step may be conducted at the same temperature as the  
 tep. The second amplification stage of (M1) is conducted under

CC different reaction conditions from that of the first amplifica  
 CC to modulate the relative rate of production of the first amplifi  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) int  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of met  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contamination  
 CC decreases the time it takes to carry out a PCR reaction. The p  
 CC sequence represents a glucuronidase (gus) PCR primer, which is  
 CC example from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0;

OY 1 CGAGTGAAGATCCCTT 17  
 |||||  
 Db 1 CGAGTGAAGATCCCTT 17

## RESULT 2

ABQ82538  
 ID ABQ82538 standard; DNA; 22 BP.

AC ABQ82538;

XX 18-DEC-2002 (first entry)

DE Beta-glucuronidase PCR primer SEQ ID NO:4.

XX Adenocarcinoma; oesophagus; malignancy; PCR primer; ss.

XX Homo sapiens.

XX WO200270751-Al.

XX 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006504.

XX 02-MAR-2001; 2001US-0273277P.

XX (UYPI-) UNIV PITTSBURGH.

XX Godfrey TE, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

XX WPI; 32795/79.

XX Multiplex PCR method for detecting malignancies, e.g. adenocarc  
 the oesophagus comprises conducting a PCR amplification on a DNA  
 a PCR reaction mixture.

XX Claim 4; Page 30; 141pp; English.

CC The present invention describes a multiplex polymerase chain re  
 CC (PCR) (M1) comprising conducting PCR on a DNA sample in a react  
 CC mixture conducted in first and second amplification stages, eac  
 CC or more PCR cycles comprising denaturing, annealing and elongat  
 CC where the elongating step may be conducted at the same temperat  
 CC annealing step. The second amplification stage of (M1) is condu  
 CC different reaction conditions from that of the first amplifica  
 CC to modulate the relative rate of production of the first amplifi  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of met  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contamination

he time it takes to carry out a PCR reaction. The present  
presents a beta-glucuronidase (beta-gus) PCR primer, which is  
example from the present invention

BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

ilarity 100.0%; Score 17; DB 6; Length 22;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
AGTGAAGATCCCTT 18

andard; DNA; 22 BP.

(first entry)

relating to the invention ZC40,575 SEQ ID NO:129.

imer; zcytor17; antiinflammatory; dermatological;  
ssive; antimicrobial; vaccine; inflammatory disease;  
y bowel disease; ulcerative colitis; Crohn's disease;  
atitis; eczema; psoriasis; endotoxaemia; septicemia;  
syndrome; infectious disease.

D-A2.

; 2003WO-US0001984.

; 2002US-0350325P.

; 2002US-0375323P.

; 2002US-0435315P.

GENETICS INC.

; Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
Gross JA, Dillon SR;

18179/58.

7 ligand polypeptides, useful for treating inflammatory  
ach as inflammatory bowel disease, ulcerative colitis, Crohn's  
pic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.

SEQ ID NO 129; 372pp; English.

on relates to a novel isolated zcytor17 ligand polypeptide. A  
of the invention has antiinflammatory, dermatological,  
ssive, and antimicrobial activity, and may have a use in a  
a polypeptide is useful for treating inflammatory diseases,  
lamatory bowel disease, ulcerative colitis, Crohn's disease,  
atitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
me or infectious diseases. The present sequence is used in  
fication of the invention.

BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

ilarity 100.0%; Score 17; DB 9; Length 22;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||

Db 2 CGAGTGAAGATCCCTT 18

RESULT 4  
AAQ12740/c  
ID AAQ12740 standard; DNA; 50 BP.  
XX  
AC AAQ12740;  
XX  
DT 25-MAR-2003 (revised)  
DT 09-JAN-2003 (revised)  
DT 26-SEP-1991 (first entry)  
XX  
DE Uida-2 probe for E. coli, S. sonnei and S. flexneri detection.  
XX  
KW Detection; probe; Uida; pathogens; PCR; Shigella.  
XX  
OS Synthetic.  
XX  
FN EP438115-A.  
XX  
PD 24-JUL-1991.  
XX  
PF 15-JAN-1991; 91EP-00100408.  
XX  
PR 19-JAN-1990; 90US-00467813.  
XX  
PA (PEKE ) PERKIN-ELMER CORP.  
XX  
PI Atlas RM, Bej AK, Mahbubani MH, Miller R, Steffan RJ;  
XX  
DR WPI; 1991-216812/30.  
XX  
PT Detection of microbial pathogens and faecal contamination indic  
PT recovering cells, lysing, recovering DNA, amplifying by polymer  
PT reaction, and detection of amplified sequence.  
XX  
PS Claim 22; Page 22; 14pp; English.  
XX  
CC A 166 bp region of the E. coli Uida gene, based upon the sequen  
CC reported by Jefferson et al., FNAS 83:8447-8451 (1986), was amp  
CC using the primers 1939E-1 (AAQ12728) and 2085R-1 (AAQ12729). Th  
CC is located between 1998 bp and 2047 bp. The primers and this pr  
CC used in the detection of E. coli, S. sonnei and S. flexneri de  
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 2  
CC to correct PA field.)  
XX  
SQ Sequence 50 BP; 11 A; 15 C; 13 G; 11 T; 0 U; 0 Other;  
XX  
Query Match 90.6%; Score 15.4; DB 2; Length 50;  
Best Local Similarity 94.1%; Pred. No. 1.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
Db 17 CGAGTGAAGATCCCTT 1  
RESULT 5  
AAQ96499/c  
ID AAX96499 standard; DNA; 20 BP.  
XX  
AC AAX96499;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
XX  
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarc  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;  
KW neutralising epitope; PCR primer; ss.  
XX  
OS Synthetic.



la pneumoniae.

2.

; 98WO-IB001890.

; 97FR-00014673.

; 98US-0107078P.

SET.

57842/30.

ence of Chlamydia pneumoniae.

Disclosure; 1912pp; English.

7517 represent PCR primers used to amplify open reading frames nucleic acid sequences from the genome of Chlamydia pneumoniae 90). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in se, sarcoidosis, sinusitis, purulent otitis media, erythema pharyngitis. The polypeptides encoded by the open reading he C. pneumoniae genome (see AAY34584-AAY35879) can be used nic compositions as vaccines. Vectors containing C. pneumoniae sequences can also be used as immunogenic compositions, where the vector directs the expression of a neutralising C. pneumoniae

BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

ilarity 78.8%; Score 13.4; DB 2; Length 20;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGTGAAGATCCCC 15

|||||

AATGAAGATCCCC 3

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 121677.

obe; expressed sequence tag; microarray; gene expression; iation; biallelic marker; polymorphism; human; es comparison.

IS.

.0-A1.

1.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

2;

;67953/53.

XX New array of nucleic acid probes, useful for in situ hybridizat  
PT Southern, Northern or dot-blot hybridization to identify or det  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 121677; 9pp; English.

XX The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense m  
CC Also disclosed is a method of gene expression analysis. The arr  
CC in monitoring gene expression levels by hybridisation to a DNA  
CC in analysis of genetic variation or in hybridisation of tag-lab  
CC compounds. The nucleic acid probes are specifically designed fo  
CC of at least one target sequence. The method of analysis compris  
CC hybridising at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridisation. The nuclei  
CC probes are attached to a solid support. The analysis comprises  
CC gene expression levels, identifying biallelic markers or polymo  
CC or family members of a gene and a cross-species comparison. Eac  
CC nucleic acids further comprises a tag sequence. The array of nu  
CC probes is useful in in situ hybridisation, in Southern, Norther  
CC blot hybridisation to identify or detect the sequence or specif  
CC mutations of any gene, in mapping the 5' termini of mRNA molecu  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b  
CC isolated and previously sequenced. The sequence presented is on  
CC nucleic acid probes incorporated in the microarray. Note: The s  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BF; 10 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 8; Length 25;

Best Local Similarity 93.3%; Pred. No. 1.6e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15

|||||

Db 9 CGAGTGAAGATCCCC 23

RESULT 7

ABA05396/c

ID ABA05396 standard; DNA; 32 BP.

XX ABA05396;

XX 26-FEB-2002 (first entry)

XX Human IL-1beta PCR primer R1.

XX Human; IL-1 beta gene; IL-1M; IL-1beta; PCR primer; ss.

XX Homo sapiens.

XX CN1307138-A.

XX 08-AUG-2001.

XX 28-JAN-2000; 2000CN-00100695.

XX 28-JAN-2000; 2000CN-00100695.

XX (PREC-) PRECLINICAL MEDICINE INST MILITARY ACAD.

XX Ling S, Song X;

XX WPI; 2002-026898/04.

XX Expression vector pBVIL1 comprising modified human IL-1 beta ge  
PT and endoenzyme sites, useful for antigen expression.

XX

3TGAAGATCCCCT	16
3TGAAGATCCCCT	26

XX	T lymphocyte specific transcription factor TCF-111-99 probe #2.
DE	
XX	
KW	Human; T lymphocyte specific transcription factor TCF-111.99; c
XW	kW infection: immunological disease: gene therapy: probe: ss.

3. The present invention provides the protein and coding sequences of T lymphocyte specific transcription factor TCF-111.99. The sequence is used in the treatment of infections, cancer and immunological diseases. The present sequence is a probe for the coding sequence of the invention.

XX Sequence 41 BP; 12 A; 11 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCT 16  
| | | | | | | | | | | | | | | |  
Db 2 GAGTGAAGATCCCAT 16

RESULT 12  
ABA94074  
ID ABA94074 standard; DNA; 41 BP.  
XX AC ABA94074;  
XX  
XX 07-MAY-2002 (first entry)  
XX DT  
XX DE Human oestrogen receptor related protein 9.13 probe 2 SEQ ID NO  
XX  
XX KW Human; oestrogen receptor related protein 9.13; cytostatic; haem  
XX KW virucide; immunomodulatory; antiinflammatory; gene therapy; haem  
XX KW malignant tumour; human immunodeficiency virus infection; HIV i  
XX KW immunological disease; inflammation; probe; ss.  
XX OS Homo sapiens.  
XX OS  
XX PN WO200196387-A1.  
XX  
XX PD 20-DEC-2001.  
XX  
XX PF 04-JUN-2001; 2001WO-CN000891.  
XX  
XX PR 05-JUN-2000; 2000CN-00116318.  
XX  
XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
XX PI Mao Y, Xie Y;  
XX  
XX DR WPI; 2002-075586/10.  
XX  
XX PT Estrogen-receptor related protein 9.13 and encoding polynucleot  
XX PT in diagnosis and treatment of malignant tumors, hemopathy, huma  
XX PT immunodeficiency virus infection, immunological diseases and  
XX PT inflammation.  
XX  
XX PS Example 6; Page 20; 36pp; Chinese.  
XX  
XX CC The present invention describes human oestrogen-receptor relate  
XX CC 9.13 (I). (I) has cytostatic, haemostatic, virucide, immunomod  
XX CC antiinflammatory activities. The polynucleotide (II) encoding (I  
XX CC used in gene therapy. (I) and (II) can be used in the diagnosis  
XX CC treatment of malignant tumour, haemopathy, human immunodeficien  
XX CC (HIV) infection, immunological diseases and various inflammatio  
XX CC present sequence represents a probe for human oestrogen recepto  
XX CC protein 9.13, which is used in an example from the present inve  
XX  
XX SQ Sequence 41 BP; 12 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCT 16  
| | | | | | | | | | | | | | | |  
Db 2 GAGTGAAGATCCCAT 16

Page 21(Disclosure); 35pp; Chinese.

invention provides the protein and coding sequences of human  
e specific transcription factor TCF-111.99. The sequences can  
the treatment of infections, cancer and immunological  
he present sequence is a probe for the coding sequence of the

BP; 12 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

78.8%; Score 13.4; DB 6; Length 41;  
ilarity 93.3%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCT 16  
| | | | | | | | | | | | | | | |  
GTGAGATCCCAT 16

andard; DNA; 41 BP.

(first entry)

e specific transcription factor TCF-111-99 probe #1.

mphocyte specific transcription factor TCF-111.99; cancer;  
immunological disease; gene therapy; probe; ss.

us.

3. The present invention provides the protein and coding sequences of T lymphocyte specific transcription factor TCF-111.99. The sequence is used in the treatment of infections, cancer and immunological diseases. The present sequence is a probe for the coding sequence of the invention.

XX Sequence 41 BP; 12 A; 11 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCT 16  
| | | | | | | | | | | | | | | |  
Db 2 GAGTGAAGATCCCAT 16

Page 21(Disclosure); 35pp; Chinese.

invention provides the protein and coding sequences of human  
e specific transcription factor TCF-111.99. The sequences can  
the treatment of infections, cancer and immunological  
he present sequence is a probe for the coding sequence of the

BP; 12 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

78.8%; Score 13.4; DB 6; Length 41;  
ilarity 93.3%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCT 16  
| | | | | | | | | | | | | | | |  
GTGAGATCCCAT 16

andard; DNA; 41 BP.

(first entry)

e specific transcription factor TCF-111-99 probe #1.

mphocyte specific transcription factor TCF-111.99; cancer;  
immunological disease; gene therapy; probe; ss.

us.

3. The present invention provides the protein and coding sequences of T lymphocyte specific transcription factor TCF-111.99. The sequence is used in the treatment of infections, cancer and immunological diseases. The present sequence is a probe for the coding sequence of the invention.

XX Sequence 41 BP; 12 A; 11 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCT 16  
| | | | | | | | | | | | | | | |  
Db 2 GAGTGAAGATCCCAT 16

Page 21(Disclosure); 35pp; Chinese.

invention provides the protein and coding sequences of human  
e specific transcription factor TCF-111.99. The sequences can  
the treatment of infections, cancer and immunological  
he present sequence is a probe for the coding sequence of the

BP; 12 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

78.8%; Score 13.4; DB 6; Length 41;  
ilarity 93.3%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCT 16  
| | | | | | | | | | | | | | | |  
GTGAGATCCCAT 16

andard; DNA; 41 BP.

(first entry)

e specific transcription factor TCF-111-99 probe #1.

mphocyte specific transcription factor TCF-111.99; cancer;  
immunological disease; gene therapy; probe; ss.

us.

3. The present invention provides the protein and coding sequences of T lymphocyte specific transcription factor TCF-111.99. The sequence is used in the treatment of infections, cancer and immunological diseases. The present sequence is a probe for the coding sequence of the invention.

XX Sequence 41 BP; 12 A; 11 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 6; Length 41;  
Best Local Similarity 93.3%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCT 16  
| | | | | | | | | | | | | | | |  
Db 2 GAGTGAAGATCCCAT 16

Page 21(Disclosure); 35pp; Chinese.

invention provides the protein and coding sequences of human  
e specific transcription factor TCF-111.99. The sequences can  
the treatment of infections, cancer and immunological  
he present sequence is a probe for the coding sequence of the

BP; 12 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

78.8%; Score 13.4; DB 6; Length 41;  
ilarity 93.3%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCT 16  
| | | | | | | | | | | | | | | |  
GTGAGATCCCAT 16

andard; DNA; 41 BP.

(first entry)

e specific transcription factor TCF-111-99 probe #1.

mphocyte specific transcription factor TCF-111.99; cancer;  
immunological disease; gene therapy; probe; ss.

us.

probe; expressed sequence tag; microarray; gene expression; mutation; polymorphism; polymorphic marker; human; comparison.

0-A1.  
 .  
 ; 2002US-00098263.  
 ; 2001US-0276759P.  
 YMETRIX INC.  
 ;  
 67953/53.  
 f nucleic acid probes, useful for in situ hybridization, in  
 orthern or dot-blot hybridization to identify or detect the  
 specific mutations of any gene.  
 Q ID NO 14835; 9pp; English.  
 on discloses a microarray comprising a plurality of nucleic  
 acid probes including one of 2,018,500 fully defined sequences,  
 ch, perfect mismatch, antisense match or antisense mismatch.  
 sed is a method of gene expression analysis. The array is used  
 ng gene expression levels by hybridisation to a DNA library,  
 of genetic variation or in hybridisation of tag-labelled  
 The nucleic acid probes are specifically designed for analysis  
 one target sequence. The method of analysis comprises  
 at least one or more nucleic acids to at least two or more  
 d probes and detecting the hybridisation. The nucleic acid  
 attached to a solid support. The analysis comprises monitoring  
 sion levels, identifying biallelic markers or polymorphisms,  
 embers of a gene and a cross-species comparison. Each of the  
 ds further comprises a tag sequence. The array of nucleic acid  
 sful in situ hybridisation, in Southern, Northern or dot-  
 isation to identify or detect the sequence or specific  
 f any gene, in mapping the 5' termini of mRNA molecules by  
 nsions or in screening cDNA or genomic libraries or subclones  
 nal subclones containing segments of DNA that have been  
 d previously sequenced. The sequence presented is one of the  
 d probes incorporated in the microarray. Note: The sequence  
 is patent can also be obtained in electronic format directly  
 at seqdata.uspto.gov/sequence.html  
 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;  
 75.3%; Score 12.8; DB 8; Length 25;  
 ilarity 87.5%; Pred. No. 3.5e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 AGTGAAGATCCCT 16  
 |||||  
 AGTGAAGACCTCT 23  
 andard; DNA; 25 BP.  
 (first entry)  
 array DNA oligonucleotide SEQ ID NO 60404.  
 obe; expressed sequence tag; microarray; gene expres-  
 sion; biallelic marker; polymorphism; human;  
 es comparison.  
 US.  
 0-A1.  
 XX PD 05-JUN-2003.  
 XX XX  
 XX PF 15-MAR-2002; 2002US-00098263.  
 XX XX  
 XX PR 16-MAR-2001; 2001US-0276759P.  
 XX XX  
 XX PA (AFFY-) AFFYMETRIX INC.  
 XX XX  
 XX PI Mittmann MP;  
 XX DR WPI; 2003-567953/53.  
 XX XX  
 XX PT New array of nucleic acid probes, useful for in situ hybridizat  
 XX PT Southern, Northern or dot-blot hybridization to identify or det  
 XX FS Claim 1; SEQ ID NO 60404; 9pp; English.  
 XX CC The invention discloses a microarray comprising a plurality of  
 CC acid probes including one of 2,018,500 fully defined sequences,  
 CC perfect match, perfect mismatch, antisense match or antisense m  
 CC Also disclosed is a method of gene expression analysis. The arr  
 CC in monitoring gene expression levels by hybridisation to a DNA  
 CC in analysis of genetic variation or in hybridisation of tag-lab  
 CC compounds. The nucleic acid probes are specifically designed fo  
 CC of at least one target sequence. The method of analysis compris  
 CC hybridising at least one or more nucleic acids to at least two  
 CC nucleic acid probes and detecting the hybridisation. The nuclei  
 CC probes are attached to a solid support. The analysis comprises  
 CC gene expression levels, identifying biallelic markers or polymo  
 CC or family members of a gene and a cross-species comparison. Eac  
 CC nucleic acids further comprises a tag sequence. The array of nu  
 CC probes is useful in situ hybridisation, in Southern, Northern  
 CC blot hybridisation to identify or detect the sequence or specif  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecu  
 CC primer extensions or in screening cDNA or genomic libraries or  
 CC for additional subclones containing segments of DNA that have b  
 CC isolated and previously sequenced. The sequence presented is o  
 CC nucleic acid probes incorporated in the microarray. Note: The s  
 CC data for this patent can also be obtained in electronic format  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX SQ Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 8; Length 25;  
 Best Local Similarity 87.5%; Pred. No. 3.5e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;  
 Qy 1 CGAGTGAAGATCCCT 16  
 |||||  
 Db 8 CGAGTGAAGATCCCT 23  
 RESULT 17  
 ACI30900  
 ID ACI30900 standard; DNA; 25 BP.  
 XX AC ACI30900;  
 XX AC ACI30900;  
 DT 13-OCT-2003 (first entry)  
 XX DE  
 XX DE Human microarray DNA oligonucleotide SEQ ID NO 30891.  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expres  
 KW genetic variation; biallelic marker; polymorphism; human;  
 XX cross-species comparison.  
 OS Homo sapiens.  
 XX OS  
 XX US2003104410-A1.  
 XX PD 05-JUN-2003.

2002US-00098263.

2001US-0276759P.

METRIX INC.

7953/53.

nucleic acid probes, useful for in situ hybridization, in Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

ID NO 30891; 9pp; English.

in discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids is further comprised in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format (from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html))

BP; 9 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;

Best Local Similarity 87.5%; Pred. NO. 3.5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16

||||| |||

GTGAAGACCTCT 16

undard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 109878.

be; expressed sequence tag; microarray; gene expression; ation; biallelic marker; polymorphism; human; is comparison.

;

-Al.

2002US-00098263.

XX

PR 16-MAR-2001; 2001US-0276759P.

XX

PA (AFFY-) AFFYMETRIX INC.

XX

PI Mitmann MP;

XX

PI MPI; 2003-567953/53.

XX

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 109878; 9pp; English.

XX

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acids is further comprised in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format (from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html))

Sequence 25 BP; 6 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;

Best Local Similarity 87.5%; Pred. NO. 3.5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16

||||| |||

Db 16 CGAGTGAAGATCCCT 1

RESULT 19

AAI65129/c

ID AAI65129 standard; DNA; 29 BP.

XX

AC AAI65129;

XX

DT 29-NOV-2001 (first entry)

XX

DE PCR primer #6.

XX

KW PCR primer; Charcot-Leyden Crystal 2; CLL2; ss.

XX

OS Unidentified.

XX

PN CN1303940-A.

XX

PD 18-JUL-2001.

XX

PF 27-OCT-1999; 99CN-00119870.

XX

PR 27-OCT-1999; 99CN-00119870.

XX

PA (UYFU-) UNIV FUDAN.

ion relates to a system for detecting gene expression, which is the same as the one described above. The system is useful because the gene corresponds to any of 8143 oligonucleotides (AZ08152) each having 50 base pairs (bp). The system is useful for gene expression profiling. It is particularly useful for a disease, monitoring (rate of) progression of a disease, therapeutic outcome, determining prognosis for a patient, disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection.

09:38:23 2004

us-10-090-326-17.max.rng

printed specification, but was obtained in electronic format  
m WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 12 A; 16 C; 18 G; 14 T; 0 U; 0 Other;  
75.3%; Score 12.8; DB 6; Length 60;  
larity 87.5%; Pred. No. 3.8e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAAGATCCGCTT 17  
|||||  
TCAAGATCGCTT 12

ndard; RNA; 17 BP.

(first entry)

arbon nuclear transport substrate sequence SEQ ID NO:551.

hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
ha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
ibozyme; angiogenic factor; cytosolic; antidiabetic;  
ic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
al; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
macular degeneration; inflammation; neovascular glaucoma;  
eration; psoriasis; verruca vulgaris; angiofibroma;  
erosis; pot-wine stain; Sturge Weber syndrome;  
unay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

99WO-US006507.

98US-0079678P.

RYME PHARM INC.

oberts E, Jarvis T, Coeshott C, Mcswiggen JA;

1315/50.

mes for modulating the synthesis, expression and/or stability  
ncoding an angiogenic factors.

age 72; 305pp; English.

invention describes enzymatic nucleic acid molecules with RNA  
ivity, which specifically cleave RNA encoded by an aryl  
nuclear transporter (ARNT) gene, an integrin subunit beta 3  
egrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
i AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
3 to AAA17560 and AAA17623 to AAA17684 represent their  
ng target sequences; AAA17685 to AAA18385 and AAA19087 to  
present ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
5 to AAA19222 represent their corresponding target sequences;  
AAA20361 and AAA21501 to AAA21595 represent ribozyme  
or integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
AAA21688 represent their corresponding target sequences;  
AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
a subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
present their corresponding target sequences. The ribozymes of  
n are used for modulating the synthesis, expression and/or  
f an mRNA encoding angiogenic factor, especially ARNT,  
unit beta-3, integrin subunit alpha-6, or Tie-2. They are

CC especially used to treat cancer, diabetic retinopathy, age relat  
CC macular degeneration (ARMD), inflammation, and arthritis, as well  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca v  
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Webe  
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu sy  
CC and other syndromes and diseases related to the levels of ARNT,  
CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 17 BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 2; Length 17;  
Best Local Similarity 92.9%; Pred. No. 5.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACTGAAGATCCGCTT 16  
|||||  
Db 17 AGTGAAGATACGCTT 4

RESULT 23  
AAA17326/c  
ID AAA17326 standard; RNA; 17 BP.

XX AC AAA17326;

XX 19-JUN-2000 (first entry)

DT Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:  
DE Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angioge  
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin riboz  
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic  
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic;  
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arti  
KW age related macular degeneration; inflammation; neovascular glau  
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or  
of an mRNA encoding an angiogenic factors.

XX Claim 53; Page 72; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules  
cleaving activity, which specifically cleave RNA encoded by an  
hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit  
gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA167  
AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent the  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA190  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to  
CC and AAA19155 to AAA19222 represent their corresponding target s  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozym  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA2150  
CC AAA21596 to AAA21688 represent their corresponding target sequ  
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozym



a subunit beta 3, and AAA22476 to AAA23262, AAA23343 to present their corresponding target sequences. The ribozymes of on are used for modulating the synthesis, expression and/or f an mRNA encoding angiogenic factor, especially ARNT, bunit beta-3, integrin subunit alpha-6, or Tie-2. They are used to treat cancer, diabetic retinopathy, age related generation (ARMD), inflammation, and arthritis, as well as glaucoma, myopic degeneration, psoriasis, verruca vulgaris, a of tuberous sclerosis, pot-wine stains, Sturge Weber ippel-Treanunay-Weber syndrome, Osler-Weber-Rendu syndrome, yndromes and diseases related to the levels of ARNT, Tie-2, bunit alpha-6, or integrin subunit beta-3

BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

72.9%; Score 12.4; DB 2; Length 17;

ilarity 92.9%; Pred. No. 5.5e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGAAGATCCCTT 16

|||||  
TGAAGATCCCTT 2

andard; DNA; 29 BP.

(first entry)

PCR primer SEQ ID NO:9.

4; PCR primer; ss.

S.

; 98CN-00126050.

; 98CN-00126050.

V FUDAN.

Y, Tu Q;

44299/50.

in Rab24, its coding sequence, preparation and usage.

Page 13; 22pp; Chinese.

invention describes human Rab24. The human Rab24 protein is to mouse Rab24. The present sequence represents a PCR primer ab24 which is used in an example from the present invention

BP; 8 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 3; Length 29;

ilarity 92.9%; Pred. No. 5.8e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGAAGATCCCTT 17

|||||

TGAAGATCCCTT 1

ID AAQ41588 standard; DNA; 32 BP.  
XX  
AC AAQ41588;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-AUG-1993 (first entry)  
XX  
DE ZXY construct primer Y BAM.  
XX  
KW Human T cell reactive feline protein; TRFP; epitope; recombitop  
XX  
OS Synthetic.  
XX  
PN WO9308280-A1.  
XX  
PD 29-APR-1993.  
XX  
PF 16-OCT-1992; 92WO-US008694.  
XX  
PR 16-OCT-1991; 91US-00777859.  
PR 13-DEC-1991; 91US-00807529.  
XX  
PA (IMMU-) IMMULOGIC PHARM CORP.  
XX  
PI Rogers BL, Mergenstern JP, Bond JF, Garman RD, Kuo M, Morv  
XX  
DR WPI; 1993-152473/18.  
XX  
PT Recombitope peptide having T-cell stimulating activity - for th  
PT diagnosis and treatment of sensitivity to protein allergens,  
PT auto:antigens and protein antigens.  
XX  
PS Disclosure; Fig 10; 73pp; English.  
XX  
CC The primer is used in the construction of recombitope peptides  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 32 BF; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;  
  
Query Match 72.9%; Score 12.4; DB 2; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;  
  
Oy 2 GAGTGAAGATCCCC 15  
Db 14 GAGTGAAGATCCCC 1  
  
RESULT 26  
AAZ88659/c  
ID AAZ88659 standard; DNA; 32 BP.  
XX  
AC AAZ88659;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Human TRFP derived primer #8.  
XX  
KW T-cell reactive feline protein; TRFP; T cell epitope; T cell re  
KW down regulation; immune response; allergen; immunoglobulin E;  
KW sensitivity; cat protein allergen; human; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6019972-A.  
XX  
PD 01-FEB-2000.  
XX  
PF 02-SEP-1994; 94US-00300928.  
XX  
PR 03-NOV-1989; 89US-00431565.  
PR 28-FEB-1991; 91US-00662276.  
PR 13-DEC-1991; 91US-00807529.

; 92US-00857311.  
; 92US-00884718.  
; 93US-00006116.

JLOGIC PHARM CORP.

Greenstein JL, Kuo M, Briner TJ, Morville M;

16862/13.

human T cell reactive feline protein for treating sensitivity  
in allergens comprise at least one T cell epitope recognized  
receptor specific for the human T cell reactive feline

Col 123-124; 105pp; English.

ion describes a novel peptide (I) of human T cell reactive  
sin (hTRFP) having at least one T cell epitope recognized by a  
prior specific for the human T cell reactive feline protein,  
consisting of at least 7-30 amino acids, and having an amino  
ce derived from an amino acid sequence comprising 94, 96, 97,  
residues, given in the specification. The peptides down,  
a immune response to the allergen. The peptides have reduced  
in E binding and reduce T cell responsiveness. The peptide  
all in compositions for treating sensitivity to a cat protein  
a subject. This sequence represents a primer used to  
aptides comprising of two or more regions of human TRFP

BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 3; Length 32;  
ilarity 92.9%; Pred. No. 5.9e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCC 15  
|||||  
GTGAGGATCCCC 1

undard; cDNA; 32 BP.

(first entry)

; human T cell reactive feline protein; hTRFP; immunotherapy;

1.

; 95US-00431184.  
; 89US-00431565.  
; 91US-00662276.  
; 91US-00807529.  
; 92US-00857311.  
; 92US-00884718.  
; 93US-00006116.  
; 94US-00300928.

JLOGIC PHARM CORP.

Garman RD, Greenstein JL, Bond JF;

XX WPI; 2000-601477/57.

XX Detecting, preventing and treating sensitivity to cat protein a  
PT comprises combining a biological sample with a human T cell rea  
PT feline protein and determining the extent of binding that occur  
XX Disclosure; Col 123; 106pp; English.

XX The present invention relates to the detection of sensitivity t  
CC protein allergen by combining a blood sample from a subject wit  
CC peptide of human T cell reactive feline protein (hTRFP). This m  
CC the hTRFP peptides are useful for diagnosing, preventing and tr  
CC allergies by reducing or abolishing an individual's allergic re  
CC a cat allergen. DNA encoding the TRFP may be used as probes to  
CC equivalent sequences present in other species. These may furthe  
CC to study the mechanism of immunotherapy of cat allergy, and to  
CC modified derivatives, analogues or functional equivalents usefu  
CC immunotherapy. The present sequence was used in the invention

XX Sequence 32 BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCC 15  
|||||  
Db 14 GAGTGAAGATCCCC 1

RESULT 28

AAA07479/c

ID AAA07479 standard; DNA; 32 BP.

XX AAA07479;

XX 13-JUL-2000 (first entry)

XX Oligonucleotide used in isolation of TRFP coding sequence.

XX Cat; TRFP; human T-cell reactive feline protein; cat protein al  
XX house dust; Fel d I; cat allergy; Felis domesticus sensitivity;  
XX diagnosis; goat; sheep; horse; rabbit; dog; ss.

XX Synthetic.

XX US6025162-A.

XX 15-FEB-2000.

XX 28-APR-1995; 95US-00430944.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Morgenstern JP, Griffith IJ, Rogers BL;

XX WPI; 2000-181812/16.

XX New human T cell reactive feline protein, useful for desensitizi  
PT allergic individuals to cat allergens.

XX Disclosure; Col 123-124; 108pp; English.

XX This sequence is an oligonucleotide used to isolate TRFP. The ir

1 09:38:23 2004

us-10-090-326-17.max.rng

a human T cell reactive feline protein (TRFP). The protein is an allergen, and was isolated from a vacuum bag extract of house dust collected from several cats. TRFP is composed of two covalently linked peptide chains. TRFP is also referred to as Fel d I. TRFP and its peptides are reducing or preventing the adverse effects that exposure to feline allergens has on cat allergic individuals (i.e. to individuals to cat allergens or block the effect of the TRFP is also used in methods of diagnosing sensitivity to feline allergens in an individual. DNA sequences encoding TRFP can be used to locate equivalent sequences present in other species, sheep, horse, rabbit and dog, that may be useful in diagnostic and therapeutic applications

BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;  
Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCC 15  
|||||  
GTGAGATCCCC 1

standard; DNA; 32 BP.

(first entry)

in construction of TRFP derived peptides ZXY.

active feline protein; TRFP; Fel d I; cat allergen; primer;  
c; T cell stimulator; diagnostic; immunotherapy; ss.

95US-00430014.

89US-00431565.  
91US-00662276.  
91US-00807529.  
92US-00857311.  
92US-00894718.  
93US-00006116.  
94US-00300928.

ULOGIC PHARM CORP.

ers BL, Gefter ML, Morgenstern JP, Brauer AW;  
JL, Griffith IJ, Garman RD;

16905/27.

cell reactive feline protein useful for reducing or individual's allergic response to cat allergen comprising two covalently linked peptide chains.

Col 123-124; 106pp; English.

ion describes a novel naturally occurring cat protein allergen T cell reactive feline protein (TRFP), comprising two covalently linked peptide chains with a molecular weight of 20 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD under reducing conditions. The products of the invention have T cell activity and act as human T cell stimulators. TRFP is useful

for reducing or preventing the adverse effects of cat allergens on allergic individuals and in ex vivo diagnostic tests to determine cat allergen sensitivity so as to selectively use them to desensitize individual. Purified TRFP is also useful for studying mechanism of immunotherapy of cat allergy and to design modified derivatives, analogs or functional equivalents that are more useful in immunotherapy against cat allergy. DNA sequences encoding TRFP as probes to locate equivalent sequences present in other species (sheep, dogs, rabbits or horses) that may be useful in diagnostic therapeutics. Fully defined and characterized TRFP provides a very simple desensitization therapy. This sequence represents a used in the construction of TRFP derived peptides ZXY, YXZ and XX are used in the method of the invention

Sequence 32 BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAGATCCCC 15  
|||||  
Db 14 GAGTGAGATCCCC 1

RESULT 30

ABZ47913/C

ID ABZ47913 standard; DNA; 41 BP.

AC ABZ47913;

DT 26-JUN-2003 (first entry)

DE Human ATP-binding cassette ABOG1 gene polymorphic site, #4697.

Human; drug metabolising enzyme; gene; drug metabolism; chromosomal polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism;

Homo sapiens.

Key Location/Qualifiers

variation replace(21,A)

/\*tag= a

/standard\_name= "Single nucleotide polymorphism

WO200252044-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-JP011592.

27-DEC-2000; 2000JP-00399443.

02-MAY-2001; 2001JP-00135256.

27-AUG-2001; 2001JP-00256862.

(RIKE ) RIKEN KK.

Nakamura Y, Sekine A, Iida A, Saito S;

WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, c detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.

Claim 23; Page 153; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within encoding enzymes associated with drug metabolism. The invention to methods and compositions for identifying individuals who have

phism in such drug metabolising enzyme-encoding genes. The ns may be identified in a nucleic acid sample using probes or specific for a sequence selected from ABZ43217-ABZ50887 using a detection assays, including hybridisation assays, nucleic acid PCR-based methods. The invention also encompasses methods of and screening drugs using genetic polymorphism data. Genetic n data, particularly that relating to single nucleotide s (SNPs), may be used in studying the relationship between a variations and human diseases, conditions, and responses to are also useful as polymorphism markers for discovering genes or exacerbate certain diseases. SNPs are particularly useful a respects as they are stable in populations, occur and have lower mutation rates than other genome variations ating sequences. The detection and analysis of polymorphisms oding drug metabolising enzymes allows the customisation of les based upon the genetic profile of individual patients. not only take the guesswork out of selecting the drug with the arapeutic effect for a particular patient, but would also likelihood of adverse reactions, thereby increasing safety. he invention are also useful in the drug discovery and cesses. For example, individuals could be selected for als only if their genetic profiles indicate that they are responding to a particular drug or drug class, and previously candidates could be revived if they were matched with more patient populations. The methods, data and compositions of n may therefore lead to an increase in the range of g targets and decreases in the number of adverse drug ailed drug trials, the time taken for a drug to be approved, f time patients are on medication and the number of different a patient needs to take before finding an effective therapy

BP; 9 A; 9 C; 17 G; 6 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 6; Length 41;

ilarity 92.9%; Pred. No. 6e+03; Length 41;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCCCC 15

|||||  
GTGAAGATCCCC 26

indard; DNA; 41 BP.

(first entry)

itive 3' diphosphate nucleotidase 11.99 probe #1.

ite nucleotidase 11.99; enzyme; human; acidosis; gene therapy;

3.

; 2000CN-00116599.

; 2000CN-00116599.

UGHAI BIODOOR GENE DEV CO LTD.

Y;

05422/35.

peptide-human lithium sensitive 3' diphosphate nucleotidase  
ly nucleotide for coding this polypeptide.

XX Example 6; Page 22 (Disclosure); 35pp; Chinese.  
XX The present invention relates to novel human lithium sensitive  
CC diphosphate nucleotidase 11.99 (see AB875982). The enzyme and i  
CC sequence are useful for treating several diseases, such as horm  
CC related dysfunction disease and metabolic acid-base disequilib  
CC (acidosis). The present sequence is a probe, which was used in  
CC from the invention  
XX  
SQ Sequence 41 BP; 9 A; 9 C; 8 G; 15 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 6; Length 41;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 4 GTGAAGATCCCCCT 17

Db 16 GTGATGATCCCCCT 29

RESULT 32

ABK0658/c

ID ABK0658 standard; RNA; 17 BP.

AC ABK00658;

XX 12-MAR-2002 (first entry)

DE Human NOGO Hammerhead Ribozyme #658.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; hae  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead  
KW DNazyme; inozyme; G-cleaver; ambrzyme; zinzyme; lymphoma; leuk  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leuka  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell l  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; demen  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sc  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerativ

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIKA B M.

XX Blatt L, Mcswiggen J, Chowrika BM;

PI WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antise  
PT constructs, which down regulate expression of a CD20 gene or ne  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leuk  
PT central nervous system injury.

XX Claim 88; Page 76; 200pp; English.

on relates to a nucleic acid molecule which down regulates of a CD20 gene and a nucleic acid molecule which down expression of a neurite growth inhibitor gene (NOCO). The 3s may be enzymatic nucleic acids (e.g. a ribozyme or a inozyme (an endolytic nucleic acid cleaving an RNA molecule an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr e (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA motif). The CD20-targeting nucleic acid is used to cleave RNA the presence of a divalent cation that is preferably Mg<sup>2+</sup>, it may be contacted with a cell to reduce CD20 activity of e treat a patient having a condition associated with the level e treatment may further comprise the use of one or more In particular, the CD20 targeting nucleic acid may be used to oma, leukaemia, B-cell lymphoma, low-grade or follicular non- lymphoma (NHL), bulky low-grade or follicular NHL, mantle-cell HIV (human immunodeficiency virus) associated NHL, mantle-cell (CLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, mbocytopenia, and inflammatory arthropathy. The NOGO- nucleic acid is used to cleave RNA of the NOGO gene in the a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the d may be contacted with a cell to reduce NOGO activity of the eat a patient having a condition associated with the level of e treatment may further comprise the use of one or more In particular, the NOGO-targeting nucleic acid may be used to al nervous system (CNS) injury and cerebrovascular accident e), Alzheimer's disease, dementia, multiple sclerosis (MS), y-induced neuropathy, amyotrophic lateral sclerosis (ALS), disease, ataxia, Huntington's disease, Creutzfeldt-Jakob uscular dystrophy, and/or other neurodegenerative disease h respond to the modulation of NOGO expression. The present ; a hammerhead ribozyme of the invention

BP; 5 A; 1 C; 5 G; 0 T; 6 U; 0 Other;

71.8%; Score 12.2; DB 4; Length 17;

ilarity 82.4%; Pred.No. 7.1e+03; Mismatches 3; Indels 0; Gaps 0;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

ATGATATCCCTT 1

andard; DNA; 24 BP.

) (first entry)

alcohol dehydrogenase promoter primer 3.

alcohol dehydrogenase; genetic engineering; PCR; amplification; us protein; gene expression; primer; ss.

s oryzae.

-A.

9.

8; 98JP-00105712.

8; 98JP-00105712.

ANO PHARM KK.  
ENCY OF IND SCI & TECHNOLOGY.

626935/54.

oter derived from an Aspergillus genus microbe - useful for

PT producing exotic proteins.  
XX  
XX Example 2; Page 4; 1lpp; Japanese.  
XX  
XX Primers AAZ30689-Z30691 were used to PCR amplify the promoter s from the alcohol dehydrogenase gene (AAZ30680) from Aspergillus CC the invention relates to novel gene promoters (AAZ30680-Z30685) CC from Aspergillus oryzae which can be used in genetic engineering CC express heterologous proteins in Aspergillus XX  
SQ Sequence 24 BP; 5 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 2; Length 24;  
Best Local Similarity 82.4%; Pred.No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

|||||

20 CCAGTGAAGATCCCTT 4

RESULT 34

ABQ00239

ID ABQ00239 standard; DNA; 24 BP.

XX ABQ00239;

AC ABQ00239;

XX 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 230.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.

XX 25-AUG-2000; 2000US-0227948P.

XX 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or target nucleic acid sequence, has different addresses comprising different specific capture probes.

XX Claim 1; Page 49; 26lpp; English.

XX The invention relates to an oligonucleotide array (I) comprising 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the given in ABQ00010-ABQ13409. (I) is useful for immobilising a nucleic acid sequence by attaching a adapter nucleic acid (ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The above method is useful for detecting a target nucleic acid, which comprises detecting the presence of the modified target nucleic acid.

XX Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 24;

Best Local Similarity 82.4%; Pred.No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

||||| ||| ||  
GTGAGACCCCAATT 17

ndard; DNA; 24 BP.

(first entry)

ide adapter/capture probe 4469.

ide array; adapter sequence; probe; ss.

A2.

2001WO-US026519.

2000US-0227948P.

2000US-0228854P.

MINA INC.

12068/33.

ing adapter sequences useful for immobilizing or detecting a  
ic acid sequence, has different addresses comprising  
pecific capture probes.

ie 145; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least  
; addresses (adapter sequences) with each comprising a  
pture probe selected from a group consisting of the sequences  
00010-ABQ13409. (I) is useful for immobilizing a target  
l sequence by attaching a adapter nucleic acid (ABQ00010-  
; a target nucleic acid to form a modified target nucleic acid  
ng the modified target nucleic acid with (I). The steps of  
l is useful for detecting a target nucleic acid, which further  
etecting the presence of the modified target nucleic acid

BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

71.8%; Score 12.2; DB 6; Length 24;

ilarity 82.4%; Pred. No. 7.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

||||| ||| ||

GTGAGACCCCAATT 17

andard; DNA; 24 BP.

(first entry)

ide adapter/capture probe 10756.

ide array; adapter sequence; probe; ss.

XX WO200216649-A2.  
XX 28-FEB-2002.  
XX 27-AUG-2001; 2001WO-US026519.  
XX 25-AUG-2000; 2000US-0227948P.  
XX 29-AUG-2000; 2000US-0228854P.  
XX (ILLU-) ILLUMINA INC.  
XX Gunderson K;  
XX WPI; 2002-292068/33.  
XX Array comprising adapter sequences useful for immobilizing or de  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX Claim 1; Page 222; 261pp; English.  
XX The invention relates to an oligonucleotide array (I) comprising  
CC 25 different addresses (adapter sequences) with each comprising  
CC different capture probe selected from a group consisting of the  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a tar  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00  
CC ABQ13409) to a target nucleic acid to form a modified target nuc  
CC and contacting the modified target nucleic acid with (I). The st  
CC above method is useful for detecting a target nucleic acid, whic  
CC comprises detecting the presence of the modified target nucleic  
XX Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 24;

Best Local Similarity 82.4%; Pred. No. 7.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

OY 1 CGAGTGAAGATCCCTT 17

||||| ||| ||

Db 1 CGCGTGAGACCCCAATT 17

RESULT 37

ABQ10806/c

ID ABQ10806 standard; DNA; 24 BP.

XX ABQ10806;

XX AC

DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 10797.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.

XX 25-AUG-2000; 2000US-0227948P.

XX 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or d

elic acid sequence, has different addresses comprising specific capture probes.

ge 222; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least t addresses (adapter sequences) with each comprising a capture probe selected from a group consisting of the sequences Q00010-ABQ13409. (I) is useful for immobilising a target d sequence by attaching a adapter nucleic acid (ABQ00010- o a target nucleic acid to form a modified target nucleic acid ing the modified target nucleic acid with (I). The steps of d is useful for detecting a target nucleic acid, which further detecting the presence of the modified target nucleic acid

BP; 4 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

ilarity 71.8%; Score 12.2; DB 6; Length 24;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
CGTGAAGATCCCAT 8

andard; DNA; 24 BP.

; (first entry)

stide adapter/capture probe 4510.

stide array; adapter sequence; probe; ss.

3-A2.

2.

1; 2001WO-US026519.

0; 2000US-0227948P.

0; 2000US-0228854P.

LUMINA INC.

K;

292068/33.

rising adapter sequences useful for immobilizing or detecting a leic acid sequence, has different addresses comprising specific capture probes.

age 145; 261pp; English.

ion relates to an oligonucleotide array (I) comprising at least nt addresses (adapter sequences) with each comprising a capture probe selected from a group consisting of the sequences BQ00010-ABQ13409. (I) is useful for immobilising a target id sequence by attaching a adapter nucleic acid (ABQ00010- to a target nucleic acid to form a modified target nucleic acid ing the modified target nucleic acid with (I). The steps of od is useful for detecting a target nucleic acid, which further detecting the presence of the modified target nucleic acid

4 BP; 4 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||  
DB 24 CGCGTGAAGATCCCAT 8

RESULT 39

AAD27956/c

ID AAD27956 standard; DNA; 25 BP.

XX AAD27956;

XX 16-JUL-2002 (first entry)

XX Human D3 dopamine receptor nucleic acid amplifying primer #1.

XX Mental disorder; neurodegenerative disorder; schizophrenia;

KW manic depression; Tourette's syndrome; Parkinson's disease;

KW Alzheimer's disease; Huntington's disease; PCR primer; human;

KW D3 dopamine receptor; ss.

XX Homo sapiens.

XX WO200214547-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-IL000761.

XX 15-AUG-2000; 2000IL-00137865.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Fuchs S, Ilani T, Perl O;

XX WPI; 2002-315412/35.

Diagnosing neurodegenerative disorder in an individual by eval ratio of D3 dopamine receptor mRNA and/or alpha7 nicotinic ace receptor mRNA of test individual, to control gene mRNA of heal individual.

Example 1; Page 8; 33pp; English.

The invention relates to a method of diagnosing a mental disorder neurodegenerative disorder that involves measuring mRNA of D3 receptor and/or alpha7 nicotinic acetylcholine receptor (alpha7) and of a control gene in peripheral blood lymphocytes (PBLS) of individual and of at least one healthy control individual, calculating the ratio between D3 dopamine receptor mRNA and the control gene and/or the ratio between alpha7 ACHR mRNA and the control gene each individual, evaluating the ratios obtained for the tested individual and the healthy control individual. An increase in D3 dopamine mRNA and/or decrease in alpha7 ACHR mRNA in the tested individual comparison to the control individual indicates that the tested individual has a highly likelihood of having the disorder. The method is diagnosis and follow up of a mental disorder e.g. schizophrenia depression, Tourette's syndrome and a neurodegenerative disorder Parkinson's disease, Alzheimer's disease or Huntington's disease individual. The present sequence is a PCR primer for amplification of human D3 dopamine receptor nucleic acid

Sequence 25 BP; 8 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 25;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||||

AGTGAAGATCCCTTT 9

andard; DNA; 25 BP.

(first entry)

tide adapter/capture probe 12333.

tide array; adapter sequence; probe; ss.

-A2.

; 2001WO-US026519.

; 2000US-0227948P.

; 2000US-0228854P.

UMINA INC.

;

92068/33.

using adapter sequences useful for immobilizing or detecting a nucleic acid sequence, has different addresses comprising specific capture probes.

ge 241; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of the above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

BP; 4 A; 6 C; 9 G; 6 T; 0 U; 0 Other;

71.8%; Score 12.2; DB 6; Length 25;

ilarity 82.4%; Pred. No. 7.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTTT 17

|||||

CGTGAAGACCCCAT 9

andard; DNA; 25 BP.

(first entry)

tide adapter/capture probe 12292.

tide array; adapter sequence; probe; ss.

PN WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.

XX 25-AUG-2000; 2000US-0227948P.

PR 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

PI

XX WPI; 2002-292068/33.

DR

XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.

PT

XX Claim 1; Page 241; 261pp; English.

PS

XX The invention relates to an oligonucleotide array (I) comprising 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of the above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

CC

XX Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 U; 0 Other;

SQ

Query Match 71.8%; Score 12.2; DB 6; Length 25;

Best Local Similarity 82.4%; Pred. No. 7.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTTT 17

|||

Db 2 CGCGTGAAGACCCCAT 18

|||||

RESULT 42

ACI15438/c

ID ACI15438 standard; DNA; 25 BP.

XX ACI15438;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 15429.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression variation; biallelic marker; polymorphism; human; cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization

PT



northern or dot-blot hybridization to identify or detect the specific mutations of any gene.

3Q ID NO 15429; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. The array is used as a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises members of a gene and a cross-species comparison. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids is useful in situ hybridisation, in Southern, Northern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules or in screening cDNA or genomic libraries or polyclonal subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

5 BP; 8 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 8; Length 25;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

3AGTGAAGATCCCTT 17  
|||||  
3ATTGAAGTTCACCTT 1

standard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 109787.

robe; expressed sequence tag; microarray; gene expression; radiation; biallelic marker; polymorphism; human; comparison.

as.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

P;

567953/53.

of nucleic acid probes, useful for in situ hybridization, in Northern or dot-blot hybridization to identify or detect the specific mutations of any gene.

XX

PS Claim 1; SEQ ID NO 109787; 9pp; English.

XX

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. The array is used as a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises members of a gene and a cross-species comparison. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules or in screening cDNA or genomic libraries or polyclonal subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 8; Length 25;

Best Local Similarity 82.4%; Pred. No. 7.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

Db 23 CGTCTGAGGTCCCTT 7

RESULT 44

AAH96915

ID AAH96915 standard; RNA; 38 BP.

XX AAH96915;

XX 09-OCT-2001 (first entry)

XX Human Chk1 ribozyme SEQ ID NO: 2340.

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene th RNA cleavage; cancer; ss.

XX Homo sapiens.

XX WO200157206-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003504.

XX 03-FEB-2000; 2000US-0179983P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (FATT/) FATTAEY A R.

XX Fattaey AR, Jarvis T, Mcswiggen J, Boother RN, Holman PS;

XX WPI; 2001-496922/54.

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid molecules, which downregulate expression of a checkpoint kinase useful for treating colorectal, lung, breast or prostate cancer

XX Claim 5; Page 72; 115pp; English.

PS

invention provides nucleic acid molecules capable of  
ing the expression of the human checkpoint kinase-1 (Chk1)  
may be antisense or ribozyme sequences, and are useful in the  
f diseases associated with conditions affected by Chk1 levels,  
ancer. The present sequence is an oligonucleotide described in  
fication of the invention

BP; 12 A; 10 C; 9 G; 0 T; 7 U; 0 Other;

71.8%; Score 12.2; DB 4; Length 38;

ilarity 58.8%; Pred. No. 7.7e+03; Indels 0; Gaps 0;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

||: ||| : |||:

AGUCAAGGUCUCCU 34

andard; RNA; 38 BP.

(first entry)

Zinzyne substrate sequence #355.

antisense therapy; cytostatic; antiinflammatory; haemostatic;  
ective; nootropic; neuroprotective; antiparkinsonian;  
D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
ozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;  
homa; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
odeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
cytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
Y arthropathy; central nervous system injury;  
ular accident; CVA; Alzheimer's disease; multiple sclerosis;  
Y-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
disease; ataxia; Huntington's disease; substrate sequence;  
-Jakob disease; muscular dystrophy; neurodegenerative disease.

S.

-A2.

; 2001WO-US004273.

; 2000US-0181797P.

; 2000US-0185516P.

; 2000US-0187128P.

OZYME PHARM INC.

TT L.

WIGGEN J.

WRIRA B M.

Icswiggen J, Chowrira BM;

.07195/69.

d molecules, e.g., enzymatic nucleic acids and antisense  
which down regulate expression of a CD20 gene or neurite  
bitor gene useful for treating, e.g., lymphoma, leukemia, and  
vous system injury.

age 101; 200pp; English.

on relates to a nucleic acid molecule which down regulates  
of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO).  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme c  
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving a an RN  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyne (cle  
CC with a YGY motif). The CD20-targeting nucleic acid is used to  
CC of CD20 in the presence of a divalent cation that is preferably  
CC Furthermore, it may be contacted with a cell to reduce CD20 act  
CC the cell and treat a patient having a condition associated with  
CC of CD20. The treatment may further comprise the use of one or n  
CC therapies. In particular, the CD20 targeting nucleic acid may  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follic  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, n  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, n  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic ly  
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOG  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthe  
CC nucleic acid may be contacted with a cell to reduce NOGO activi  
CC cell and treat a patient having a condition associated with the  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may  
CC treat central nervous system (CNS) injury and cerebrovascular a  
CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-  
CC disease, muscular dystrophy, and/or other neurodegenerative dis  
CC states which respond to the modulation of NOGO expression. The  
CC sequence is a substrate sequence for a nucleic acid of the inve  
CC based on the human NOGO sequence

XX Sequence 38 BP; 10 A; 9 C; 11 G; 0 T; 8 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 4; Length 38;

Best Local Similarity 58.8%; Pred. No. 7.7e+03;

Matches 10; Conservative 4; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17

||||: ||| : |||:

Db 18 CGAGUCAAGGUCUCCU 34

Search completed: February 29, 2004, 09:03:59

Job time : 170.052 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 08:44:24 ; Search time 32.013 Seconds

(without alignments)

294.698 Million cell updates/sec

US-10-090-326-17

17

1 c9agtgaagatccccctt 17

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 874574

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
lived by analysis of the total score distribution.

# SUMMARIES

Query	Match	Length	DB	ID	Description
78.8	20	4	US-09-198-452A-5825	Sequence 5825, Ap	
72.9	32	1	US-07-807-529A-70	Sequence 70, Appl	
72.9	32	3	US-08-300-928C-101	Sequence 101, App	
72.9	32	3	US-08-430-944D-101	Sequence 101, App	
72.9	32	3	US-08-430-014-101	Sequence 101, App	
72.9	32	3	US-08-431-184-101	Sequence 101, App	
71.8	36	4	US-09-474-432B-265	Sequence 265, App	
71.8	37	4	US-09-476-387-264	Sequence 264, App	
71.8	38	4	US-09-474-432B-1199	Sequence 1199, Ap	
71.8	38	4	US-09-474-432B-1257	Sequence 1257, Ap	
71.8	38	4	US-09-474-432B-1303	Sequence 1303, Ap	
71.8	38	4	US-09-474-432B-1332	Sequence 1332, Ap	
71.8	38	4	US-09-476-387-1198	Sequence 1198, Ap	
71.8	38	4	US-09-476-387-1256	Sequence 1256, Ap	
71.8	38	4	US-09-476-387-1302	Sequence 1302, Ap	
71.8	38	4	US-09-476-387-1331	Sequence 1331, Ap	
71.8	46	3	US-09-070-408-67	Sequence 67, Appl	
70.6	31	4	US-09-302-357-2	Sequence 2, Appli	
70.6	43	1	US-07-936-533A-3	Sequence 3, Appli	
70.6	43	1	US-07-936-533A-32	Sequence 32, Appl	
70.6	43	1	US-08-344-257A-3	Sequence 3, Appli	
69.4	27	3	US-08-638-931-17	Sequence 17, Appl	
69.4	33	4	US-09-462-941-25	Sequence 25, Appl	
69.4	50	4	US-09-182-145-114	Sequence 114, App	
69.4	52	4	US-08-956-171E-2265	Sequence 2265, Ap	
69.4	57	3	US-08-908-643C-56	Sequence 56, Appl	
67.1	17	1	US-08-390-850-641	Sequence 641, App	

C	28	11.4	67.1	17	1	US-08-435-634-641	Sequence
C	29	11.4	67.1	20	4	US-09-198-452A-3355	Sequence
C	30	11.4	67.1	20	4	US-09-198-452A-4698	Sequence
C	31	11.4	67.1	20	4	US-09-198-452A-6352	Sequence
C	32	11.4	67.1	21	4	US-09-302-620B-48	Sequence
C	33	11.4	67.1	26	3	US-08-789-329C-15	Sequence
C	34	11.4	67.1	33	4	US-09-013-895A-10	Sequence
C	35	11.4	67.1	33	4	US-09-565-918-11	Sequence
C	36	11.4	67.1	33	4	US-09-448-868-10	Sequence
C	37	11.4	67.1	33	4	US-09-144-428-31	Sequence
C	38	11.4	67.1	36	1	US-08-299-498A-29	Sequence
C	39	11.4	67.1	36	5	PCT-US95-10813-29	Sequence
C	40	11.4	67.1	41	1	US-08-681-935-15	Sequence
C	41	11.4	67.1	41	3	US-08-939-323-15	Sequence
C	42	11.4	67.1	42	1	US-08-681-935-14	Sequence
C	43	11.4	67.1	42	3	US-08-939-323-14	Sequence
C	44	11.4	67.1	42	4	US-09-302-620B-60	Sequence
C	45	11.4	67.1	45	1	US-08-434-730-1	Sequence
C	46	11.4	67.1	45	1	US-08-434-730-10	Sequence
C	47	11.4	67.1	47	1	US-09-422-978-584	Sequence
C	48	11.4	67.1	47	4	US-09-422-978-3742	Sequence
C	49	11.2	65.9	20	4	US-09-422-978-8968	Sequence
C	50	11.2	65.9	20	4	US-09-198-452A-2986	Sequence
C	51	11.2	65.9	22	1	US-08-379-078-686	Sequence
C	52	11.2	65.9	22	1	US-08-379-078-687	Sequence
C	53	11.2	65.9	22	1	US-08-379-078-689	Sequence
C	54	11.2	65.9	22	1	US-08-379-078-690	Sequence
C	55	11.2	65.9	22	1	US-08-446-530-23	Sequence
C	56	11.2	65.9	22	2	US-09-097-562-23	Sequence
C	57	11.2	65.9	22	4	US-07-974-409C-243	Sequence
C	58	11.2	65.9	22	4	US-07-974-409C-245	Sequence
C	59	11.2	65.9	22	4	US-07-974-409C-249	Sequence
C	60	11.2	65.9	22	4	US-07-974-409C-251	Sequence
C	61	11.2	65.9	22	5	PCT-US93-00977-243	Sequence
C	62	11.2	65.9	22	5	PCT-US93-00977-245	Sequence
C	63	11.2	65.9	22	5	PCT-US93-00977-249	Sequence
C	64	11.2	65.9	22	5	PCT-US93-00977-251	Sequence
C	65	11.2	65.9	30	1	US-08-102-567-31	Sequence
C	66	11.2	65.9	30	3	US-08-462-947-31	Sequence
C	67	11.2	65.9	30	4	US-09-364-539-150	Sequence
C	68	11.2	65.9	31	1	US-08-467-420A-74	Sequence
C	69	11.2	65.9	31	1	US-08-470-110A-74	Sequence
C	70	11.2	65.9	31	1	US-08-667-769A-74	Sequence
C	71	11.2	65.9	31	2	US-08-940-371-74	Sequence
C	72	11.2	65.9	31	5	PCT-US95-17082A-74	Sequence
C	73	11.2	65.9	36	1	US-07-997-133-8	Sequence
C	74	11.2	65.9	36	5	US-07-997-133-8	Sequence
C	75	11.2	65.9	37	1	US-08-021-623C-12	Sequence
C	76	11.2	65.9	38	4	US-09-474-432B-1173	Sequence
C	77	11.2	65.9	38	4	US-09-474-432B-1178	Sequence
C	78	11.2	65.9	38	4	US-09-474-432B-1218	Sequence
C	79	11.2	65.9	38	4	US-09-474-432B-1236	Sequence
C	80	11.2	65.9	38	4	US-09-474-432B-1272	Sequence
C	81	11.2	65.9	38	4	US-09-474-432B-1275	Sequence
C	82	11.2	65.9	38	4	US-09-474-432B-1277	Sequence
C	83	11.2	65.9	38	4	US-09-474-432B-1301	Sequence
C	84	11.2	65.9	38	4	US-09-474-432B-1392	Sequence
C	85	11.2	65.9	38	4	US-09-474-432B-1401	Sequence
C	86	11.2	65.9	38	4	US-09-474-432B-1425	Sequence
C	87	11.2	65.9	38	4	US-09-474-432B-1453	Sequence
C	88	11.2	65.9	38	4	US-09-474-432B-1462	Sequence
C	89	11.2	65.9	38	4	US-09-476-387-1172	Sequence
C	90	11.2	65.9	38	4	US-09-476-387-1177	Sequence
C	91	11.2	65.9	38	4	US-09-476-387-1217	Sequence
C	92	11.2	65.9	38	4	US-09-476-387-1235	Sequence
C	93	11.2	65.9	38	4	US-09-476-387-1271	Sequence
C	94	11.2	65.9	38	4	US-09-476-387-1274	Sequence
C	95	11.2	65.9	38	4	US-09-476-387-1276	Sequence
C	96	11.2	65.9	38	4	US-09-476-387-1300	Sequence
C	97	11.2	65.9	38	4	US-09-476-387-1391	Sequence
C	98	11.2	65.9	38	4	US-09-476-387-1400	Sequence
C	99	11.2	65.9	38	4	US-09-476-387-1424	Sequence
C	100	11.2	65.9	38	4	US-09-476-387-1452	Sequence



62.4	38	4	US-09-476-387-1203	Sequence 1203, Ap	C 320	10.4	61.2	32	4	US-09-923-246-71	Sequence
62.4	38	4	US-09-476-387-1207	Sequence 1207, Ap	C 321	10.4	61.2	32	4	US-09-923-246-75	Sequence
62.4	38	4	US-09-476-387-1255	Sequence 1255, Ap	C 322	10.4	61.2	32	4	US-10-295-723-62	Sequence
62.4	38	4	US-09-476-387-1284	Sequence 1284, Ap	C 323	10.4	61.2	32	4	US-10-295-723-71	Sequence
62.4	38	4	US-09-476-387-1290	Sequence 1290, Ap	C 324	10.4	61.2	32	4	US-10-295-723-75	Sequence
62.4	38	4	US-09-476-387-1355	Sequence 1355, Ap	C 325	10.4	61.2	33	1	US-08-207-900B-7	Sequence
62.4	38	4	US-09-476-387-1405	Sequence 1405, Ap	C 326	10.4	61.2	33	3	US-08-930-605-12	Sequence
62.4	38	4	US-09-476-387-1410	Sequence 1410, Ap	C 327	10.4	61.2	33	3	US-09-073-569-14	Sequence
62.4	38	4	US-09-476-387-1416	Sequence 1416, Ap	C 328	10.4	61.2	33	4	US-09-169-205D-13	Sequence
62.4	38	4	US-09-476-387-1426	Sequence 1426, Ap	C 329	10.4	61.2	34	4	US-09-198-119C-20	Sequence
62.4	38	4	US-09-476-387-1455	Sequence 1455, Ap	C 330	10.4	61.2	35	1	US-08-683-877-7	Sequence
62.4	38	4	US-09-476-387-1476	Sequence 1476, Ap	C 331	10.4	61.2	35	1	US-08-683-877-9	Sequence
62.4	39	2	US-08-249-687C-12	Sequence 12, Appl	C 332	10.4	61.2	38	1	US-08-338-992B-20	Sequence
62.4	44	1	US-08-462-388-11	Sequence 11, Appl	C 333	10.4	61.2	38	4	US-09-010-733-20	Sequence
62.4	59	2	US-07-662-764D-42	Sequence 42, Appl	C 334	10.4	61.2	47	4	US-09-422-978-221	Sequence
62.4	59	2	US-07-662-764D-42	Sequence 42, Appl	C 335	10.4	61.2	47	4	US-09-422-978-1315	Sequence
62.4	59	4	US-09-193-390A-42	Sequence 42, Appl	C 336	10.4	61.2	47	4	US-09-422-978-2778	Sequence
62.4	59	4	US-09-193-390A-42	Sequence 42, Appl	C 337	10.4	61.2	49	4	US-09-538-709-973	Sequence
62.4	60	2	US-07-662-764D-26	Sequence 26, Appl	C 338	10.4	61.2	57	2	US-08-612-858-34	Sequence
62.4	60	2	US-07-662-764D-26	Sequence 26, Appl	C 339	10.4	61.2	57	4	US-09-522-217-65	Sequence
62.4	60	4	US-09-193-390A-26	Sequence 26, Appl	C 340	10.4	61.2	57	4	US-09-523-246-65	Sequence
62.4	60	4	US-09-193-390A-26	Sequence 26, Appl	C 341	10.4	61.2	57	4	US-10-295-723-65	Sequence
61.2	12	1	US-07-974-447-6	Sequence 6, Appli	C 342	10.4	61.2	60	3	US-09-448-280-13	Sequence
61.2	12	1	US-08-149-199-6	Sequence 4, Appli	C 343	10.2	60.0	17	1	US-08-166-664-11	Sequence
61.2	12	2	US-08-993-118-4	Sequence 4, Appli	C 344	10.2	60.0	17	4	US-09-866-108A-10481	Sequence
61.2	12	3	US-08-748-130-26	Sequence 4, Appli	C 345	10.2	60.0	17	4	US-09-866-108A-10482	Sequence
61.2	12	3	US-08-845-528C-4	Sequence 6, Appli	C 346	10.2	60.0	19	4	US-09-422-978-4438	Sequence
61.2	12	3	US-09-115-061-6	Sequence 11, Appl	C 347	10.2	60.0	20	1	US-08-065-078-2	Sequence
61.2	12	3	US-08-969-815-11	Sequence 11, Appl	C 348	10.2	60.0	20	3	US-08-932-445-2	Sequence
61.2	12	3	US-09-120-025-11	Sequence 6, Appli	C 349	10.2	60.0	20	4	US-09-198-452A-4378	Sequence
61.2	12	3	US-09-178-573B-6	Sequence 6, Appli	C 350	10.2	60.0	20	4	US-09-068-506-32	Sequence
61.2	12	3	US-09-261-079-6	Sequence 6, Appli	C 351	10.2	60.0	20	4	US-09-068-506-33	Sequence
61.2	12	4	US-09-419-568F-6	Sequence 6, Appli	C 352	10.2	60.0	21	1	US-08-644-271-19	Sequence
61.2	12	4	US-09-354-243B-6	Sequence 11, Appl	C 353	10.2	60.0	21	3	US-08-860-038-3	Sequence
61.2	12	4	US-09-710-481-11	Sequence 12, Appl	C 354	10.2	60.0	21	4	US-09-077-955-19	Sequence
61.2	12	4	US-09-656-952-12	Sequence 4, Appli	C 355	10.2	60.0	21	4	US-09-422-978-10728	Sequence
61.2	12	4	US-08-493-260A-4	Sequence 4, Appli	C 356	10.2	60.0	22	2	US-08-117-952-691	Sequence
61.2	12	4	US-09-066-281B-4	Sequence 1, Appl	C 357	10.2	60.0	22	3	US-09-189-060B-6	Sequence
61.2	12	4	US-09-553-875-11	Sequence 4, Appli	C 358	10.2	60.0	22	3	US-09-189-060B-8	Sequence
61.2	12	4	US-08-488-446-4	Sequence 11, Appl	C 359	10.2	60.0	22	3	US-09-084-303B-109	Sequence
61.2	12	4	US-09-768-670-11	Sequence 4, Appli	C 360	10.2	60.0	24	2	US-08-790-813-1	Sequence
61.2	12	4	US-08-467-344A-4	Sequence 4, Appli	C 361	10.2	60.0	24	3	US-08-646-861-23	Sequence
61.2	12	4	US-09-468-433C-4	Sequence 4, Appli	C 362	10.2	60.0	24	3	US-09-201-078-1	Sequence
61.2	17	1	US-08-390-850-642	Sequence 642, App	C 363	10.2	60.0	25	1	US-08-387-315A-13	Sequence
61.2	17	1	US-08-435-634-642	Sequence 642, App	C 364	10.2	60.0	25	4	US-08-754-559-13	Sequence
61.2	17	4	US-08-584-040-7577	Sequence 7577, Ap	C 365	10.2	60.0	25	4	US-09-866-108A-15373	Sequence
61.2	17	4	US-08-584-040-7578	Sequence 7578, Ap	C 366	10.2	60.0	25	4	US-09-866-108A-15375	Sequence
61.2	17	4	US-09-371-772B-3373	Sequence 3373, Ap	C 367	10.2	60.0	25	4	US-09-866-108A-15376	Sequence
61.2	17	4	US-09-371-772B-3374	Sequence 3374, Ap	C 368	10.2	60.0	25	4	US-09-866-108A-15377	Sequence
61.2	18	3	US-08-717-294-43	Sequence 43, Appl	C 369	10.2	60.0	25	4	US-09-866-108A-15378	Sequence
61.2	20	1	US-08-634-331-8	Sequence 8, Appli	C 370	10.2	60.0	25	4	US-09-866-108A-15379	Sequence
61.2	20	3	US-09-198-452A-4423	Sequence 4423, Ap	C 371	10.2	60.0	25	4	US-09-866-108A-15380	Sequence
61.2	22	3	US-08-943-731-521	Sequence 521, App	C 372	10.2	60.0	25	4	US-09-866-108A-15381	Sequence
61.2	23	1	US-08-017-664-6	Sequence 6, Appli	C 373	10.2	60.0	25	4	US-09-866-108A-15382	Sequence
61.2	24	2	US-08-702-105A-36	Sequence 8, Appli	C 374	10.2	60.0	25	4	US-09-866-108A-15383	Sequence
61.2	24	2	US-09-075-395-8	Sequence 36, Appl	C 375	10.2	60.0	26	4	US-09-194-285-16	Sequence
61.2	24	3	US-08-702-110A-36	Sequence 36, Appl	C 376	10.2	60.0	26	4	US-09-741-171-2	Sequence
61.2	24	3	US-08-789-329C-17	Sequence 17, Appl	C 377	10.2	60.0	27	4	US-08-609-443B-25	Sequence
61.2	24	3	US-09-325-571-36	Sequence 36, Appl	C 378	10.2	60.0	28	2	US-08-851-896-25	Sequence
61.2	24	4	US-09-848-585-36	Sequence 36, Appl	C 379	10.2	60.0	28	4	US-09-437-585A-16	Sequence
61.2	25	4	US-09-538-709-317	Sequence 317, App	C 380	10.2	60.0	28	4	PCT-US95-07542-7	Sequence
61.2	25	4	US-09-585-174-95	Sequence 95, Appl	C 381	10.2	60.0	28	5	US-09-565-596-1	Sequence
61.2	27	1	US-08-185-424B-4	Sequence 4, Appli	C 382	10.2	60.0	29	3	US-08-215-749A-1	Sequence
61.2	29	1	US-08-106-981-7	Sequence 7, Appli	C 383	10.2	60.0	30	1	US-08-814-052-38	Sequence
61.2	29	3	US-09-338-671-7	Sequence 11, Appl	C 384	10.2	60.0	30	3	US-08-812-829-30	Sequence
61.2	29	5	PCT-US94-12883-11	Sequence 16, Appl	C 385	10.2	60.0	30	3	US-09-230-180-11	Sequence
61.2	30	2	US-08-962-284-16	Sequence 22, Appl	C 386	10.2	60.0	30	3	US-09-230-180-12	Sequence
61.2	32	1	US-08-338-992B-22	Sequence 22, Appl	C 387	10.2	60.0	30	3	US-09-230-180-11	Sequence
61.2	32	4	US-09-522-217-62	Sequence 62, Appl	C 388	10.2	60.0	30	3	US-09-230-180-12	Sequence
61.2	32	4	US-09-522-217-71	Sequence 71, Appl	C 389	10.2	60.0	31	3	US-09-284-878-8	Sequence
61.2	32	4	US-09-522-217-75	Sequence 75, Appl	C 390	10.2	60.0	31	3	US-08-485-355B-19	Sequence
61.2	32	4	US-09-010-733-22	Sequence 22, Appl	C 391	10.2	60.0	31	5	PCT-US92-06045-6	Sequence
61.2	32	4	US-09-923-246-62	Sequence 62, Appl	C 392	10.2	60.0	34	3	US-09-110-517-10	Sequence

60.0	34	4	US-09-474-432B-235	Sequence 235, App	466	10.2	60.0	38	4	US-09-476-387-1408	Sequence
60.0	34	4	US-09-474-432B-242	Sequence 242, App	467	10.2	60.0	38	4	US-09-476-387-1427	Sequence
60.0	34	4	US-09-474-432B-252	Sequence 252, App	468	10.2	60.0	38	4	US-09-476-387-1430	Sequence
60.0	34	4	US-09-474-432B-284	Sequence 284, App	469	10.2	60.0	38	4	US-09-476-387-1438	Sequence
60.0	34	4	US-09-474-432B-293	Sequence 293, App	470	10.2	60.0	38	4	US-09-476-387-1442	Sequence
60.0	35	3	US-08-920-413-4	Sequence 4, Appl	471	10.2	60.0	38	4	US-09-476-387-1466	Sequence
60.0	35	4	US-09-476-387-234	Sequence 234, App	c 472	10.2	60.0	39	3	US-09-105-678A-10	Sequence
60.0	35	4	US-09-476-387-241	Sequence 241, App	c 473	10.2	60.0	39	3	US-09-105-678A-16	Sequence
60.0	35	4	US-09-476-387-251	Sequence 251, App	c 474	10.2	60.0	39	3	US-09-105-678A-22	Sequence
60.0	35	4	US-09-476-387-283	Sequence 283, App	c 475	10.2	60.0	39	3	US-09-421-208-10	Sequence
60.0	35	4	US-09-476-387-292	Sequence 292, App	c 476	10.2	60.0	39	3	US-09-421-208-16	Sequence
60.0	36	4	US-09-474-432B-253	Sequence 253, App	c 477	10.2	60.0	40	1	US-08-440-548-54	Sequence
60.0	36	4	US-09-474-432B-285	Sequence 285, App	c 478	10.2	60.0	40	1	US-08-466-344-54	Sequence
60.0	36	4	US-09-474-432B-294	Sequence 294, App	c 479	10.2	60.0	40	1	US-08-896-116-7	Sequence
60.0	37	2	US-09-028-361A-17	Sequence 17, Appl	c 480	10.2	60.0	40	3	US-08-896-122-7	Sequence
60.0	37	3	US-09-025-580-19	Sequence 19, Appl	c 481	10.2	60.0	40	3	US-08-896-122-7	Sequence
60.0	37	4	US-09-476-387-252	Sequence 252, App	c 482	10.2	60.0	40	5	PCT-US95-08487-7	Sequence
60.0	37	4	US-09-476-387-293	Sequence 293, App	c 483	10.2	60.0	42	3	US-09-189-060B-9	Sequence
60.0	37	4	US-09-476-387-293	Sequence 293, App	c 484	10.2	60.0	43	3	US-08-721-458B-58	Sequence
60.0	38	4	US-09-474-432B-1148	Sequence 1148, App	c 485	10.2	60.0	45	1	US-07-744-282C-95	Sequence
60.0	38	4	US-09-474-432B-1149	Sequence 1149, App	c 486	10.2	60.0	45	1	US-08-944-982-1	Sequence
60.0	38	4	US-09-474-432B-1151	Sequence 1151, App	c 487	10.2	60.0	45	3	US-09-105-678A-13	Sequence
60.0	38	4	US-09-474-432B-1155	Sequence 1155, App	c 488	10.2	60.0	45	3	US-09-105-678A-19	Sequence
60.0	38	4	US-09-474-432B-1158	Sequence 1158, App	c 489	10.2	60.0	45	3	US-09-105-678A-25	Sequence
60.0	38	4	US-09-474-432B-1165	Sequence 1165, App	c 490	10.2	60.0	45	3	US-09-421-208-13	Sequence
60.0	38	4	US-09-474-432B-1198	Sequence 1198, App	c 491	10.2	60.0	45	3	US-09-421-208-19	Sequence
60.0	38	4	US-09-474-432B-1233	Sequence 1233, App	c 492	10.2	60.0	45	3	US-09-421-208-25	Sequence
60.0	38	4	US-09-474-432B-1258	Sequence 1258, App	c 493	10.2	60.0	45	5	PCT-US92-06821A-78	Sequence
60.0	38	4	US-09-474-432B-1261	Sequence 1261, App	c 494	10.2	60.0	47	4	US-09-422-978-1291	Sequence
60.0	38	4	US-09-474-432B-1262	Sequence 1262, App	c 495	10.2	60.0	47	4	US-09-422-978-1413	Sequence
60.0	38	4	US-09-474-432B-1271	Sequence 1271, App	c 496	10.2	60.0	49	3	US-08-282-055-1	Sequence
60.0	38	4	US-09-474-432B-1276	Sequence 1276, App	c 497	10.2	60.0	50	4	US-09-227-595-21	Sequence
60.0	38	4	US-09-474-432B-1281	Sequence 1281, App	c 498	10.2	60.0	50	5	PCT-US95-06726-38	Sequence
60.0	38	4	US-09-474-432B-1281	Sequence 1281, App	c 499	10.2	60.0	51	1	US-08-629-600-3	Sequence
60.0	38	4	US-09-474-432B-1314	Sequence 1314, App	c 500	10.2	60.0	51	3	US-09-130-663-19	Sequence
60.0	38	4	US-09-474-432B-1341	Sequence 1341, App	c 501	10.2	60.0	51	3	US-09-432-335-19	Sequence
60.0	38	4	US-09-474-432B-1342	Sequence 1342, App	c 502	10.2	60.0	51	3	US-09-076-761-3	Sequence
60.0	38	4	US-09-474-432B-1348	Sequence 1348, App	c 503	10.2	60.0	51	4	US-09-614-022-19	Sequence
60.0	38	4	US-09-474-432B-1357	Sequence 1357, App	c 504	10.2	60.0	51	4	US-09-474-178-2	Sequence
60.0	38	4	US-09-474-432B-1361	Sequence 1361, App	c 505	10.2	60.0	51	4	US-08-956-171E-2064	Sequence
60.0	38	4	US-09-474-432B-1372	Sequence 1372, App	c 506	10.2	60.0	51	4	US-09-443-199C-567	Sequence
60.0	38	4	US-09-474-432B-1384	Sequence 1384, App	c 507	10.2	60.0	53	4	US-09-012-895-11	Sequence
60.0	38	4	US-09-474-432B-1393	Sequence 1393, App	c 508	10.2	60.0	54	1	US-08-390-850-1089	Sequence
60.0	38	4	US-09-474-432B-1394	Sequence 1394, App	c 509	10.2	60.0	54	1	US-08-435-634-1089	Sequence
60.0	38	4	US-09-474-432B-1409	Sequence 1409, App	c 510	10.2	60.0	55	1	US-07-744-282C-93	Sequence
60.0	38	4	US-09-474-432B-1428	Sequence 1428, App	c 511	10.2	60.0	55	4	US-09-116-492A-35	Sequence
60.0	38	4	US-09-474-432B-1431	Sequence 1431, App	c 512	10.2	60.0	55	5	PCT-US92-06821A-76	Sequence
60.0	38	4	US-09-474-432B-1439	Sequence 1439, App	c 513	10.2	60.0	57	1	US-08-330-163-30	Sequence
60.0	38	4	US-09-474-432B-1443	Sequence 1443, App	c 514	10.2	60.0	57	1	US-08-330-163-35	Sequence
60.0	38	4	US-09-474-432B-1467	Sequence 1467, App	c 515	10.2	60.0	57	1	US-08-482-111-30	Sequence
60.0	38	4	US-09-476-387-1147	Sequence 1147, App	c 516	10.2	60.0	57	1	US-08-482-111-35	Sequence
60.0	38	4	US-09-476-387-1148	Sequence 1148, App	c 517	10.2	60.0	57	3	US-09-439-887-36	Sequence
60.0	38	4	US-09-476-387-1150	Sequence 1150, App	c 518	10.2	60.0	60	4	US-08-407-620A-36	Sequence
60.0	38	4	US-09-476-387-1154	Sequence 1154, App	c 519	10.2	60.0	60	4	US-08-182-968A-247	Sequence
60.0	38	4	US-09-476-387-1157	Sequence 1157, App	c 520	10.2	60.0	60	4	US-08-182-968A-247	Sequence
60.0	38	4	US-09-476-387-1164	Sequence 1164, App	c 521	10.2	60.0	60	4	US-08-774-306A-247	Sequence
60.0	38	4	US-09-476-387-1197	Sequence 1197, App	c 522	10.2	60.0	60	4	US-09-064-156A-247	Sequence
60.0	38	4	US-09-476-387-1232	Sequence 1232, App	c 523	10.2	60.0	60	4	US-08-390-850-643	Sequence
60.0	38	4	US-09-476-387-1257	Sequence 1257, App	c 524	10.2	60.0	60	4	US-08-435-634-643	Sequence
60.0	38	4	US-09-476-387-1260	Sequence 1260, App	c 525	10.2	60.0	60	4	US-08-474-450A-61	Sequence
60.0	38	4	US-09-476-387-1261	Sequence 1261, App	c 526	10.2	60.0	60	4	US-08-983-466-92	Sequence
60.0	38	4	US-09-476-387-1270	Sequence 1270, App	c 527	10.2	60.0	60	4	US-08-928-692-41	Sequence
60.0	38	4	US-09-476-387-1275	Sequence 1275, App	c 528	10.2	60.0	60	4	US-09-205-860-28	Sequence
60.0	38	4	US-09-476-387-1280	Sequence 1280, App	c 529	10.2	60.0	60	4	US-09-256-496-13	Sequence
60.0	38	4	US-09-476-387-1313	Sequence 1313, App	c 530	10.2	60.0	60	4	US-09-256-496-15	Sequence
60.0	38	4	US-09-476-387-1340	Sequence 1340, App	c 531	10.2	60.0	60	4	US-09-085-686-7	Sequence
60.0	38	4	US-09-476-387-1341	Sequence 1341, App	c 532	10.2	60.0	60	4	US-09-339-972-41	Sequence
60.0	38	4	US-09-476-387-1347	Sequence 1347, App	c 533	10.2	60.0	60	4	US-08-417-629B-2	Sequence
60.0	38	4	US-09-476-387-1356	Sequence 1356, App	c 534	10.2	60.0	60	4	US-09-205-860-3	Sequence
60.0	38	4	US-09-476-387-1360	Sequence 1360, App	c 535	10.2	60.0	60	4	US-08-630-019A-37	Sequence
60.0	38	4	US-09-476-387-1371	Sequence 1371, App	c 536	10.2	60.0	60	4	US-08-630-019A-42	Sequence
60.0	38	4	US-09-476-387-1383	Sequence 1383, App	c 537	10.2	60.0	60	4	US-09-357-071-36	Sequence
60.0	38	4	US-09-476-387-1392	Sequence 1392, App	c 538	10.2	60.0	60	4	US-08-838-545-42	Sequence
60.0	38	4	US-09-476-387-1393	Sequence 1393, App	c 539	10.2	60.0	60	4	US-08-838-545-47	Sequence

58.8	20	3	US-09-487-445-30	Sequence 30, Appl	612	9.8	57.6	19	4	US-09-422-978-5995	Sequence
58.8	20	3	US-09-349-532-42	Sequence 42, Appl	c 613	9.8	57.6	19	4	US-09-422-978-9121	Sequence
58.8	20	3	US-09-349-532-47	Sequence 47, Appl	614	9.8	57.6	19	4	US-09-747-391-229	Sequence
58.8	20	4	US-08-469-260A-670	Sequence 670, Appl	c 615	9.8	57.6	20	1	US-08-308-892A-2	Sequence
58.8	20	4	US-08-488-446-670	Sequence 670, App	c 616	9.8	57.6	20	2	US-08-117-952-435	Sequence
58.8	20	4	US-09-138-452A-4312	Sequence 4312, Ap	617	9.8	57.6	20	3	US-09-487-445-39	Sequence
58.8	20	4	US-09-138-452A-5714	Sequence 5714, Ap	618	9.8	57.6	20	3	US-09-487-368A-230	Sequence
58.8	20	4	US-08-467-344A-670	Sequence 670, App	c 619	9.8	57.6	20	3	US-09-489-868A-26	Sequence
58.8	21	4	US-09-557-910-4	Sequence 4, Appli	620	9.8	57.6	20	4	US-09-517-467B-300	Sequence
58.8	22	4	US-09-535-008-12	Sequence 12, Appl	621	9.8	57.6	20	4	US-09-517-467B-343	Sequence
58.8	22	4	US-09-636-735A-24	Sequence 24, Appl	622	9.8	57.6	20	4	US-09-091-952A-190	Sequence
58.8	27	3	US-08-985-162-850	Sequence 850, App	623	9.8	57.6	20	4	US-09-629-644A-230	Sequence
58.8	28	4	US-09-401-063-850	Sequence 850, App	c 624	9.8	57.6	20	4	US-09-060-239-252	Sequence
58.8	28	4	US-08-859-998-1194	Sequence 1194, Ap	c 625	9.8	57.6	20	4	US-09-402-923A-252	Sequence
58.8	28	4	US-09-225-928-1194	Sequence 1194, Ap	c 626	9.8	57.6	20	4	US-09-198-452A-2140	Sequence
58.8	28	4	US-09-225-201B-1194	Sequence 1194, Ap	c 627	9.8	57.6	20	4	US-09-198-452A-4476	Sequence
58.8	29	1	US-08-073-197-15	Sequence 15, Appl	628	9.8	57.6	20	4	US-09-909-595-23	Sequence
58.8	29	1	US-08-073-197-20	Sequence 20, Appl	629	9.8	57.6	20	4	US-09-629-644A-230	Sequence
58.8	29	1	US-08-451-313-15	Sequence 15, Appl	630	9.8	57.6	21	3	US-08-952-796-7	Sequence
58.8	29	1	US-08-451-313-20	Sequence 20, Appl	c 631	9.8	57.6	21	4	US-09-162-631-4	Sequence
58.8	30	1	US-08-266-451B-13	Sequence 13, Appl	c 632	9.8	57.6	21	4	US-09-328-174A-6	Sequence
58.8	30	2	US-08-608-584-25	Sequence 25, Appl	c 633	9.8	57.6	21	4	US-09-328-174A-24	Sequence
58.8	30	2	US-08-748-725-13	Sequence 13, Appl	634	9.8	57.6	21	4	US-09-422-978-8744	Sequence
58.8	31	1	US-08-390-850-275	Sequence 275, App	c 635	9.8	57.6	21	4	US-09-422-978-10758	Sequence
58.8	31	1	US-08-390-850-276	Sequence 276, App	c 636	9.8	57.6	22	2	US-08-596-387B-119	Sequence
58.8	31	1	US-08-390-850-277	Sequence 277, App	c 637	9.8	57.6	22	2	US-08-874-266-31	Sequence
58.8	31	1	US-08-390-850-278	Sequence 278, App	c 638	9.8	57.6	22	4	US-09-067-615-119	Sequence
58.8	31	1	US-08-390-850-279	Sequence 279, App	c 639	9.8	57.6	22	5	PCT-US95-09816A-119	Sequence
58.8	31	1	US-08-390-850-280	Sequence 280, App	c 640	9.8	57.6	23	1	US-08-446-918A-8	Sequence
58.8	31	1	US-08-390-850-281	Sequence 281, App	c 641	9.8	57.6	23	2	US-08-580-806-8	Sequence
58.8	31	1	US-08-435-634-275	Sequence 275, App	c 642	9.8	57.6	23	4	US-09-564-805-208	Sequence
58.8	31	1	US-08-435-634-276	Sequence 276, App	c 643	9.8	57.6	24	3	US-09-046-158A-24	Sequence
58.8	31	1	US-08-435-634-277	Sequence 277, App	644	9.8	57.6	24	6	5164366-9	Patent No
58.8	31	1	US-08-435-634-278	Sequence 278, App	645	9.8	57.6	25	3	US-08-996-441B-88	Sequence
58.8	31	1	US-08-435-634-279	Sequence 279, App	646	9.8	57.6	25	3	US-08-993-722A-88	Sequence
58.8	31	1	US-08-435-634-280	Sequence 280, App	647	9.8	57.6	25	3	US-08-993-170A-88	Sequence
58.8	31	1	US-08-435-634-281	Sequence 281, App	648	9.8	57.6	25	3	US-08-993-775B-88	Sequence
58.8	33	1	US-08-255-670A-8	Sequence 8, Appli	649	9.8	57.6	25	4	US-09-427-770-88	Sequence
58.8	38	4	US-09-371-772B-12197	Sequence 12197, A	650	9.8	57.6	25	4	US-09-427-769-88	Sequence
58.8	38	4	US-09-371-772B-13772	Sequence 13772, A	651	9.8	57.6	25	4	US-09-866-108A-15480	Sequence
58.8	39	2	US-08-841-178-16	Sequence 16, Appl	652	9.8	57.6	25	4	US-09-866-108A-15481	Sequence
58.8	42	1	US-07-911-473B-178	Sequence 178, App	653	9.8	57.6	25	4	US-09-866-108A-15482	Sequence
58.8	42	1	US-07-714-131C-178	Sequence 178, App	654	9.8	57.6	25	4	US-09-866-108A-15483	Sequence
58.8	42	1	US-08-412-110-178	Sequence 178, App	655	9.8	57.6	25	4	US-09-866-108A-15484	Sequence
58.8	42	1	US-08-409-442A-178	Sequence 178, App	656	9.8	57.6	25	4	US-09-866-108A-15485	Sequence
58.8	42	2	US-08-469-609A-178	Sequence 178, App	657	9.8	57.6	25	4	US-09-866-108A-15486	Sequence
58.8	42	2	US-09-143-190-178	Sequence 178, App	658	9.8	57.6	25	4	US-09-866-108A-15487	Sequence
58.8	42	4	US-09-502-344-178	Sequence 178, App	659	9.8	57.6	25	4	US-09-866-108A-15488	Sequence
58.8	47	4	US-09-671-317-640	Sequence 640, App	660	9.8	57.6	25	4	US-09-866-108A-15489	Sequence
58.8	47	4	US-09-422-978-1646	Sequence 1646, Ap	661	9.8	57.6	25	4	US-09-866-108A-15490	Sequence
57.6	16	1	US-08-218-303-14	Sequence 14, Appl	662	9.8	57.6	25	4	US-09-866-108A-15491	Sequence
57.6	17	4	US-08-584-040-5411	Sequence 5411, Ap	663	9.8	57.6	25	4	US-09-866-108A-15492	Sequence
57.6	17	4	US-08-584-040-7272	Sequence 7272, Ap	664	9.8	57.6	26	1	US-08-379-078-619	Sequence
57.6	17	4	US-08-584-040-7273	Sequence 7273, Ap	665	9.8	57.6	26	4	US-07-974-409C-619	Sequence
57.6	17	4	US-08-584-040-7274	Sequence 7274, Ap	c 666	9.8	57.6	26	4	US-09-606-324-1	Sequence
57.6	17	4	US-09-371-772B-2310	Sequence 2310, Ap	667	9.8	57.6	26	5	PCT-US93-00977-619	Sequence
57.6	17	4	US-09-371-772B-3081	Sequence 3081, Ap	c 668	9.8	57.6	27	1	US-08-464-531-33	Sequence
57.6	17	4	US-09-371-772B-3082	Sequence 3082, Ap	c 669	9.8	57.6	27	2	US-08-461-598-33	Sequence
57.6	17	4	US-09-371-772B-3083	Sequence 3083, Ap	c 670	9.8	57.6	27	3	US-08-985-162-1335	Sequence
57.6	17	4	US-09-866-108A-10588	Sequence 10588, A	c 671	9.8	57.6	27	3	US-08-467-023-181	Sequence
57.6	17	4	US-09-866-108A-10589	Sequence 10589, A	c 672	9.8	57.6	27	3	US-08-322-137-33	Sequence
57.6	17	4	US-09-866-108A-10590	Sequence 10590, A	c 673	9.8	57.6	27	4	US-09-508-264A-11	Sequence
57.6	17	4	US-09-866-108A-10591	Sequence 10591, A	674	9.8	57.6	28	4	US-09-401-063-1335	Sequence
57.6	17	4	US-09-866-108A-10592	Sequence 10592, A	c 675	9.8	57.6	28	4	US-09-417-197-19	Sequence
57.6	18	1	US-08-139-862-5	Sequence 5, Appli	c 676	9.8	57.6	29	1	US-08-683-877-12	Sequence
57.6	18	2	US-08-117-952-34	Sequence 34, Appl	c 677	9.8	57.6	29	3	US-09-257-799-21	Sequence
57.6	18	3	US-08-150-805-12	Sequence 12, Appl	c 678	9.8	57.6	29	3	US-08-320-919A-21	Sequence
57.6	18	3	US-08-996-069A-12	Sequence 12, Appl	c 679	9.8	57.6	30	1	US-08-235-503B-63	Sequence
57.6	18	4	US-09-721-822A-102	Sequence 102, App	680	9.8	57.6	30	1	US-08-238-963A-5	Sequence
57.6	18	4	US-09-357-487B-35	Sequence 35, Appl	681	9.8	57.6	30	1	US-08-367-175A-11	Sequence
57.6	18	4	US-09-555-554-12	Sequence 12, Appl	682	9.8	57.6	30	1	US-08-555-678-63	Sequence
57.6	18	4	US-09-897-259C-8	Sequence 8, Appli	683	9.8	57.6	30	2	US-08-117-952-647	Sequence
57.6	19	4	US-09-422-978-5785	Sequence 5785, Ap	684	9.8	57.6	30	2	US-08-479-275D-48	Sequence

57.6	30	2	US-08-488-271B-48	Sequence 48, Appl	758	9.8	57.6	42	1	US-08-154-916-4	Sequence
57.6	30	2	US-08-701-339-11	Sequence 11, Appl	759	9.8	57.6	42	4	US-09-214-909-19	Sequence
57.6	30	3	US-08-746-397-5	Sequence 5, Appl	c 760	9.8	57.6	43	1	US-07-763-512-8	Sequence
57.6	30	3	US-08-746-397-9	Sequence 9, Appl	761	9.8	57.6	43	1	US-07-931-473B-256	Sequence
57.6	30	3	US-08-523-894-56	Sequence 56, Appl	762	9.8	57.6	43	1	US-07-714-131C-256	Sequence
57.6	30	4	US-09-359-361-5	Sequence 5, Appl	763	9.8	57.6	43	1	US-08-412-110-256	Sequence
57.6	30	4	US-09-462-843A-18	Sequence 18, Appl	764	9.8	57.6	43	1	US-08-409-442A-256	Sequence
57.6	30	4	US-09-937-832-3	Sequence 3, Appl	765	9.8	57.6	43	2	US-08-469-609A-256	Sequence
57.6	30	5	PT-US95-05265-63	Sequence 63, Appl	766	9.8	57.6	43	3	US-09-143-190-256	Sequence
57.6	31	1	US-08-066-281-3	Sequence 3, Appl	767	9.8	57.6	43	4	US-09-320-344-256	Sequence
57.6	31	1	US-08-066-281-7	Sequence 7, Appl	c 768	9.8	57.6	43	4	US-09-390-134B-26	Sequence
57.6	31	2	US-09-018-628-21	Sequence 21, Appl	769	9.8	57.6	45	2	US-08-379-057-5	Sequence
57.6	31	3	US-09-273-378-21	Sequence 21, Appl	770	9.8	57.6	45	3	US-08-989-251-16	Sequence
57.6	31	3	US-09-280-766-7	Sequence 7, Appl	771	9.8	57.6	45	3	US-09-340-250-16	Sequence
57.6	31	3	US-09-303-064-10	Sequence 10, Appl	772	9.8	57.6	45	4	US-09-528-108-16	Sequence
57.6	31	3	US-09-018-635-52	Sequence 52, Appl	773	9.8	57.6	46	4	US-09-486-241-19	Sequence
57.6	31	4	US-09-086-503-10	Sequence 10, Appl	c 774	9.8	57.6	47	4	US-09-641-638-981	Sequence
57.6	31	4	US-09-813-781-71	Sequence 71, Appl	c 775	9.8	57.6	47	4	US-09-486-241-11	Sequence
57.6	31	4	US-09-912-962-52	Sequence 52, Appl	c 776	9.8	57.6	47	4	US-09-422-978-1174	Sequence
57.6	32	3	US-09-358-382-4	Sequence 4, Appl	c 777	9.8	57.6	47	4	US-09-422-978-1370	Sequence
57.6	33	1	US-08-138-608-41	Sequence 41, Appl	778	9.8	57.6	47	4	US-09-422-978-1420	Sequence
57.6	33	1	US-08-583-318-6	Sequence 38, Appl	779	9.8	57.6	49	1	US-08-171-389-136	Sequence
57.6	33	2	US-08-479-275D-38	Sequence 39, Appl	780	9.8	57.6	49	1	US-08-422-978-1682	Sequence
57.6	33	2	US-08-479-275D-39	Sequence 39, Appl	781	9.8	57.6	49	1	US-08-123-936-136	Sequence
57.6	33	2	US-08-488-271B-38	Sequence 38, Appl	782	9.8	57.6	49	2	US-08-475-228A-136	Sequence
57.6	33	2	US-08-488-271B-39	Sequence 39, Appl	783	9.8	57.6	49	3	US-08-482-080A-136	Sequence
57.6	33	2	US-08-488-271B-40	Sequence 40, Appl	784	9.8	57.6	49	4	US-09-354-947-136	Sequence
57.6	33	2	US-08-488-271B-41	Sequence 41, Appl	785	9.8	57.6	49	4	US-09-350-969-35	Sequence
57.6	33	2	US-08-667-939A-25	Sequence 25, Appl	786	9.8	57.6	49	5	PCT-US93-12388-136	Sequence
57.6	33	3	US-08-722-719-51	Sequence 51, Appl	787	9.8	57.6	50	4	US-08-849-567A-57	Sequence
57.6	33	3	US-08-840-316-107	Sequence 107, Appl	788	9.8	57.6	50	4	US-08-849-567A-72	Sequence
57.6	33	3	US-09-232-468A-38	Sequence 38, Appl	c 789	9.8	57.6	51	4	US-09-443-199C-34	Sequence
57.6	33	3	US-08-809-523-107	Sequence 107, Appl	c 790	9.8	57.6	51	4	US-09-443-199C-709	Sequence
57.6	33	3	US-08-471-971-107	Sequence 107, Appl	c 791	9.8	57.6	51	4	US-09-443-199C-710	Sequence
57.6	33	4	US-08-433-123-25	Sequence 25, Appl	c 792	9.8	57.6	51	4	US-09-443-199C-1111	Sequence
57.6	33	4	US-09-334-951-51	Sequence 51, Appl	c 793	9.8	57.6	51	4	US-09-443-199C-1112	Sequence
57.6	33	4	US-09-402-776-107	Sequence 107, Appl	c 794	9.8	57.6	51	6	5198542-16	Patent No
57.6	33	4	US-09-334-923A-51	Sequence 51, Appl	c 795	9.8	57.6	52	1	US-08-260-202A-27	Sequence
57.6	33	4	US-09-170-496D-135	Sequence 135, Appl	c 796	9.8	57.6	52	4	US-08-608-151A-24	Sequence
57.6	33	4	US-09-784-984B-32	Sequence 32, Appl	c 797	9.8	57.6	54	2	US-08-479-275D-45	Sequence
57.6	33	4	US-09-334-954A-51	Sequence 51, Appl	798	9.8	57.6	54	2	US-08-488-271B-45	Sequence
57.6	35	1	US-08-591-989-87	Sequence 87, Appl	799	9.8	57.6	54	2	US-08-701-339-8	Sequence
57.6	35	2	US-08-334-545-12	Sequence 12, Appl	c 800	9.8	57.6	55	3	US-08-485-355B-16	Sequence
57.6	35	4	US-09-450-072-37	Sequence 37, Appl	801	9.8	57.6	56	3	US-09-150-805-2	Sequence
57.6	35	4	US-09-351-348-37	Sequence 37, Appl	802	9.8	57.6	56	3	US-08-996-069A-2	Sequence
57.6	36	2	US-08-809-267-27	Sequence 27, Appl	c 803	9.8	57.6	56	3	US-09-390-867A-45	Sequence
57.6	36	3	US-09-232-468A-15	Sequence 15, Appl	c 804	9.8	57.6	56	3	US-09-390-867A-46	Sequence
57.6	36	3	US-09-338-420-8	Sequence 8, Appl	c 805	9.8	57.6	56	4	US-09-548-260-45	Sequence
57.6	36	4	US-09-158-863C-29	Sequence 29, Appl	c 806	9.8	57.6	56	4	US-09-548-260-46	Sequence
57.6	36	4	US-09-784-984B-12	Sequence 12, Appl	c 807	9.8	57.6	60	2	US-07-662-764D-22	Sequence
57.6	36	5	PCT-US95-13662A-27	Sequence 27, Appl	c 808	9.8	57.6	60	2	US-07-662-764D-22	Sequence
57.6	37	4	US-09-813-781-16	Sequence 16, Appl	809	9.8	57.6	60	2	US-07-662-764D-34	Sequence
57.6	38	4	US-09-373-845-13	Sequence 13, Appl	c 810	9.8	57.6	60	2	US-07-662-764D-34	Sequence
57.6	38	4	US-09-483-846B-3	Sequence 3, Appl	811	9.8	57.6	60	3	US-09-150-805-1	Sequence
57.6	38	4	US-09-348-953-8	Sequence 8, Appl	812	9.8	57.6	60	3	US-08-996-069A-1	Sequence
57.6	39	1	US-08-232-537-3	Sequence 3, Appl	813	9.8	57.6	60	4	US-09-193-390A-22	Sequence
57.6	39	2	US-08-782-760-7	Sequence 7, Appl	c 814	9.8	57.6	60	4	US-09-193-390A-22	Sequence
57.6	39	3	US-08-435-568A-28	Sequence 28, Appl	815	9.8	57.6	60	4	US-09-193-390A-34	Sequence
57.6	39	3	US-09-306-290-40	Sequence 40, Appl	c 816	9.8	57.6	60	4	US-09-193-390A-34	Sequence
57.6	39	3	US-09-367-953B-14	Sequence 14, Appl	817	9.6	56.5	17	4	US-09-866-108A-455	Sequence
57.6	39	4	US-08-417-551-5	Sequence 5, Appl	818	9.6	56.5	17	4	US-09-866-108A-456	Sequence
57.6	39	4	US-09-097-319A-22	Sequence 22, Appl	819	9.6	56.5	18	2	US-09-200-141-39	Sequence
57.6	39	4	US-09-813-781-58	Sequence 58, Appl	c 820	9.6	56.5	18	3	US-08-912-272-73	Sequence
57.6	39	4	US-08-316-385-5	Sequence 5, Appl	c 821	9.6	56.5	18	3	US-09-205-143-20	Sequence
57.6	39	5	PCT-US96-00995-7	Sequence 7, Appl	822	9.6	56.5	18	3	US-08-784-582-68	Sequence
57.6	40	1	US-07-938-084-8	Sequence 8, Appl	c 823	9.6	56.5	18	3	US-09-723-534-39	Sequence
57.6	40	2	US-08-960-756-21	Sequence 21, Appl	c 824	9.6	56.5	18	3	US-09-723-534-40	Sequence
57.6	40	2	US-08-960-756-24	Sequence 24, Appl	c 825	9.6	56.5	18	3	US-09-723-534-41	Sequence
57.6	40	3	US-08-748-547-15	Sequence 15, Appl	c 826	9.6	56.5	18	4	US-09-026-039-73	Sequence
57.6	40	3	US-08-748-547-16	Sequence 16, Appl	c 827	9.6	56.5	19	4	US-09-143-571-31	Sequence
57.6	40	4	US-09-060-299-253	Sequence 253, Appl	828	9.6	56.5	19	4	US-09-563-826-5	Sequence
57.6	40	4	US-09-402-923A-253	Sequence 253, Appl	c 829	9.6	56.5	20	2	US-08-904-901-61	Sequence
57.6	41	2	US-08-343-443B-21	Sequence 21, Appl	c 830	9.6	56.5	20	2	US-08-904-901-119	Sequence





ug-10-090-326-17.max.rni

STREET: One Kendall Square, Building 600  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02139  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/807,529A  
FILING DATE: 19911213  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA: US 07/662,276  
FILING DATE: 28-FEB-1991  
APPLICATION NUMBER: US 07/431,565  
FILING DATE: 03-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Channing, Stacey L.  
REGISTRATION NUMBER: 31,095  
REFERENCE/DOCKET NUMBER: IPC-027/im1-015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 494-0060  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-07-807-529A-70

ATTENTION: Affairs, R.  
NTTTON: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
E: 9710-003-999  
CATION NUMBER: US/09/198, 452A  
IG DATE: 1998-11-24  
ID NOS: 6849

```

78.8%; Score 13.4; DB 4; Length 20;
ularity 93.3%; Pred. No. 2.2e+02;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

10/c  
Application US/07807529A

MEMORIAL LIFE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/300,928C  
FILING DATE: September 2, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,529  
FILING DATE: December 13, 1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

09:38:23 2004

us-10-090-326-17.max.rni

E. MANDRAGOURAS  
ON NUMBER: 36,207  
DOCKET NUMBER: 002.6US(IMI-044)  
ACTION INFORMATION:  
(617) 227-7400  
OR SEQ ID NO: 101:  
CHARACTERISTICS:  
12 base pairs  
leic acid  
SS: single  
linear  
PE: CDNA  
YES  
11

72.9%; Score 12.4; DB 3; Length 32;  
larity 92.9%; Pred. No. 8.3e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCCCC 15  
|||||  
GTGAGATCCCC 1

11/c  
Application US/08430944D  
162  
ACTION:  
Bruce L. Rogers et al.  
VENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
SEQUENCES: 103  
ICE ADDRESS:  
LAHIVE & COCKFIELD, LLP  
18 State Street  
Boston  
Massachusetts  
USA  
09

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
ICATION DATA:  
IN NUMBER: US/08/430,944D  
PE: 28-APR-1995  
ACTION DATA:  
IN NUMBER: US 08/430,014  
PE: 27-APR-1995  
ACTION DATA:  
IN NUMBER: US 08/300,928  
PE: 02-SEPT-1994  
ACTION INFORMATION:  
/ E. Mandragouras  
ON NUMBER: 36,207  
DOCKET NUMBER: IMI-044DV2  
ACTION INFORMATION:  
(617) 227-7400  
OR SEQ ID NO: 101:  
CHARACTERISTICS:  
12 base pairs  
leic acid  
SS: single  
linear  
PE: CDNA  
YES  
11

Best Local Similarity 92.9%; Pred. No. 8.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCC 15  
|||||  
DB 14 GAGTGAAGATCCCC 1

RESULT 5  
US-08-430-014-101/c  
; Sequence 101, Application US/08430014  
; Patent No. 6048962  
; GENERAL INFORMATION:  
; APPLICANT: GEFFER, Malcolm L. et al.  
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS: 101  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02145  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,014  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/300,928  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: AMY E. MANDRAGOURAS  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ANTI-SENSE: YES  
US-08-430-014-101

Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 8.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCC 15  
|||||  
DB 14 GAGTGAAGATCCCC 1

RESULT 6  
US-08-431-184-101/c  
; Sequence 101, Application US/08431184  
; Patent No. 6120769  
; GENERAL INFORMATION:  
; APPLICANT: Bruce L. Rogers et al.  
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:

09:38:23 2004

us-10-090-326-17.max.rni

LAHIVE & COCKFIELD, LLP  
28 State Street  
Boston  
Massachusetts  
USA  
09

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
LICATION DATA:  
ON NUMBER: US/08/431,184  
TE: 28-APR-1995  
CATION DATA:  
ON NUMBER: US 08/430,014  
TE: 27-APR-1995  
CATION DATA:  
ON NUMBER: US 08/300,328  
TE: 02-SEPT-1994  
ENT INFORMATION:  
IV E. Mandragouras  
ION NUMBER: 36,207  
/DOCKET NUMBER: IMI-044DV3  
CATION INFORMATION:  
: (617)227-7400  
(617)742-4214  
OR SEQ ID NO: 101:  
ARACTERISTICS:  
32 base pairs  
cleic acid  
ESS: single  
linear  
PE: cDNA  
YES  
1

72.9%; Score 12.4; DB 3; Length 32;  
ilarity 92.9%; Pred. No. 8.3e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCCCC 15  
|||||  
GTGAGGATCCCC 1

65 Application US/09474432B  
8640  
ATION:  
bozyme Pharmaceuticals, Inc.  
eigelman, Leo  
urigin, Alex  
beaudry, Amber  
karpeisky, Alex  
ademic, Jasenka  
weedler, David  
innen, Shawn  
NTION: Nucleotide triphosphate and their incorporation into oligonucleot  
E: MBH00-831-B (247/276)  
ICATION NUMBER: US/09/474,432B  
G DATE: 1999-12-19  
ATION NUMBER: US 60/064,866  
DATE: 1997-11-05  
ATION NUMBER: US 60/084,727  
DATE: 1998-04-29  
ATION NUMBER: US 09/186,675  
DATE: 1998-11-04  
ATION NUMBER: US 09/301,511  
DATE: 1999-04-28  
Q ID NOS: 1526  
entin version 3.0

SEQ ID NO 265  
LENGTH: 36  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
NAME/KEY: misc feature  
LOCATION: (1)..(4)  
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage  
NAME/KEY: misc feature  
LOCATION: (1)..(7)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (9)..(15)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (19)..(19)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (21)..(24)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (27)..(27)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (29)..(36)  
OTHER INFORMATION: 2'-O-Methyl  
NAME/KEY: misc feature  
LOCATION: (17)..(17)  
OTHER INFORMATION: 2'-deoxy-2'-amino  
NAME/KEY: misc feature  
LOCATION: (28)..(28)  
OTHER INFORMATION: 2'-deoxy-2'-amino  
NAME/KEY: misc feature  
LOCATION: (36)..(36)  
OTHER INFORMATION: 3'-end phosphate attached to an inverted deox  
US-09-474-432B-265

Query Match 71.8%; Score 12.2; DB 4; Length 36;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCCCTT 17  
|||||  
Db 17 CGAGUCAGGUCUCUU 33

RESULT 8  
US-09-476-387-264  
Sequence 264, Application US/09476387  
Patent No. 6617438  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leo  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex  
APPLICANT: Adamic, Jasenka Matulic  
APPLICANT: Sweedler, Dave  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide Triphosphate and their incorporation  
FILE REFERENCE: MBH00-831-C (249/073)  
CURRENT APPLICATION NUMBER: US/09/476,387  
CURRENT FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 09/474,432  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/301,511  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: 60/083,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/064,866  
PRIOR FILING DATE: 1997-11-05

09:38:23 2004

us-10-090-326-17.max.rni

ID NOS: 1524  
antin version 3.0

ificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

sc feature

)- (4)

ATION: Phosphorothioate 3'-internucleotide Linkage

sc feature

)- (7)

ATION: 2'-O-Methyl

sc feature

)- (15)

ATION: 2'-O-Methyl

sc feature

9)- (19)

ATION: 2'-O-Methyl

sc feature

1)- (24)

ATION: 2'-O-Methyl

sc feature

7)- (27)

ATION: 2'-O-Methyl

sc feature

9)- (36)

ATION: 2'-O-Methyl

sc feature

7)- (17)

ATION: 2'-deoxy-2'-amino

sc feature

3)- (28)

ATION: 2'-deoxy-2'-amino

sc feature

7)- (37)

ATION: n stands for inverted deoxybasic derivative

4

ilarity 71.8%; Score 12.2; DB 4; Length 37;

Conservative 58.8%; Pred.No.1.le+03; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

AGUCAAGGUCUCCU 33

199

Application US/09474432B

9640

ATION:

bozyme Pharmaceuticals, Inc.

argelman, Leo

argin, Alex

audry, Amber

arpeisky, Alex

amic, Jasenka

weedler, David

innen, Shawn

ATION: Nucleotide triphosphate and their incorporation into oligonucleot

E: MBH00-831-B (247/276)

CATION NUMBER: US/09/474,432B

G DATE: 1999-12-19

TION NUMBER: US 60/064,866

DATE: 1997-11-05

TION NUMBER: US 60/084,727

DATE: 1998-04-29

TION NUMBER: US 09/186,675

DATE: 1998-11-04

TION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 1526  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1199  
; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymati

US-09-474-432B-1199

Query Match

Best Local Similarity 71.8%; Score 12.2; DB 4; Length 38;

Matches 10; Conservative 58.8%; Pred.No.1.le+03;

Mismatches 4; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

Db 18 CGAGUCAAGGUCUCCU 34

RESULT 10

US-09-474-432B-1257

; Sequence 1257, Application US/09474432B

; Patent No. 6528640

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo

; APPLICANT: Burgin, Alex

; APPLICANT: Beaudry, Amber

; APPLICANT: Karpeisky, Alex

; APPLICANT: Adamic, Jasenka

; APPLICANT: Sweedler, David

; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporati

; FILE REFERENCE: MBH00-831-B (247/276)

; CURRENT APPLICATION NUMBER: US/09/474,432B

; CURRENT FILING DATE: 1999-12-19

; PRIOR APPLICATION NUMBER: US 60/064,866

; PRIOR FILING DATE: 1997-11-05

; PRIOR APPLICATION NUMBER: US 60/084,727

; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: US 09/186,675

; PRIOR FILING DATE: 1998-11-04

; PRIOR APPLICATION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28

; NUMBER OF SEQ ID NOS: 1526

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1257

; LENGTH: 38

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymati

US-09-474-432B-1257

Query Match

Best Local Similarity 71.8%; Score 12.2; DB 4; Length 38;

Matches 10; Conservative 58.8%; Pred.No.1.le+03;

Mismatches 4; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

Db 18 CGAGUCAAGGUCUCCU 34

RESULT 11

US-09-474-432B-1303

; Sequence 1303, Application US/09474432B

; Patent No. 6528640

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Beigelman, Leo

; APPLICANT: Burgin, Alex

; APPLICANT: Beaudry, Amber

arpeisky, Alex  
 adamic, Jasenka  
 weedler, David  
 zinnen, Shawn  
 NITION: Nucleotide triphosphate and their incorporation into oligonucleot  
 E: MBHB00-831-B (247/276)  
 CATION NUMBER: US/09/474,432B  
 IG DATE: 1999-12-19  
 TION NUMBER: US 60/064,866  
 DATE: 1997-11-05  
 TION NUMBER: US 60/084,727  
 DATE: 1998-04-29  
 TION NUMBER: US 09/186,675  
 DATE: 1998-11-04  
 TION NUMBER: US 09/301,511  
 DATE: 1999-04-28  
 ID NOS: 1526  
 tentIn version 3.0

# Artificial Sequence

NATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 303

71.8%; Score 12.2; DB 4; Length 38;  
 milarity 58.8%; Pred.No.1.le+03;  
 Conservative 4; Mismatches 3; Indels 0; Gaps 0;

HAGTGAAGATCCCTT 17  
 ||||:||||:||||:  
 HAGUCAGGUCUCCUU 34

1332  
 Application US/09474432B  
 28640

NATION:  
 ibozyme Pharmaceuticals, Inc.

Beigelman, Leo  
 Burgin, Alex  
 Beaudry, Amber  
 Karpeisky, Alex  
 Adamic, Jasenka  
 Sweedler, David  
 Zinnen, Shawn

ENTION: Nucleotide triphosphate and their incorporation into oligonucleot  
 CE: MBHB00-831-B (247/276)

ICATION NUMBER: US/09/474,432B

NG DATE: 1999-12-19

ATION NUMBER: US 60/064,866

DATE: 1997-11-05

ATION NUMBER: US 60/084,727

DATE: 1998-04-29

ATION NUMBER: US 09/186,675

ATION NUMBER: US 09/301,511

DATE: 1999-04-28

ID NOS: 1526

tentIn version 3.0

2

# Artificial Sequence

NATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 1332

71.8%; Score 12.2; DB 4; Length 38;

milarity 58.8%; Pred.No.1.le+03;

Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGTGAAGATCCCTT 17  
 ||||:||||:||||:  
 Db 18 CGAGUCAGGUCUCCUU 34

## RESULT 13

US-09-476-387-1198  
 ; Sequence 1198, Application US/09476387  
 ; Patent No. 6617438  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporat  
 ; FILE REFERENCE: MBHB00-831-C (249/073)  
 ; CURRENT APPLICATION NUMBER: US/09/476,387  
 ; CURRENT FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: 60/083,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; NUMBER OF SEQ ID NOS: 1524  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1198  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymat  
 US-09-476-387-1198

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
 Best Local Similarity 58.8%; Pred.No.1.le+03;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
 ||||:||||:||||:  
 Db 18 CGAGUCAGGUCUCCUU 34

## RESULT 14

US-09-476-387-1256  
 ; Sequence 1256, Application US/09476387  
 ; Patent No. 6617438  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporat  
 ; FILE REFERENCE: MBHB00-831-C (249/073)  
 ; CURRENT APPLICATION NUMBER: US/09/476,387  
 ; CURRENT FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04

us-10-090-326-17.max.rni

```

/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Beigelman, Leo
/ APPLICANT: Beaudry, Amber
/ APPLICANT: Karpeisky, Alex
/ APPLICANT: Adamic, Jasenka Matulic
/ APPLICANT: Sweedler, Dave
/ APPLICANT: Zinnen, Shawn
/ TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporati
/ FILE REFERENCE: MBHB00-831-C (249/073)
/ CURRENT APPLICATION NUMBER: US/09/476,387
/ CURRENT FILING DATE: 2001-04-04
/ PRIOR APPLICATION NUMBER: 09/474,432
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: 09/301,511
/ PRIOR FILING DATE: 1999-04-28
/ PRIOR APPLICATION NUMBER: 09/186,675
/ PRIOR FILING DATE: 1998-11-04
/ PRIOR APPLICATION NUMBER: 60/083,727
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/064,866
/ PRIOR FILING DATE: 1997-11-05
/ NUMBER OF SEQ ID NOS: 1524
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1331
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymati
US-09-476-387-1331

```

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
36

```

/ ERROR APPLICATION NUMBER: 09/083,721
/ ERROR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 09/186,675
/ PRIOR FILING DATE: 1998-11-04
/ PRIOR APPLICATION NUMBER: 60/083,727
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/064,866
/ PRIOR FILING DATE: 1997-11-05
/ NUMBER OF SEQ ID NOS: 1524
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1331
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic
US-09-476-387-1331

```

```

/ 1998-04-29
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/064,866
/ PRIOR FILING DATE: 1997-11-05
/ NUMBER OF SEQ ID NOS: 1524
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1331
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic
US-09-476-387-1331

```

```

; ORGANISM: Artificial Sequence
; TYPE: RNA
; LENGTH: 38
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic
US-09-476-387-1331

```

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

18 CGAGUCAGGUCUCCUU 34

RESULT 17  
US-09-070-408-67/c  
; Sequence 67, Application US/09070408  
; Patent No. 6180341  
; GENERAL INFORMATION:  
; APPLICANT: Iverson, Brent L.  
; APPLICANT: Georgiou, George  
; APPLICANT: Burks, Elizabeth A.  
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS  
; TITLE OF INVENTION: OF PROTEINS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,408  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/045,409  
FILING DATE: 01-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363

UNRECORDED RELEASE #100, VERSION #1.00  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,408  
FILING DATE: Concurrently Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/045,409  
FILING DATE: 01-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363

REFLECTION NUMBER: 05 00/043,403  
FILING DATE: 01-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: McMillian, Nabeela R.  
REGISTRATION NUMBER: P-43,363

09:38:23 2004

us-10-090-326-17.max.rni

/DOCKET NUMBER: UT5B:593

/CATION INFORMATION:

: 512/418-3000

OR SEQ ID NO: 67:

ARACTERISTICS:

46 base pairs

cleic acid

ESS: single

linear

71.8%; Score 12.2; DB 3; Length 46;

ilarity 82.4%; Pred. No. 1.1e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

|||||

GGTGATGATCCCAT 19

C plication US/09302357

0070

ATION:

KAJIMA, Hiroki

GASAWA, Akitsu

INTION: METHOD FOR GIVING RESISTANCE TO WEED CONTROL COMPOUNDS

INTION: TO PLANTS

E: 20-4555P

CATION NUMBER: US/09302,357

G DATE: 1999-04-30

ID NOS: 65

entIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: Synthetic

ATION: Oligonucleotide Primer to amplify bchH gene

70.6%; Score 12; DB 4; Length 31;

ilarity 100.0%; Pred. No. 1.4e+03;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGTGAAGATC 12

|||||

AGTGAAGATC 12

plication US/07936533A

/4718

ATION:

Philip Hammond

Anthony Endozo

VENTION: NUCLEIC ACID PROBES

VENTION: TO CHLAMYDIA PNEUMONIAE

SEQUENCES: 40

ENCE ADDRESS:

3: Lyon & Lyon

611 West Sixth Street

Los Angeles

California

USA

317

EADABLE FORM:

YPE: 3.5" Diskette, 1.44 Mb

: IBM Compatible

/OPERATING SYSTEM: IBM P.C.DOS (Version 5.0)

/SOFTWARE: WordPerfect (Version 5.1)

/CURRENT APPLICATION DATA:

/APPLICATION NUMBER: US/07/936,533A

/FILING DATE: 19920826

/CLASSIFICATION: 435

/PRIOR APPLICATION DATA:

/PRIOR APPLICATION DATA: including application

/PRIOR APPLICATION DATA: described below:

/APPLICATION NUMBER:

/FILING DATE:

/ATTORNEY/AGENT INFORMATION:

/NAME: Warburg, Richard J.

/REGISTRATION NUMBER: 32,327

/REFERENCE/DOCKET NUMBER: 198/175

/TELECOMMUNICATION INFORMATION:

/TELEPHONE: (213) 489-1600

/TELEFAX: (213) 955-0440

/TELEX: 67-3510

/INFORMATION FOR SEQ ID NO: 3:

/SEQUENCE CHARACTERISTICS:

/LENGTH: 43

/TYPE: NUCLEIC ACID

/STRANDEDNESS: single

/TOPOLOGY: linear

US-07-936-533A-3

Query Match 70.6%; Score 12; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 6 GAAGATCCCTT 17

|||||

DB 14 GAAGATCCCTT 25

RESULT 20

US-07-936-533A-32/c

; Sequence 32, Application US/07936533A

; Patent No. 5374718

; GENERAL INFORMATION:

; APPLICANT: Philip Hammond

; APPLICANT: Anthony Endozo

; TITLE OF INVENTION: NUCLEIC ACID PROBES

; TITLE OF INVENTION: TO CHLAMYDIA PNEUMONIAE

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C.DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/936,533A

; FILING DATE: 19920826

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 198/175

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

non

nor



09:38:23 2004

us-10-090-326-17.max.rni

```
(213) 955-0440
7-3510
OR SEQ ID NO: 32:
CHARACTERISTICS:
3
NUCLEIC ACID
SS: single
linear
;

70.6%; Score 12; DB 1; Length 43;
ilarity 100.0%; Pred. No. 1.4e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AGATCCCTT 17
|||||
AGATCCCTT 19

Application US/08344257A
8870
ATION:
Philip Hammond
Anthony Ednoza
VENTION: NUCLEIC ACID PROBES
ENTION: TO CHLAMYDIA PNEUMONIAE
SEQUENCES: 30
ICE ADDRESS:
; Lyon & Lyon
; 33 West Fifth Street
; Suite 4700
; Angeles
; California
; U.S.A.
71
ADABLE FORM:
PE: 3.5" Diskette, 1.44 Mb
PE: storage
IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
ICATION DATA:
ON NUMBER: US/08/344,257A
PE: No. 5683870ember 23, 1994
ATION: 435
ATION DATA:
ATION DATA: including application
ATION DATA: described below:
ATION: 435
ONT INFORMATION:
per, Sheldon O
ION NUMBER: 38,179
/DOCKET NUMBER: 209/248
ATION INFORMATION:
: (213) 489-1600
(213) 955-0440
7-3510
OR SEQ ID NO: 3:
CHARACTERISTICS:
3
NUCLEIC ACID
SS: single
linear
;

70.6%; Score 12; DB 1; Length 43;
ilarity 100.0%; Pred. No. 1.4e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AGATCCCTT 17
|||||

Db 14 GAAGATCCCTT 25

RESULT 22
US-08-638-931-17
; Sequence 17, Application US/08638931
; Patent No. 6194145
; GENERAL INFORMATION:
; APPLICANT: HEIDRICH, Bj rn
; APPLICANT: ROBINSON, Peter-Nicholas
; APPLICANT: TIECKE, Frank
; APPLICANT: ROLFS, Arndt
; TITLE OF INVENTION: Genus and species-specific identification
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,931
; FILING DATE: 25-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 15 891.1
; FILING DATE: 29-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-638-931-17

Query Match 69.4%; Score 11.8; DB 3; Length 27;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 GAGTGAAGATCCCTT 16
|||
Db 5 GAATGAATATCCCTT 19

RESULT 23
US-09-462-941-25/c
; Sequence 25, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Pro
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
```

## Artificial Sequence

ATON: Description of Artificial Sequence:PCR Primer

69.4%; Score 11.8; DB 4; Length 33;  
 ilarity 86.7%; Pred. No. 1.8e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
 |||||  
 AGTGAAGATCCCC 2

4/c

Application US/09182145B  
 7657

ATION:

stein, David A.

hen, Robert

ddard, Audrey

dney, Austin L.

llan, Kenneth J.

wrence, David A.

vine, Arnold J.

nnica, Diane

y, Margaret Ann

od, William I.

NTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

E: P117682

CATION NUMBER: US/09/182,145B

IG DATE: 1998-10-29

CATION NUMBER: US 60/063,704

IG DATE: 1997-10-29

CATION NUMBER: US 60/073,612

IG DATE: 1998-02-04

CATION NUMBER: US 60/081,695

IG DATE: 1998-04-14

ID NOS: 156

Artificial sequence

.sc\_feature

50-

ATION: Sequence is synthesized.

7657

4

69.4%; Score 11.8; DB 4; Length 50;  
 ilarity 86.7%; Pred. No. 1.9e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
 |||||  
 AGTGAAGATCCCC 35

2265/c

Application US/08956171E

93114

ORMATION:

ANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon  
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides a  
 NUMBER OF SEQUENCES: 5256  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 2265:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

US-08-956-171E-2265

Query Match

Best Local Similarity 69.4%; Score 11.8; DB 4; Length 52;

Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCCCTT 17

||| |||||

Db 39 AGTTAAGCTCCCTT 25

RESULT 26

US-08-908-643C-56

; Sequence 56, Application US/08908643C

; Patent No. 6120995

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; Pearlman, Joshua M.

; Barber, Michael T.

; Schultz, Stephanie

; Parkinson, Scott J.

; TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO  
 COLORECTAL CANCER CELLS AND METHODS OF  
 USING THE SAME

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6;

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

09:38:23 2004

us-10-090-326-17.max.rni

BRATING SYSTEM: PC-DOS/MS-DOS  
TWARE: WordPerfect 6.1  
APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,643C  
LING DATE: 07-Aug-1997  
ASSIFICATION: N/A  
PLICATION DATA:  
PLICATION NUMBER: <Unknown>  
LING DATE: <Unknown>  
//AGENT INFORMATION:  
E: Mark Deluca  
ISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-2209  
UNICATION INFORMATION:  
EPHONE: 215-568-3100  
EFAX: 215-568-3439  
OR SEQ ID NO: 56:  
3 CHARACTERISTICS:  
E: nucleic acid  
RANDEDNESS: double  
OLOGY: linear  
3 DESCRIPTION: SEQ ID NO: 56:

69.4%; Score 11.8; DB 3; Length 57;  
ilarity 86.7%; Pred. No. 1.9e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16  
|||||  
GAGAGATCCCT 42

l/c  
Application US/08/90850  
3215

ATION:  
Draper, Kenneth G.  
Pavco, Pamela  
McSwiggen, James  
Gustofson, John  
Stinchcomb, Dan T.  
ENTION: METHOD AND REAGENT FOR TREATMENT  
ENTION: OF ARTHRITIC CONDITIONS  
SEQUENCES: 1151  
CE ADDRESS:  
: Lyon & Lyon  
333 West Fifth Street  
Suite 4700  
s Angeles  
alifornia  
U.S.A.  
71

ADABLE FORM:  
PE: 3.5" Diskette, 1.44 Mb  
PE: storage  
IBM Compatible  
SYSTEM: IBM P.C. DOS 5.0  
FastSeq Version 1.5  
ICATION DATA:  
ON NUMBER: US/08/390,850  
TE: February 17, 1995  
CATION DATA:  
ON NUMBER: 08/354,920  
TE: December 13, 1994  
ON NUMBER: 08/152,487  
TE: No. 5612215ember 12, 1993  
ON NUMBER: 07/989,848  
TE: December 7, 1992  
ENT INFORMATION:  
tburg, Richard

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 641:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-390-850-641  
Query Match 67.1%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 2.7e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 4 GTGAAGATCCCT 16  
|||||  
Db 14 GTGAAGATCCACT 2

RESULT 28

US-08-435-634-641/c  
Sequence 641, Application US/08435634  
Patent No. 5731295  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Gustofson, John  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
OF ARTHRITIC CONDITIONS  
NUMBER OF SEQUENCES: 1151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,634  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,850  
FILING DATE: February 17, 1995  
APPLICATION NUMBER: 08/354,920  
FILING DATE: December 13, 1994  
APPLICATION NUMBER: 08/152,487  
FILING DATE: No. 5731295ember 12, 1993  
APPLICATION NUMBER: 07/989,848  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 641:  
SEQUENCE CHARACTERISTICS:

```
17 base pairs
cleic acid
ESS: single
linear
1
67.1%; Score 11.4; DB 1; Length 17;
ilarity 92.3%; Pred. No. 2.7e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
GAAGATCCCT 16
|||||
GAAGATCCACT 2
355/c
Application US/09198452A
9294
TION:
iffais, R.
TION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TION: thereof and uses thereof, in particular for the diagnosis, prevention: and treatment of infection
E: 9710-003-999
TION NUMBER: US/09/198,452A
G DATE: 1998-11-24
ID NOS: 6849
Chlamydia pneumoniae
355
67.1%; Score 11.4; DB 4; Length 20;
ilarity 92.3%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
GAAGATCCCT 16
|||||
GAAGATCCACT 2
Application US/09198452A
9294
TION:
iffais, R.
TION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TION: thereof and uses thereof, in particular for the diagnosis, prevention: and treatment of infection
E: 9710-003-999
TION NUMBER: US/09/198,452A
G DATE: 1998-11-24
ID NOS: 6849
Chlamydia pneumoniae
698
Application US/09198452A
9294
TION:
iffais, R.
TION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TION: thereof and uses thereof, in particular for the diagnosis, prevention: and treatment of infection
E: 9710-003-999
TION NUMBER: US/09/198,452A
G DATE: 1998-11-24
ID NOS: 6849
Chlamydia pneumoniae
698
67.1%; Score 11.4; DB 4; Length 20;
ilarity 92.3%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
GAAGATCCCT 16
|||||
GAAGATCCCT 13
352/c
Sequence 6352, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 6352
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6352
Query Match 67.1%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
QY 4 GTGAAGATCCCT 16
|||||
Db 14 GTGAAGATCCACT 2
RESULT 32
US-09-302-620B-48
Sequence 48, Application US/09302620B
Patent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 MONOOXYGENASE GENES AND PROTEINS RELATED TO CYTOCHROME P450 MONOOXYGENASE
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND HYDROXYLASE
FILE REFERENCE: 1010-16.seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 48
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-302-620B-48
Query Match 67.1%; Score 11.4; DB 4; Length 21;
Best Local Similarity 92.3%; Pred. No. 2.8e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
QY 4 GTGAAGATCCCT 16
|||||
Db 6 GTGAAGATCCCAT 18
RESULT 33
US-08-789-329C-15/c
Sequence 15, Application US/08789329C
Patent No. 6165755
GENERAL INFORMATION:
APPLICANT: SHERWOOD ET AL.
```

09:38:23 2004

us-10-090-326-17.max.rni

VENTION: CHICKEN NEUROPEPTIDE GENE USEFUL  
VENTION: FOR IMPROVED POULTRY PRODUCTION  
SEQUENCES: 20

ICE ADDRESS:  
Klarquist Sparkman Campbell Leigh &  
Whinston, LLP

One World Trade Center  
21 S.W. Salmon Street  
Suite 1600  
Portland, Oregon

United States of America

4-2986

ADABLE FORM:  
E: Disk, 3-1/2 inch

IBM PC compatible

SYSTEM: Windows NT

WordPerfect 7.0 & ASCII

ICATION DATA: US/08/789,329C

IN NUMBER: 15

TE: 01/23/97

ATION: 435

TATION DATA:

IN NUMBER:

TE: INFORMATION:

NT INFORMATION:

ON NUMBER: 41,401

DOCKET NUMBER: 2847-46468/DJE

TATION INFORMATION:

(503) 226-7391

(503) 228-9446

OR SEQ ID NO: 15:

CHARACTERISTICS:

6bp

leic acid

SS: single

linear

67.1%; Score 11.4; DB 3; Length 26;

larity 92.3%; Pred. No. 2.8e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAAGATCCCT 16

|||||

AAAGATCCCAT 8

)/c  
Application US/09013895A

3363

TATION:

Ni, Jian

Rosen, Craig A.

Pan, James G.

Gentz, Reiner L.

Dixit, Vishva M.

VENTION: Death Domain Containing Receptor 4 (DR4: Death

VENTION: Receptor 4), Member of the TNF-Receptor

VENTION: Superfamily and Binding to Trail (AP02-L)

SEQUENCES: 12

ACE ADDRESS:

: HUMAN GENOME SCIENCES, INC.

9410 KEY WEST AVENUE

TXVILLE

US

50

ADABLE FORM:

FE: Floppy disk

IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/013,895A

FILING DATE: 27-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1300002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-013-895A-10

Query Match 67.1%; Score 11.4; DB 4; Length 33;  
Best Local Similarity 92.3%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCC 14

|||||

Db 15 GAGTGAAGATCCC 3

RESULT 35

US-09-565-918-11/c

; Sequence 11, Application US/09565918

; Patent No. 6433147

GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A.

; APPLICANT: Pan, James G.

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Dixit, Vishva M.

; TITLE OF INVENTION: Death Domain Containing Receptor 4

; FILE REFERENCE: 1488.1300005

; CURRENT APPLICATION NUMBER: US/09/565,918

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: US 60/132,922

; PRIOR FILING DATE: 1999-05-06

; PRIOR APPLICATION NUMBER: US 09/013,895

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: US 60/037,829

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: US 60/035,722

; PRIOR FILING DATE: 1997-01-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 11

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNA Prime;

US-09-565-918-11

Query Match 67.1%; Score 11.4; DB 4; Length 33;  
Best Local Similarity 92.3%; Pred. No. 2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCC 14

|||||

Db 15 GAGTGAAGATCCC 3

RESULT 36

```

/c
application US/09448868
1823
MATION:
  Ni, Jian
  Rosen, Craig A.
  Pan, James G.
  Gentz, Reiner L.
  Dixit, Vishva M.
VENTION: Death Domain Containing Receptor 4 (DR4: Death
VENTION: Receptor 4), Member of the TNF-Receptor
VENTION: Superfamily and Binding to Trail (AP02-L)
SEQUENCES: 12
NCE ADDRESS:
: HUMAN GENOME SCIENCES, INC.
9410 KEY WEST AVENUE
CKVILLE
D
US
50
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
LOCATION DATA:
ON NUMBER: US/09/448,868
TE: HEREWITH
ACTION:
CATION DATA:
ON NUMBER: 09/013,895
TE: 27-JAN-1998
ACTION:
ENT INFORMATION:
EFFE, ERIC K.
ION NUMBER: 36,688
/DOCKET NUMBER: 1498.1300004
CATION INFORMATION:
: (202) 371-2540
OR SEQ ID NO: 10:
33 base pairs
nucleic acid
ESS: single
linear
PE: DNA (genomic)

67.1%; Score 11.4; DB 4; Length 33;
ilarity 92.3%; Pred.No.2.9e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCCC 14
|||||
GTGAGGATCCC 3

/c
application US/09144428
13108
NATION:
BAYER CORPORATION, The
TAMBURINI, Paul P
DAVIS, Gary
DELARIA, Katherine A
MARLOR, Christopher W
MULLER, Daniel K
VENTION: HUMAN BIKUNIN
SEQUENCES: 71
NCE ADDRESS:
3: McDonnell Boehnen Hulbert & Berghoff

```

```

; STREET: 30C S. Wacker Drive Suite 3200
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,428
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,106
; FILING DATE: 11-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,793
; FILING DATE: 14-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/725,251
; FILING DATE: 04-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 96,223-II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-09-144-428-31

Query Match 67.1%; Score 11.4; DB 4; Length 35;
Best Local Similarity 92.3%; Pred.No.2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 3 AGTGAAGATCCCC 15
Db 13 AGTGAGGATCCCC 1

RESULT 38
US-08-299-498A-29
; Sequence 29, Application US/08299498A
; Patent No. 5688670
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Lorsch, Jon R.
; APPLICANT: Wilson, Charles
; TITLE OF INVENTION: NOVEL RIBOZYMES AND NOVEL RIBOZYME
; TITLE OF INVENTION: SELECTION SYSTEMS
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

09:38:23 2004

us-10-090-326-17.max.rni

SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30B  
ICATION DATA:  
N NUMBER: US/08/299,498A  
E: 01-SEP-1994  
TION: 435  
NT INFORMATION:  
rk, Paul T.  
ON NUMBER: 30,162  
DOCKET NUMBER: 00786/245001  
ATION INFORMATION:  
(617) 542-5070  
(617) 542-8906  
0154  
R SEQ ID NO: 29:  
ARACTERISTICS:  
16 base pairs  
leic acid  
SS: single  
linear

67.1%; Score 11.4; DB 1; Length 36;  
larity 84.6%; Pred. No. 2.9e+03;  
Conservative 1; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCC 13  
|||||:  
GGGAGAUCC 14

plication PC/TUS9510813  
ATION:  
Szostak, Jack W.  
Lorsch, Jon R.  
Wilson, Charles  
ENTION: NOVEL RIBOZYMES AND NOVEL RIBOZYME  
ENTION: SELECTION SYSTEMS  
SEQUENCES: 91

ACE ADDRESS:  
Fish & Richardson  
25 Franklin Street  
Boston  
Massachusetts  
U.S.A.  
10-2804

ADABLE FORM:  
E: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30B  
ICATION DATA:  
N NUMBER: PC/US95/10813  
E:  
ATION:

ATION DATA:  
N NUMBER: 08/299,498  
E: 01-SEP-1994  
ENT INFORMATION:  
rk, Paul T.  
ION NUMBER: 30,162  
/DOCKET NUMBER: 00786/245001  
ATION INFORMATION:  
(617) 542-5070  
(617) 542-8906  
0154  
R SEQ ID NO: 29:  
ARACTERISTICS:  
16 base pairs  
leic acid  
SS: single

TOPOLOGY: linear  
PCT-US95-10813-29

Query Match 67.1%; Score 11.4; DB 5; Length 36;  
Best Local Similarity 84.6%; Pred. No. 2.9e+03;  
Matches 11; Conservative 1; Mismatches 1; Indels 0;

QY 1 CGAGTGAAGATCC 13  
|||||:  
Db 2 CGAGGAGAUCC 14

RESULT 40  
US-08-681-935-15  
; Sequence 15, Application US/08681935  
; Patent No. 5710248  
; GENERAL INFORMATION:  
; APPLICANT: GROSE, CHARLES F.  
; TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND  
; TITLE OF INVENTION: IMMUNOPURIFICATION  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
; STREET: 119 NORTH FOURTH STREET, SUITE 201  
; CITY: MINNEAPOLIS  
; STATE: MINNESOTA  
; COUNTRY: USA  
; ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/681,935  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MCCORMACK, MYRA H.  
REGISTRATION NUMBER: 36,602  
REFERENCE/DOCKET NUMBER: 140.00040101  
TELEPHONE: 612-305-1225  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-681-935-15

Query Match 67.1%; Score 11.4; DB 1; Length 41;  
Best Local Similarity 92.3%; Pred. No. 3e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 5 TGAAGATCCCTT 17  
|||||:  
Db 4 TGAAGATCACCIT 16

RESULT 41  
US-08-939-323-15  
; Sequence 15, Application US/08939323  
; Patent No. 6255462  
; GENERAL INFORMATION:  
; APPLICANT: GROSE, CHARLES F.  
; TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND  
; TITLE OF INVENTION: IMMUNOPURIFICATION  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

09:38:23 2004

us-10-090-326-17.max.rni

119 NORTH FOURTH STREET, SUITE 203  
MINNEAPOLIS

USA

21

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/08/939,323

TE: 29-SEP-1997

ATION: 435

CATION DATA:

ON NUMBER: US 08/681,935

TE: 29-JUL-1996

ENT INFORMATION:

ETING MS., ANN M.

ION NUMBER: 33,977

/DOCKET NUMBER: 140.00040102

CATION INFORMATION:

: (612) 305-1217

OR SEQ ID NO: 15:

ARACTERISTICS:

41 base pairs

cleic acid

BSS: single

linear

PE: other nucleic acid

67.1%; Score 11.4; DB 3; Length 41;

ilarity 92.3%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAGATCCCTT 17

|||||

AAGATCACCTT 16

/c

Publication US/08681935

0248

MATION:

GROSE, CHARLES F.

VENTION: PEPTIDE TAG FOR IMMUNODETECTION AND

VENTION: IMMUNOPURIFICATION

SEQUENCES: 18

NCE ADDRESS:

: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.

119 NORTH FOURTH STREET, SUITE 201

MINNEAPOLIS

MINNESOTA

01

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/08/681,935

TE:

ATION: 435

ENT INFORMATION:

CORMACK, MYRA H.

ION NUMBER: 36,602

/DOCKET NUMBER: 140.00040101

CATION INFORMATION:

: 612-305-1225

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-681-935-14

Query Match

Best Local Similarity 67.1%; Score 11.4; DB 1; Length 42;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 5 TGAAGATCCCTT 17

|||||

Db 23 TGAAGATCACCTT 11

RESULT 43

US-08-939-323-14/c

Sequence 14, Application US/08939323

Patent No. 6255462

GENERAL INFORMATION:

APPLICANT: GROSE, CHARLES F.

TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND

TITLE OF INVENTION: IMMUNOPURIFICATION

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,323

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/681,935

FILING DATE: 29-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: MUETING MS., ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 140.00040102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1217

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-08-939-323-14

Query Match

Best Local Similarity 67.1%; Score 11.4; DB 3; Length 42;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 5 TGAAGATCCCTT 17

|||||

Db 23 TGAAGATCACCTT 11

RESULT 44



Publication US/09302620B  
420  
TION:  
son, C. Ron  
aft, David L.  
rich, Dudley  
hoo, Mark  
dduri, Krishna M.  
rnett, Cathy A.  
enner, Alfred A.  
ng, Maria  
per, John C.  
eeson, Martin  
TION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450  
TION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA  
TION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS  
TION: RELATING THERETO  
: 1010-16.seq  
TION NUMBER: US/09/302,620B  
DATE: 1999-04-30  
ID NOS: 109  
ntIn Ver. 2.1

Official Sequence

TION: Description of Artificial Sequence: Primer

67.1%; Score 11.4; DB 4; Length 42;  
larity 92.3%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGATCCCCCT 16  
|||||||  
AGATCCCCAT 18

Publication US/08434730  
463  
TION:  
Dalton, Stephen  
Kochan, Jarema P  
Osborne, Mark A  
ENTION: METHOD TO DETECT PROTEIN-PROTEIN  
ENTION: INTERACTIONS  
QUENCES: 16  
ICE ADDRESS:  
Hoffmann-La Roche Inc  
40 Kingsland Street  
ley

USA  
0  
TABLE FORM:  
E: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
ICATION DATA:  
N NUMBER: US/08/434,730  
E: 04-MAY-1995  
TION: 435  
NT INFORMATION:  
lonow, Raina  
ON NUMBER: 39022  
DOCKET NUMBER: 9069  
ATION INFORMATION:  
(201)235-4391

TELEFAX: (201)235-2363  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-434-730-1  
  
Query Match 67.1%; Score 11.4; DB 1; Length 45;  
Best Local Similarity 92.3%; Pred. No. 3e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;  
  
QY 1 CGAGTGAAGATCC 13  
Db 25 CGACTGAAGATCC 37  
  
Search completed: February 29, 2004, 11:22:32  
Job time : 39.013 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 09:43:45 ; Search time 104.429 Seconds  
(without alignments)  
587.262 Million cell updates/sec

JS-10-090-326-17

1 csgatgaagatccccc 17

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2353733 seqs, 1803733377 residues

hits satisfying chosen parameters: 1448676

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Published Applications NA: \*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09D\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB ID	Description
100.0	22	15	US-10-351-157-144
78.8	20	15	Sequence 144, App
78.8	25	14	Sequence 5825, App
75.3	25	14	Sequence 121677, App
75.3	25	14	Sequence 14835, A
75.3	25	14	Sequence 30891, A
75.3	25	14	Sequence 60404, A
75.3	25	14	Sequence 66622, A
75.3	25	14	Sequence 109878, A
75.3	50	15	Sequence 934, App
75.3	60	10	Sequence 31862, A
72.9	32	8	US-08-464-363-70
71.8	17	10	US-09-780-533A-658
71.8	24	10	Sequence 658, App
71.8	25	10	US-09-940-185-246
71.8	25	10	Sequence 4227, App
71.8	25	14	Sequence 15429, A

14	US-10-098-263B-109787	25	14	US-10-098-263B-109787	Sequence
37	US-09-825-805-264	37	10	US-09-825-805-264	Sequence
38	US-09-825-805-1198	38	10	US-09-825-805-1198	Sequence
38	US-09-825-805-1256	38	10	US-09-825-805-1256	Sequence
38	US-09-825-805-1302	38	10	US-09-825-805-1302	Sequence
38	US-09-825-805-1331	38	10	US-09-825-805-1331	Sequence
38	US-09-730-289B-2852	38	10	US-09-730-289B-2852	Sequence
38	US-09-780-533A-4834	38	10	US-09-780-533A-4834	Sequence
38	US-09-776-474-2129	38	10	US-09-776-474-2129	Sequence
38	US-09-930-423-3137	38	10	US-09-930-423-3137	Sequence
38	US-09-792-818-1504	38	10	US-09-792-818-1504	Sequence
38	US-09-745-237A-3137	38	10	US-09-745-237A-3137	Sequence
25	US-10-098-263B-13896	25	14	US-10-098-263B-13896	Sequence
25	US-10-098-263B-122706	25	14	US-10-098-263B-122706	Sequence
17	US-09-780-533A-2313	17	10	US-09-780-533A-2313	Sequence
25	US-10-215-112-11134	25	14	US-10-215-112-11134	Sequence
25	US-10-098-263B-52155	25	14	US-10-098-263B-52155	Sequence
25	US-10-098-263B-52783	25	14	US-10-098-263B-52783	Sequence
25	US-10-098-263B-68974	25	14	US-10-098-263B-68974	Sequence
25	US-10-098-263B-121678	25	14	US-10-098-263B-121678	Sequence
33	US-10-046-232-6	33	14	US-10-046-232-6	Sequence
33	US-10-400-377-25	33	14	US-10-400-377-25	Sequence
33	US-10-400-708-25	33	14	US-10-400-708-25	Sequence
33	US-10-298-148-25	33	14	US-10-298-148-25	Sequence
50	US-10-112-267-114	50	14	US-10-112-267-114	Sequence
50	US-10-131-827-5679	50	15	US-10-131-827-5679	Sequence
52	US-08-781-986A-2265	52	8	US-08-781-986A-2265	Sequence
60	US-09-908-975-8556	60	10	US-09-908-975-8556	Sequence
60	US-09-908-975-15573	60	10	US-09-908-975-15573	Sequence
17	US-09-780-533A-2674	17	10	US-09-780-533A-2674	Sequence
17	US-09-780-533A-2675	17	10	US-09-780-533A-2675	Sequence
20	US-10-289-762-3355	20	15	US-10-289-762-3355	Sequence
20	US-10-289-762-4898	20	15	US-10-289-762-4898	Sequence
21	US-09-976-800-48	21	10	US-09-976-800-48	Sequence
21	US-10-138-838-48	21	14	US-10-138-838-48	Sequence
21	US-10-139-031-48	21	14	US-10-139-031-48	Sequence
21	US-10-138-905-48	21	14	US-10-138-905-48	Sequence
21	US-10-405-660-48	21	14	US-10-405-660-48	Sequence
21	US-10-138-898-48	21	15	US-10-138-898-48	Sequence
22	US-09-908-008A-90	22	11	US-09-908-008A-90	Sequence
23	US-10-216-540-8	23	14	US-10-216-540-8	Sequence
25	US-10-215-112-13649	25	14	US-10-215-112-13649	Sequence
25	US-10-098-263B-8288	25	14	US-10-098-263B-8288	Sequence
25	US-10-098-263B-24028	25	14	US-10-098-263B-24028	Sequence
25	US-10-098-263B-72473	25	14	US-10-098-263B-72473	Sequence
25	US-10-098-263B-81949	25	14	US-10-098-263B-81949	Sequence
25	US-10-098-263B-84787	25	14	US-10-098-263B-84787	Sequence
25	US-10-098-263B-96750	25	14	US-10-098-263B-96750	Sequence
25	US-10-098-263B-102940	25	14	US-10-098-263B-102940	Sequence
29	US-10-276-302-8	29	14	US-10-276-302-8	Sequence
30	US-09-845-042-2	30	10	US-09-845-042-2	Sequence
31	US-10-316-233-14	31	15	US-10-316-233-14	Sequence
33	US-10-226-296-10	33	14	US-10-226-296-10	Sequence
33	US-10-226-318-10	33	14	US-10-226-318-10	Sequence
33	US-10-175-902-11	33	14	US-10-175-902-11	Sequence
35	US-09-974-026-31	35	10	US-09-974-026-31	Sequence
42	US-09-976-800-60	42	10	US-09-976-800-60	Sequence
42	US-10-138-838-60	42	14	US-10-138-838-60	Sequence
42	US-10-139-031-60	42	14	US-10-139-031-60	Sequence
42	US-10-138-905-60	42	14	US-10-138-905-60	Sequence
42	US-10-138-916-60	42	14	US-10-138-916-60	Sequence
42	US-10-139-296-60	42	14	US-10-139-296-60	Sequence
42	US-10-139-218-60	42	14	US-10-139-218-60	Sequence
42	US-10-405-660-60	42	14	US-10-405-660-60	Sequence
42	US-10-138-898-60	42	15	US-10-138-898-60	Sequence
47	US-09-981-286A-16	47	9	US-09-981-286A-16	Sequence
47	US-10-349-143-584	47	15	US-10-349-143-584	Sequence
47	US-10-349-143-3742	47	15	US-10-349-143-3742	Sequence





62.4	38	10	US-09-825-805-1203	Sequence 1203, Ap	454	10.6	62.4	39	14	US-10-005-956-1382	Sequence
62.4	38	10	US-09-825-805-1207	Sequence 1207, Ap	c 455	10.6	62.4	40	15	US-10-411-066-80	Sequence
62.4	38	10	US-09-825-805-1255	Sequence 1255, Ap	456	10.6	62.4	50	9	US-09-822-698A-14	Sequence
62.4	38	10	US-09-825-805-1284	Sequence 1284, Ap	c 457	10.6	62.4	50	15	US-10-131-827-2284	Sequence
62.4	38	10	US-09-825-805-1290	Sequence 1290, Ap	c 458	10.6	62.4	50	15	US-10-131-827-3877	Sequence
62.4	38	10	US-09-825-805-1355	Sequence 1355, Ap	c 459	10.6	62.4	51	9	US-09-828-995B-7	Sequence
62.4	38	10	US-09-825-805-1405	Sequence 1405, Ap	c 460	10.6	62.4	51	9	US-09-828-995B-9	Sequence
62.4	38	10	US-09-825-805-1410	Sequence 1410, Ap	461	10.6	62.4	60	10	US-09-908-975-9176	Sequence
62.4	38	10	US-09-825-805-1426	Sequence 1426, Ap	462	10.6	62.4	60	10	US-09-908-975-12591	Sequence
62.4	38	10	US-09-825-805-1455	Sequence 1455, Ap	c 463	10.6	62.4	60	10	US-09-908-975-20521	Sequence
62.4	38	10	US-09-825-805-1476	Sequence 1476, Ap	c 464	10.6	62.4	60	10	US-09-908-975-21470	Sequence
62.4	38	10	US-09-730-289B-2807	Sequence 2807, Ap	c 465	10.4	61.2	12	8	US-08-424-550B-4	Sequence
62.4	38	10	US-09-730-289B-2813	Sequence 2813, Ap	c 466	10.4	61.2	12	9	US-09-751-797-6	Sequence
62.4	38	10	US-09-730-289B-2841	Sequence 2841, Ap	c 467	10.4	61.2	12	10	US-09-930-334-12	Sequence
62.4	38	10	US-09-730-289B-2850	Sequence 2850, Ap	c 468	10.4	61.2	12	10	US-10-311-795-20	Sequence
62.4	38	10	US-09-730-289B-2851	Sequence 2851, Ap	c 469	10.4	61.2	12	13	US-10-032-626-12	Sequence
62.4	38	10	US-09-730-289B-2855	Sequence 2855, Ap	c 470	10.4	61.2	12	13	US-10-067-813-11	Sequence
62.4	38	10	US-09-780-533A-4516	Sequence 4516, Ap	c 471	10.4	61.2	12	13	US-10-085-108-4	Sequence
62.4	38	10	US-09-780-533A-4517	Sequence 4517, Ap	c 472	10.4	61.2	12	14	US-10-235-264-9	Sequence
62.4	38	10	US-09-780-533A-4552	Sequence 4552, Ap	c 473	10.4	61.2	12	14	US-10-193-451A-12	Sequence
62.4	38	10	US-09-780-533A-4652	Sequence 4652, Ap	c 474	10.4	61.2	12	14	US-10-348-190-27	Sequence
62.4	38	10	US-09-780-533A-4685	Sequence 4685, Ap	c 475	10.4	61.2	12	14	US-10-134-345-12	Sequence
62.4	38	10	US-09-780-533A-4729	Sequence 4729, Ap	c 476	10.4	61.2	12	14	US-10-096-534-72	Sequence
62.4	38	10	US-09-780-533A-4742	Sequence 4742, Ap	c 477	10.4	61.2	12	14	US-10-160-237-4	Sequence
62.4	38	10	US-09-780-533A-4745	Sequence 4745, Ap	c 478	10.4	61.2	12	14	US-10-453-264-17	Sequence
62.4	38	10	US-09-780-533A-4764	Sequence 4764, Ap	c 479	10.4	61.2	17	10	US-09-882-945A-308	Sequence
62.4	38	10	US-09-780-533A-4770	Sequence 4770, Ap	480	10.4	61.2	17	10	US-09-882-945A-308	Sequence
62.4	38	10	US-09-780-533A-4804	Sequence 4804, Ap	c 481	10.4	61.2	19	10	US-09-765-555-30	Sequence
62.4	38	10	US-09-780-533A-4805	Sequence 4805, Ap	c 482	10.4	61.2	20	13	US-10-038-984-10	Sequence
62.4	38	10	US-09-780-533A-4857	Sequence 4857, Ap	c 483	10.4	61.2	20	14	US-10-305-810-47	Sequence
62.4	38	10	US-09-780-533A-4862	Sequence 4862, Ap	c 484	10.4	61.2	20	15	US-10-289-762-4423	Sequence
62.4	38	10	US-09-877-478-4393	Sequence 4393, Ap	c 4						

61.2	25	14	US-10-098-263B-113768	Sequence 113768,	C 600	10.2	60.0	17	10	US-09-817-879-3828	Sequence
61.2	25	14	US-10-098-263B-114170	Sequence 114170,	C 601	10.2	60.0	17	14	US-10-060-998-924	Sequence
61.2	25	14	US-10-098-263B-118332	Sequence 118332,	C 602	10.2	60.0	17	14	US-10-060-998-925	Sequence
61.2	25	14	US-10-098-263B-119425	Sequence 119425,	C 603	10.2	60.0	17	14	US-10-060-998-926	Sequence
61.2	25	14	US-10-098-263B-120505	Sequence 120505,	C 604	10.2	60.0	17	14	US-10-156-306-2808	Sequence
61.2	25	14	US-10-098-263B-120506	Sequence 120506,	C 605	10.2	60.0	18	15	US-10-297-068-1094	Sequence
61.2	25	14	US-10-098-263B-122705	Sequence 122705,	C 606	10.2	60.0	19	9	US-09-948-777-3	Sequence
61.2	25	14	US-10-098-263B-124534	Sequence 124534,	C 607	10.2	60.0	19	15	US-10-349-143-4438	Sequence
61.2	25	14	US-10-199-820-1	Sequence 1,	C 608	10.2	60.0	20	10	US-09-931-375A-11	Sequence
61.2	25	15	US-10-464-952-95	Sequence 95,	C 609	10.2	60.0	20	10	US-09-865-879-24	Sequence
61.2	26	12	US-10-451-892-4	Sequence 4,	C 610	10.2	60.0	20	13	US-10-078-808-14	Sequence
61.2	27	10	US-09-911-904-78	Sequence 78,	C 611	10.2	60.0	20	14	US-10-013-598-2	Sequence
61.2	30	9	US-09-843-245-13	Sequence 13,	C 612	10.2	60.0	20	15	US-10-289-762-4378	Sequence
61.2	31	9	US-09-801-274-233	Sequence 233,	C 613	10.2	60.0	21	13	US-10-016-283-19	Sequence
61.2	31	9	US-09-801-274-518	Sequence 518,	C 614	10.2	60.0	21	14	US-10-013-598-4	Sequence
61.2	31	10	US-09-904-968A-5	Sequence 5,	C 615	10.2	60.0	21	14	US-10-093-311-48	Sequence
61.2	31	14	US-10-245-802-4	Sequence 4,	C 616	10.2	60.0	21	15	US-10-349-143-10728	Sequence
61.2	31	14	US-10-128-463-11	Sequence 11,	C 617	10.2	60.0	22	14	US-10-079-528-3	Sequence
61.2	32	9	US-09-923-246-62	Sequence 62,	C 618	10.2	60.0	22	14	US-10-339-740-109	Sequence
61.2	32	9	US-09-923-246-71	Sequence 71,	C 619	10.2	60.0	23	15	US-10-321-039-449	Sequence
61.2	32	9	US-09-923-246-75	Sequence 75,	C 620	10.2	60.0	24	10	US-09-940-185-213	Sequence
61.2	32	12	US-10-382-091A-10	Sequence 10,	C 621	10.2	60.0	24	10	US-09-940-185-270	Sequence
61.2	32	14	US-10-270-176-68	Sequence 68,	C 622	10.2	60.0	24	10	US-09-902-176A-27	Sequence
61.2	32	14	US-10-295-723-62	Sequence 62,	C 623	10.2	60.0	24	14	US-10-085-906-536	Sequence
61.2	32	14	US-10-295-723-71	Sequence 71,	C 624	10.2	60.0	24	14	US-10-288-104-23	Sequence
61.2	32	14	US-10-295-723-75	Sequence 75,	C 625	10.2	60.0	24	14	US-10-168-445-8	Sequence
61.2	32	14	US-10-282-622-22	Sequence 22,	C 626	10.2	60.0	24	14	US-10-084-839-3687	Sequence
61.2	33	14	US-10-223-646-21	Sequence 21,	C 627	10.2	60.0	24	14	US-09-866-108-15373	Sequence
61.2	34	9	US-09-996-140-20	Sequence 20,	C 628	10.2	60.0	25	9	US-09-866-108-15376	Sequence
61.2	34	15	US-10-421-138A-20	Sequence 20,	C 629	10.2	60.0	25	9	US-09-866-108-15378	Sequence
61.2	35	14	US-10-004-551-49	Sequence 49,	C 630	10.2	60.0	25	9	US-09-866-108-15381	Sequence
61.2	36	9	US-09-966-955A-51	Sequence 51,	C 631	10.2	60.0	25	9	US-09-866-108-15382	Sequence
61.2	41	14	US-10-224-683-105	Sequence 105,	C 632	10.2	60.0	25	10	US-09-851-501-27	Sequence
61.2	47	15	US-10-349-143-221	Sequence 221,	C 633	10.2	60.0	25	10	US-09-883-152-84	Sequence
61.2	47	15	US-10-349-143-1315	Sequence 1315,	C 634	10.2	60.0	25	10	US-09-940-185-4194	Sequence
61.2	47	15	US-10-349-143-2778	Sequence 2778,	C 635	10.2	60.0	25	10	US-09-940-185-4251	Sequence
61.2	50	15	US-10-131-827-1331	Sequence 1331,	C 636	10.2	60.0	25	14	US-10-142-722-27	Sequence
61.2	50	15	US-10-131-827-2434	Sequence 2434,	C 637	10.2	60.0	25	14	US-10-215-112-2613	Sequence
61.2	50	15	US-10-131-827-4839	Sequence 4839,	C 638	10.2	60.0	25	14	US-10-215-112-8963	Sequence
61.2	50	15	US-10-131-827-6145	Sequence 6145,	C 639	10.2	60.0	25	14	US-10-215-112-10975	Sequence
61.2	51	10	US-09-963-761B-20	Sequence 20,	C 640	10.2	60.0	25	14	US-10-215-112-11008	Sequence
61.2	57	9	US-10-295-723-65	Sequence 65,	C 641	10.2	60.0	25	14	US-10-215-112-1101	Sequence
61.2	57	15	US-10-027-632-175875	Sequence 175875,	C 642	10.2	60.0	25	14	US-10-098-263B-11345	Sequence
61.2	57	15	US-10-027-632-175882	Sequence 175882,	C 643	10.2	60.0	25	14	US-10-098-263B-14215	Sequence
61.2	57	15	US-10-428-681-66	Sequence 66,	C 644	10.2	60.0	25	14	US-10-098-263B-17233	Sequence
61.2	59	15	US-10-027-632-75937	Sequence 75937,	C 645	10.2	60.0	25	14	US-10-098-263B-21987	Sequence
61.2	60	10	US-09-908-975-8857	Sequence 8857,	C 646	10.2	60.0	25	14	US-10-098-263B-4935	Sequence
61.2	60	10	US-09-908-975-9983	Sequence 9983,	C 647	10.2	60.0	25	14	US-10-098-263B-7682	Sequence
61.2	60	10	US-09-908-975-10285	Sequence 10285,	C 648	10.2	60.0	25	14	US-10-098-263B-10586	Sequence
61.2	60	10	US-09-908-975-10990	Sequence 10990,	C 649	10.2	60.0	25	14	US-10-098-263B-11345	Sequence
61.2	60	10	US-09-908-975-11198	Sequence 11198,	C 650	10.2	60.0	25	14	US-10-098-263B-14215	Sequence
61.2	60	10	US-09-908-975-11238	Sequence 11238,	C 651	10.2	60.0	25	14	US-10-098-263B-17233	Sequence
61.2	60	10	US-09-908-975-11448	Sequence 11448,	C 652	10.2	60.0	25	14	US-10-098-263B-21987	Sequence
61.2	60	10	US-09-908-975-13842	Sequence 13842,	C 653	10.2	60.0	25	14	US-10-098-263B-22721	Sequence
61.2	60	10	US-09-908-975-14193	Sequence 14193,	C 654	10.2	60.0	25	14	US-10-098-263B-24105	Sequence
61.2	60	10	US-09-908-975-14662	Sequence 14662,	C 655	10.2	60.0	25	14	US-10-098-263B-24106	Sequence
61.2	60	10	US-09-908-975-15184	Sequence 15184,	C 656	10.2	60.0	25	14	US-10-098-263B-24945	Sequence
61.2	60	10	US-09-908-975-22348	Sequence 22348,	C 657	10.2	60.0	25	14	US-10-098-263B-25895	Sequence
61.2	60	10	US-09-908-975-22693	Sequence 22693,	C 658	10.2	60.0	25	14	US-10-098-263B-27488	Sequence
61.2	60	10	US-09-908-975-22704	Sequence 22704,	C 659	10.2	60.0	25	14	US-10-098-263B-27679	Sequence
61.2	60	10	US-09-908-975-23153	Sequence 23153,	C 660	10.2	60.0	25	14	US-10-098-263B-29953	Sequence
61.2	60	10	US-09-908-975-31619	Sequence 31619,	C 661	10.2	60.0	25	14	US-10-098-263B-31915	Sequence
60.0	17	9	US-09-866-108-10481	Sequence 10481,	C 662	10.2	60.0	25	14	US-10-098-263B-31916	Sequence
60.0	17	9	US-09-866-108-10482	Sequence 10482,	C 663	10.2	60.0	25	14	US-10-098-263B-37287	Sequence
60.0	17	10	US-09-780-533A-659	Sequence 659,	C 664	10.2	60.0	25	14	US-10-098-263B-39176	Sequence
60.0	17	10	US-09-877-478-224	Sequence 224,	C 665	10.2	60.0	25	14	US-10-098-263B-39260	Sequence
60.0	17	10	US-09-877-478-1921	Sequence 1921,	C 666	10.2	60.0	25	14	US-10-098-263B-39280	Sequence
60.0	17	10	US-09-877-478-1922	Sequence 1922,	C 667	10.2	60.0	25	14		
60.0	17	10	US-09-740-332-2368	Sequence 2368,	C 668	10.2	60.0	25	14		
60.0	17	10	US-09-740-332-3828	Sequence 3828,	C 669	10.2	60.0	25	14		
60.0	17	10	US-09-817-879-2368	Sequence 2368,	C 670	10.2	60.0	25	14		
60.0	17	10			C 671	10.2	60.0	25	14		
60.0	17	10			C 672	10.2	60.0	25	14		



38	10	US-09-930-423-3078	Sequence 3078, Ap	c 892	10.2	60.0	60	10	US-09-908-975-4362	Sequence
38	10	US-09-930-423-3082	Sequence 3082, Ap	c 893	10.2	60.0	60	10	US-09-908-975-5680	Sequence
38	10	US-09-930-423-3091	Sequence 3091, Ap	c 894	10.2	60.0	60	10	US-09-908-975-5792	Sequence
38	10	US-09-930-423-3094	Sequence 3094, Ap	c 895	10.2	60.0	60	10	US-09-908-975-8642	Sequence
38	10	US-09-930-423-3099	Sequence 3099, Ap	c 896	10.2	60.0	60	10	US-09-908-975-9129	Sequence
38	10	US-09-930-423-3111	Sequence 3111, Ap	c 897	10.2	60.0	60	10	US-09-908-975-9181	Sequence
38	10	US-09-930-423-3112	Sequence 3112, Ap	c 898	10.2	60.0	60	10	US-09-908-975-9336	Sequence
38	10	US-09-930-423-3122	Sequence 3122, Ap	c 899	10.2	60.0	60	10	US-09-908-975-9480	Sequence
38	10	US-09-930-423-3126	Sequence 3126, Ap	c 900	10.2	60.0	60	10	US-09-908-975-10220	Sequence
38	10	US-09-930-423-3133	Sequence 3133, Ap	c 901	10.2	60.0	60	10	US-09-908-975-10583	Sequence
38	10	US-09-930-423-3141	Sequence 3141, Ap	c 902	10.2	60.0	60	10	US-09-908-975-10829	Sequence
38	10	US-09-930-423-3150	Sequence 3150, Ap	c 903	10.2	60.0	60	10	US-09-908-975-11233	Sequence
38	10	US-09-930-423-3207	Sequence 3207, Ap	c 904	10.2	60.0	60	10	US-09-908-975-11834	Sequence
38	10	US-09-930-423-3237	Sequence 3237, Ap	c 905	10.2	60.0	60	10	US-09-908-975-12020	Sequence
38	10	US-09-930-423-3237	Sequence 3237, Ap	c 906	10.2	60.0	60	10	US-09-908-975-12310	Sequence
38	10	US-09-780-164-1858	Sequence 1858, Ap	c 907	10.2	60.0	60	10	US-09-908-975-12454	Sequence
38	10	US-09-780-164-1861	Sequence 1861, Ap	c 908	10.2	60.0	60	10	US-09-908-975-12657	Sequence
38	10	US-09-780-164-1865	Sequence 1865, Ap	c 909	10.2	60.0	60	10	US-09-908-975-16589	Sequence
38	10	US-09-780-164-1890	Sequence 1890, Ap	c 910	10.2	60.0	60	10	US-09-908-975-17170	Sequence
38	10	US-09-780-164-1906	Sequence 1906, Ap	c 911	10.2	60.0	60	10	US-09-908-975-17537	Sequence
38	10	US-09-792-818-1496	Sequence 1496, Ap	c 912	10.2	60.0	60	10	US-09-908-975-17537	Sequence
38	10	US-09-792-818-1511	Sequence 1511, Ap	c 913	10.2	60.0	60	10	US-09-908-975-19659	Sequence
38	10	US-09-792-818-1516	Sequence 1516, Ap	c 914	10.2	60.0	60	10	US-09-908-975-20300	Sequence
38	10	US-09-792-818-1546	Sequence 1546, Ap	c 915	10.2	60.0	60	10	US-09-908-975-22601	Sequence
38	10	US-09-792-818-1560	Sequence 1560, Ap	c 916	10.2	60.0	60	10	US-09-908-975-23205	Sequence
38	10	US-09-792-818-1561	Sequence 1561, Ap	c 917	10.2	60.0	60	10	US-09-908-975-23348	Sequence
38	10	US-09-792-818-1566	Sequence 1566, Ap	c 918	10.2	60.0	60	10	US-09-908-975-32161	Sequence
38	10	US-09-792-818-1577	Sequence 1577, Ap	c 919	10	58.8	15	9	US-09-504-231A-269	Sequence
38	10	US-09-745-237A-3078	Sequence 3078, Ap	c 920	10	58.8	15	9	US-09-274-553D-269	Sequence
38	10	US-09-745-237A-3082	Sequence 3082, Ap	c 921	10	58.8	16	14	US-10-297-539-12	Sequence
38	10	US-09-745-237A-3091	Sequence 3091, Ap	c 922	10	58.8	17	10	US-09-740-332-1103	Sequence
38	10	US-09-745-237A-3094	Sequence 3094, Ap	c 923	10	58.8	17	10	US-09-740-332-3452	Sequence
38	10	US-09-745-237A-3099	Sequence 3099, Ap	c 924	10	58.8	17	10	US-09-817-879-1103	Sequence
38	10	US-09-745-237A-3111	Sequence 3111, Ap	c 925						



58.8 31 14 US-10-238-700-4299  
 58.8 31 16 US-10-395-741B-51  
 58.8 33 9 US-09-734-836-9  
 58.8 33 9 US-09-801-368-17  
 58.8 34 9 US-09-760-574-104  
 58.8 34 10 US-09-766-442A-104  
 58.8 34 15 US-10-368-879-56  
 58.8 37 9 US-09-760-574-106  
 58.8 37 10 US-09-766-442A-106  
 58.8 38 10 US-09-848-754A-3804  
 58.8 39 14 US-10-102-469-40  
 58.8 42 14 US-10-037-986-178  
 58.8 42 14 US-10-408-085-178  
 58.8 47 15 US-10-349-143-1646  
 58.8 48 10 US-09-730-289B-1175  
 58.8 50 15 US-10-131-827-1266  
 58.8 50 15 US-10-131-827-6440  
 58.8 50 15 US-10-131-827-6638  
 58.8 50 15 US-10-131-827-6830  
 58.8 50 15 US-10-131-827-7028  
 58.8 60 10 US-09-908-975-5397  
 58.8 60 10 US-09-908-975-7103  
 58.8 60 10 US-09-908-975-7435  
 58.8 60 10 US-09-908-975-11927  
 58.8 60 10 US-09-908-975-12765  
 58.8 60 10 US-09-908-975-12945  
 58.8 60 10 US-09-908-975-15995  
 58.8 60 10 US-09-908-975-19350  
 58.8 60 10 US-09-908-975-31335  
 58.8 60 10 US-09-908-975-31400  
 57.6 15 14 US-10-196-677-4  
 57.6 17 9 US-09-866-108-10588  
 57.6 17 9 US-09-866-108-10589  
 57.6 17 9 US-09-866-108-10590  
 57.6 17 9 US-09-866-108-10591  
 57.6 17 9 US-09-866-108-10592

## ALIGNMENTS

4 Application US/10351157  
 US20030215838A1  
 ATION:  
 recher, Cindy A.  
 ao, Zeren  
 uijper, Joseph L.  
 asovich, Maria M.  
 rant, Francis J.  
 reenell, Scott R.  
 hitmore, Theodore E.  
 ammond, Angela K.  
 ross, Jane A.  
 illon, Stacey R.  
 NITION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
 E: 02-02  
 CATION NUMBER: US/10/351,157  
 G DATE: 2003-01-21  
 TION NUMBER: US 60/435,361  
 DATE: 2002-12-19  
 TION NUMBER: US 60/389,108  
 DATE: 2002-06-14  
 TION NUMBER: US 60/350,325  
 DATE: 2002-01-18  
 ID NOS: 183  
 tSEQ for Windows Version 4.0

tificial Sequence

Sequence 4299, Ap  
 Sequence 51, Appl  
 Sequence 9, Appl  
 Sequence 17, Appl  
 Sequence 104, Appl  
 Sequence 104, Appl  
 Sequence 56, Appl  
 Sequence 106, Appl  
 Sequence 106, Appl  
 Sequence 3804, Appl  
 Sequence 40, Appl  
 Sequence 178, Appl  
 Sequence 178, Appl  
 Sequence 1646, Appl  
 Sequence 1175, Appl  
 Sequence 1266, Appl  
 Sequence 6440, Appl  
 Sequence 6638, Appl  
 Sequence 6830, Appl  
 Sequence 7028, Appl  
 Sequence 5397, Appl  
 Sequence 7103, Appl  
 Sequence 7435, Appl  
 Sequence 11927, Appl  
 Sequence 12765, Appl  
 Sequence 12945, Appl  
 Sequence 15995, Appl  
 Sequence 19350, Appl  
 Sequence 31335, Appl  
 Sequence 31400, Appl  
 Sequence 4, Appl  
 Sequence 10588, Appl  
 Sequence 10589, Appl  
 Sequence 10590, Appl  
 Sequence 10591, Appl  
 Sequence 10592, Appl

FEATURE:  
 ; OTHER INFORMATION: Primer ZC40575  
 US-10-351-157-144  
 Query Match 100.0%; Score 17; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
 Db 2 CGAGTGAAGATCCCTT 18

RESULT 2  
 US-10-289-762-5825/c  
 ; Sequence 5825, Application US/10289762  
 ; Publication No. US20040006218A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, R.  
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and po.  
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for  
 ; FILE REFERENCE: 9710-003-999  
 ; CURRENT APPLICATION NUMBER: US/10/289,762  
 ; CURRENT FILING DATE: 2003-03-27  
 ; NUMBER OF SEQ ID NOS: 6849  
 ; SEQ ID NO 5825  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Chlamydia pneumoniae  
 US-10-289-762-5825

Query Match 78.8%; Score 13.4; DB 15; Length 20;  
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CGAGTGAAGATCCCC 15  
 Db 17 CGAATGAAGATCCCC 3

RESULT 3  
 US-10-098-263B-121677  
 ; Sequence 121677, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 121677  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-121677

Query Match 78.8%; Score 13.4; DB 14; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CGAGTGAAGATCCCC 15  
 Db 9 CGAGTGAAGATCCCC 23

RESULT 4  
 US-10-098-263B-14835  
 ; Sequence 14835, Application US/10098263B

```

US20030104410A1
tman, Michael
TION: Human Microarray
: 3118.1
TION NUMBER: US/10/098,263B
DATE: 2003-01-08
ION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
array Probe Sequence Listing Generator V 1.1

75.3%; Score 12.8; DB 14; Length 25;
larity 87.5%; Pred. No. 2.6e+03;
Conservative 0; Mismatches 2; Indels 2; Gaps 0;

AGTGAAGATCCCT 16
|||||
AGTGAAGAACCTCT 23

891
Application US/10098263B
US20030104410A1
TION:
tman, Michael
TION: Human Microarray
: 3118.1
TION NUMBER: US/10/098,263B
DATE: 2003-01-08
ION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
array Probe Sequence Listing Generator V 1.1

75.3%; Score 12.8; DB 14; Length 25;
larity 87.5%; Pred. No. 2.6e+03;
Conservative 0; Mismatches 2; Indels 2; Gaps 0;

GTGAAGATCCCT 16
|||||
GTGAAGAACCTCT 16

404
Application US/10098263B
US20030104410A1
TION:
tman, Michael
TION: Human Microarray
: 3118.1
TION NUMBER: US/10/098,263B
DATE: 2003-01-08
ION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
array Probe Sequence Listing Generator V 1.1

o sapien

```

```

US-10-098-263B-60404

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 14; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 8 CGAGTGAAGTCCCT 23

RESULT 7
US-10-098-263B-66622
; Sequence 66622, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 66622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-66622

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 14; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 8 CGAGTGAAGTCCCT 23

RESULT 8
US-10-098-263B-109878/c
; Sequence 109878, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 109878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-109878

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 14; Length 25;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 16 CGAGTGAAGTCCCT 1

RESULT 9
US-10-131-827-934
; Sequence 934, Application US/10131827
; Publication No. US20040009479A1

```

ACTION: rhlgemuth, Jay  
 try, Kirk  
 foodward, Robert  
 y, Ngoc  
 INTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
 INTION: CHRONIC INFLAMMATORY DISEASES  
 RE: 506612000120  
 ACTION NUMBER: US/10/131,827  
 IG DATE: 2002-09-06  
 ACTION NUMBER: US 10/006,290  
 DATE: 2001-10-22  
 ACTION NUMBER: US 60/296,764  
 DATE: 2001-06-08  
 ID NOS: 9090  
 entin version 3.1

mo sapiens  
 75.3%; Score 12.8; DB 15; Length 50;  
 ilarity 87.5%; Pred. No. 2.7e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAGATCCCT 16  
 | | | | | | | | | |  
 AATGAGATCCCT 47

862/c  
 Application US/0908975  
 US20030165843A1  
 ACTION: KOSHAN, Avi  
 FASSERMAN, Alon  
 INTZ, Eli  
 INTZ, Liat  
 AIGLER, Simchon  
 ACTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
 INTION: THAT POPULATE A TRANSCRIPTOME  
 E: 36688-0005  
 ACTION NUMBER: US/09/908,975  
 IG DATE: 2001-07-20  
 ACTION NUMBER: US 60/287,724  
 DATE: 2001-05-02  
 ACTION NUMBER: US 60/221,607  
 DATE: 2000-07-28  
 ID NOS: 32337  
 entin version 3.0

mo sapiens  
 862  
 75.3%; Score 12.8; DB 10; Length 60;  
 ilarity 87.5%; Pred. No. 2.7e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAGATCCCT 17  
 | | | | | | | | | |  
 GTCAAGATCCCT 12

/c  
 Application US/08464363  
 US20030035815A1  
 ACTION: ROGERS, Bruce L.

APPLICANT: Morgenstern, Jay  
 APPLICANT: Bond, Julian F.  
 APPLICANT: Garman, Richard D.  
 APPLICANT: Greenstein, Julia L.  
 APPLICANT: Kuo, Mei-chang  
 APPLICANT: Morvile, Malcolm  
 TITLE OF INVENTION: RECOMBOTOPE PEPTIDES  
 NUMBER OF SEQUENCES: 76  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lahive & Cockfield  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII TEXT  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/464,363  
 FILING DATE: 05-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/807,529  
 FILING DATE: 13-DEC-1991  
 APPLICATION NUMBER: US 07/662,276  
 FILING DATE: 28-FEB-1991  
 APPLICATION NUMBER: US 07/431,565  
 FILING DATE: 03-NOV-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Amy E. Mandragouras  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: IMI-015CN  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 32 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-464-363-70

Query Match 72.9%; Score 12.4; DB 8; Length 32;  
 Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

Qy 2 GAGTGAGATCCCC 15  
 | | | | | | | | | |  
 Db 14 GAGTGAGATCCCC 1

RESULT 12  
 US-09-780-533A-658/c  
 Sequence 658, Application US/09780533A  
 Publication No. US20030060611A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Blatt, Larry  
 APPLICANT: McSwiggen, Jim  
 APPLICANT: Chowrira, Bharat  
 APPLICANT: Haeblerli, Pete  
 TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO  
 FILE REFERENCE: MBH00,878-A (400/011)  
 CURRENT APPLICATION NUMBER: US/09/780,533A  
 CURRENT FILING DATE: 2001-02-09  
 PRIOR APPLICATION NUMBER: US 60/181,797  
 PRIOR FILING DATE: 2000-02-11  
 NUMBER OF SEQ ID NOS: 6679  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 658

```
no sapiens
38
71.8%; Score 12.2; DB 10; Length 17;
ilarity 82.4%; Pred. No. 5.7e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17
|||||
AATGAATATCCCTT 1

;
Application US/09940185
US20030096239A1
TION:
iderson, Kevin
ee, Mark
TION: Probes and Decoder Oligonucleotides
: A-69605-1
TION NUMBER: US/09/940,185
; DATE: 2001-08-27
TION NUMBER: US 60/227,948
DATE: 2000-08-25
TION NUMBER: US 60/228,854
DATE: 2000-08-29
ID NOS: 4768
ntIn version 3.1

:ifficial Sequence
TION: Computer Generated Probe Sequence.

71.8%; Score 12.2; DB 10; Length 24;
ilarity 82.4%; Pred. No. 5.7e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GTGAAGATCCCTT 17
|||||
GTGAAGACCCCAT 17

7
Application US/09940185
US20030096239A1
TION:
iderson, Kevin
ee, Mark
TION: Probes and Decoder Oligonucleotides
: A-69605-1
TION NUMBER: US/09/940,185
DATE: 2001-08-27
TION NUMBER: US 60/227,948
ATE: 2000-08-25
TION NUMBER: US 60/228,854
DATE: 2000-08-29
ID NOS: 4768
ntIn version 3.1

ifficial Sequence
TION: Computer Generated Probe Sequence.
7

Query Match 71.8%; Score 12.2; DB 10; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
Db 2 CGGCTGAAGACCCCAT 18

RESULT 15
US-10-098-263B-15429/c
; Sequence 15429, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 15429
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-15429

Query Match 71.8%; Score 12.2; DB 14; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
Db 17 CGATTGAAGTTCACCTT 1

RESULT 16
US-10-098-263B-109787/c
; Sequence 109787, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 109787
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-109787

Query Match 71.8%; Score 12.2; DB 14; Length 25;
Best Local Similarity 82.4%; Pred. No. 5.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17
Db 23 CGTCTGAAGGTCCCTT 7

RESULT 17
US-09-825-805-264
; Sequence 264, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

Beigelman, Leo  
 Beaudry, Amber  
 Karpeisky, Alex  
 Adamic, Jasenka Matulic  
 Sweedler, Dave  
 Zinnen, Shawn  
 TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides  
 FILE REFERENCE: MBH00-831-F (400/009)  
 PUBLICATION NO. US20030004122A1  
 APPLICATION NO. US/09/825,805  
 CURRENT FILING DATE: 2001-09-27  
 PRIOR FILING DATE: 2000-05-23  
 PRIOR APPLICATION NUMBER: 09/476,387  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: 09/474,432  
 PRIOR FILING DATE: 1999-12-29  
 PRIOR APPLICATION NUMBER: 09/301,511  
 PRIOR FILING DATE: 1999-04-28  
 PRIOR APPLICATION NUMBER: 09/186,675  
 PRIOR FILING DATE: 1998-11-04  
 PRIOR APPLICATION NUMBER: 09/083,727  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/064,866  
 DATE: 1997-11-05  
 NUMBER OF SEQ ID NOS: 1558  
 SOFTWARE: Patent in version 3.0

## Artificial Sequence

NAME: Description of Artificial Sequence: Enzymatic Nucleic Acid

SEQ ID NO: 1  
 LENGTH: 38  
 TYPE: RNA  
 ORGANISM: Artificial Sequence

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

NAME: 2'-O-Methyl

RESULT 18  
 US-09-825-805-1198  
 ; Sequence 1198, Application US/09825805  
 ; Publication No. US20030004122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides  
 ; FILE REFERENCE: MBH00-831-F (400/009)  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 09/476,387  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: 60/083,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; NUMBER OF SEQ ID NOS: 1558  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 1198  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
 Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
 Db 18 CGAGUCAAGGUCUCCU 34

RESULT 19  
 US-09-825-805-1256  
 ; Sequence 1256, Application US/09825805  
 ; Publication No. US20030004122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides  
 ; FILE REFERENCE: MBH00-831-F (400/009)  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 09/476,387  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28

NAME: n stands for inverted deoxyabasic derivative

64

71.8%; Score 12.2; DB 10; Length 37;  
 Similarity 58.8%; Pred. No. 5.8e+03;  
 Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QAGTGAAGATCCCTT 17  
 Db 18 CGAGUCAAGGUCUCCU 33

TION NUMBER: 09/186,675  
 DATE: 1998-11-04  
 TION NUMBER: 60/083,727  
 DATE: 1998-04-29  
 TION NUMBER: 60/064,866  
 DATE: 1997-11-05  
 ID NOS: 1558  
 entin version 3.0

# Artificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 56

71.8%; Score 12.2; DB 10; Length 38;  
 ilarity 58.8%; Pred. No. 5.8e+03;  
 Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
 AGUCAAGGUCUCCU 34

02 Application US/09825805  
 . US20030004122A1  
 ATION:  
 bozyme Pharmaceuticals, Inc.  
 eigelman, Leo  
 eaudry, Amber  
 arpeisky, Alex  
 amic, Jasenka Matulic  
 weedler, Dave  
 innen, Shawn

NTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

3: MEHB00-831-F (400/009)  
 ATION NUMBER: US/09/825,805  
 3 DATE: 2001-09-27  
 TION NUMBER: 09/578,223  
 DATE: 2000-05-23  
 TION NUMBER: 09/476,387  
 DATE: 1999-12-30  
 TION NUMBER: 09/474,432  
 DATE: 1999-12-29  
 TION NUMBER: 09/301,511  
 DATE: 1999-04-28  
 TION NUMBER: 09/186,675  
 DATE: 1998-11-04  
 TION NUMBER: 60/083,727  
 DATE: 1998-04-29  
 TION NUMBER: 60/064,866  
 DATE: 1997-11-05  
 ID NOS: 1558  
 antin version 3.0

# Artificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 02

71.8%; Score 12.2; DB 10; Length 38;  
 ilarity 58.8%; Pred. No. 5.8e+03;  
 Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
 AGUCAAGGUCUCCU 34

RESULT 21  
 US-09-825-805-1331  
 ; Sequence 1331, Application US/09825805  
 ; Publication No. US20030004122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporati  
 ; FILE REFERENCE: MEHB00-831-F (400/009)  
 ; CURRENT APPLICATION NUMBER: US/09/825,805  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: 09/578,223  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 09/476,387  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: 60/083,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; NUMBER OF SEQ ID NOS: 1558  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1331  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
 US-09-825-805-1331

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
 Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
 ||||: ||||: ||||: ||||:  
 Db 18 CGAGUCAAGGUCUCCU 34

RESULT 22  
 US-09-730-289B-2852  
 ; Sequence 2852, Application US/09730289B  
 ; Publication No. US20030050259A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac D  
 ; FILE REFERENCE: MEHB00-864-A (400/006)  
 ; CURRENT APPLICATION NUMBER: US/09/730,289B  
 ; CURRENT FILING DATE: 2000-12-05  
 ; PRIOR APPLICATION NUMBER: US 60/169,100  
 ; PRIOR FILING DATE: 1999-12-06  
 ; NUMBER OF SEQ ID NOS: 3897  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2852  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
 US-09-730-289B-2852

1 09:38:23 2004

us-10-090-326-17.max.rnpb

71.8%; Score 12.2; DB 10; Length 38;  
Similarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
GAGTGAAGATCCCTT 17  
||||:||||:|  
GAGUCAAGGUCUCCU 34

4834  
; Application US/09780533A  
; Publication No. US2003006611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Howrira, Bharat  
; APPLICANT: Haeberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 60/181,797  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 6679  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; US-09-930-423-3137

Artificial Sequence

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

71.8%; Score 12.2; DB 10; Length 38;  
Similarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
GAGTGAAGATCCCTT 17  
||||:||||:|  
GAGUCAAGGUCUCCU 34

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

29  
; Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Koehler, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Attaeey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)  
; FILE REFERENCE: MBH00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 60/179,983  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 2992  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; US-09-930-423-3137

Artificial Sequence

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

71.8%; Score 12.2; DB 10; Length 38;  
Similarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0;  
CGAGTGAAGATCCCTT 17  
||||:||||:|  
CGAGUCAAGGUCUCCU 34

RESULT 25  
US-09-930-423-3137  
; Sequence 3137, Application US/09930423  
; Publication No. US2003009203A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: MBH00.918-A 400/027  
; CURRENT APPLICATION NUMBER: US/09/930,423  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 4553  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 3137  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; US-09-930-423-3137

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

RESULT 26  
US-09-792-818-1504  
; Sequence 1504, Application US/09792818  
; Publication No. US20030134806A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Von Carlowitz, Ira  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Hamblin, Paul  
; APPLICANT: Ellis, Jonathan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2  
; FILE REFERENCE: MBH00-901-A (400/013)  
; CURRENT APPLICATION NUMBER: US/09/792,818  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 2304  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1504  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; US-09-792-818-1504

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Query Match  
Best Local Similarity 58.8%; Score 12.2; DB 10; Length 38;  
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

137  
Application US/09745237A  
US20030143708A1  
ATTENTION: bozyme Pharmaceuticals, Inc.  
blatt, Larry  
McSwiggen, Jim  
NTION: Method and Reagent for the Treatment of Alzheimer's Disease  
E: 400/007 (MEH800-918-A)  
CATION NUMBER: US/09745,237A  
G DATE: 2002-04-15  
ID NOS: 4550  
entIn version 3.0

tificial Sequence  
ATTENTION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
137

71.8%; Score 12.2; DB 10; Length 38;  
ilarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||: |||: |||:  
AGUCAGGUCUCCUU 34

3896  
Application US/10098263B  
US20030104410A1  
ATTENTION: ttman, Michael  
NTION: Human Microarray  
E: 3118.1  
CATION NUMBER: US/10/098,263B  
G DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
roarray Probe Sequence Listing Generator V 1.1  
5

no sapien  
3896  
70.6%; Score 12; DB 14; Length 25;  
ilarity 100.0%; Pred. No. 7.4e+03;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
3TGAAGATCC 13  
|||||  
3TGAAGATCC 15  
22706/c  
5, Application US/10098263B  
US20030104410A1  
ATTENTION: ttman, Michael  
NTION: Human Microarray  
E: 3118.1  
CATION NUMBER: US/10/098,263B  
3 DATE: 2003-01-08  
TION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 122706  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-122706

Query Match 70.6%; Score 12; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 3 AGTGAAGATCC 14  
|||||  
Db 21 AGTGAAGATCC 10

RESULT 30  
US-09-780-533A-2313/c  
Sequence 2313, Application US/09780533A  
Publication No. US20030060611A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Blatt, Larry  
APPLICANT: McSwiggen, Jim  
APPLICANT: Chowrira, Bharat  
APPLICANT: Haeblerli, Pete  
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGC  
FILE REFERENCE: MEH800,878-A (400/011)  
CURRENT APPLICATION NUMBER: US/09/780,533A  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,797  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 6679  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2313  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-780-533A-2313

Query Match 69.4%; Score 11.8; DB 10; Length 17;  
Best Local Similarity 86.7%; Pred. No. 9.5e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 3 AGTGAAGATCCCTT 17  
|||||  
Db 17 AATGAATATCCCTT 3

RESULT 31  
US-10-215-112-11134/c  
Sequence 11134, Application US/10215112  
Publication No. US20030082596A1  
GENERAL INFORMATION:  
APPLICANT: Michael Mittmann  
TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
FILE REFERENCE: Test3  
CURRENT APPLICATION NUMBER: US/10/215,112  
CURRENT FILING DATE: 2002-08-08  
NUMBER OF SEQ ID NOS: 14936  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 11134  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-215-112-11134

Query Match 69.4%; Score 11.8; DB 14; Length 25;



1 09:38:23 2004

us-10-090-326-17.max.rnpb

```

ilarity 86.7%; Pred. No. 9.6e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 2;
GTGAAGATCCCCCTT 17
|||||
GTGAAGACCCCTTT 2
|||||

32155/c
3, Application US/10098263B
2, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray
E: 3118.1
G DATE: 2003-01-08
ATION NUMBER: US/10/098,263B
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
5

mo sapien
2155
ilarity 69.4%; Score 11.8; DB 14; Length 25;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
AGTGAAGATCCCC 15
|||||
AGGACGATCCCC 8

2783/c
, Application US/10098263B
, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray
E: 3118.1
G DATE: 2003-01-08
TION NUMBER: US/10/098,263B
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
3

mo sapien
2783
ilarity 69.4%; Score 11.8; DB 14; Length 25;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
AGTGAAGATCCCC 15
|||||
AGGACGATCCCC 9

8974
, Application US/10098263B
, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray

FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 68974
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-68974

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 14; Length 25;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCCCTT 17
|||||
DB 7 AGTGAAGATCCGTT 21
|||||

RESULT 35
US-10-098-263B-121678
; Sequence 121678, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121678
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121678

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 14; Length 25;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCC 15
|||||
DB 9 CGAGAAAGATCCCC 23
|||||

RESULT 36
US-10-046-232-6/c
; Sequence 6, Application US/10046232
; Publication No. US20030119099A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KEATKY
; APPLICANT: Ingrid DREVENY
; APPLICANT: Peter FOCHLAUER
; APPLICANT: Wolfgang SKRANC
; APPLICANT: Herbert MAYRHOFER
; APPLICANT: Irma WIRTH
; APPLICANT: Rudolf NEUHOFER
; APPLICANT: Rodolfo BONA
; TITLE OF INVENTION: New genes containing a DNA sequence coding fo
; TITLE OF INVENTION: recombinant proteins derived therefrom and h
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
```

09:38:23 2004

us-10-090-326-17.max.rnpb

DATE: 2001-01-16  
TION NUMBER: A523/2001  
DATE: 2001-04-03  
ID NOS: 24  
antIn Ver. 2.1

Official Sequence

ATION: Description of the artificial sequence: Synthetic oligonucleotide

69.4%; Score 11.8; DB 14; Length 33;  
ilarity 86.7%; Pred. No. 9.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CGAGATCCCTT 17  
|||||  
AGAGATCTCTT 16

/c  
pplication US/10400377  
. US20030162949A1  
ATION:  
x III, George N  
older Biotechnology, Inc.  
ATION: Derivatives of Growth Hormone and Related Proteins  
3: 4152-1-PUS  
CATION NUMBER: US/10/400,377  
3 DATE: 2003-03-26  
TION NUMBER: US/09/462,941  
DATE: 2000-01-14  
TION NUMBER: 60/052,516  
DATE: 1997-07-14  
ID NOS: 41  
antIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence:PCR Primer

69.4%; Score 11.8; DB 14; Length 33;  
ilarity 86.7%; Pred. No. 9.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
|||||  
AGTGAGGATCCCC 2

/c  
pplication US/10400708  
US20030166865A1  
ATION:  
x III, George N  
older Biotechnology, Inc.  
ATION: Derivatives of Growth Hormone and Related Proteins  
8: 4152-1-PUS  
CATION NUMBER: US/10/400,708  
3 DATE: 2003-03-26  
TION NUMBER: US/09/462,941  
DATE: 2000-01-14  
TION NUMBER: 60/052,516  
DATE: 1997-07-14  
ID NOS: 41  
antIn Ver. 2.0

; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer  
US-10-400-708-25

Query Match 69.4%; Score 11.8; DB 14; Length 33;  
Best Local Similarity 86.7%; Pred. No. 9.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCC 15  
Db 16 CTAGTGAGGATCCCC 2

RESULT 39  
US-10-298-148-25/c  
; Sequence 25, Application US/10298148  
; Publication No. US20030171284A1  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N  
; APPLICANT: Bolder Biotechnology, Inc.  
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Pro  
; FILE REFERENCE: 4152-1-PUS  
; CURRENT APPLICATION NUMBER: US/10/298,148  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/462,941  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/052,516  
; PRIOR FILING DATE: 1997-07-14  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer  
US-10-298-148-25

Query Match 69.4%; Score 11.8; DB 14; Length 33;  
Best Local Similarity 86.7%; Pred. No. 9.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCC 15  
Db 16 CTAGTGAGGATCCCC 2

RESULT 40  
US-10-112-267-114/c  
; Sequence 114, Application US/10112267  
; Publication No. US20030068678A1  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David A.  
; APPLICANT: Cohen, Robert  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Lawrence, David A.  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Pennica, Diane  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: P1176R2  
; CURRENT APPLICATION NUMBER: US/10/112,267  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,1  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,71

1 09:38:23 2004

us-10-090-326-17.max.rnpb

DATE: EARLIER FILING DATE: 1997-10-29  
ATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
DATE: EARLIER FILING DATE: 1998-02-04  
ATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
DATE: EARLIER FILING DATE: 1998-04-14  
ID NOS: 156

tficial sequence

.sc\_feature

50\_

ATION: Sequence is synthesized.

.4

69.4%; Score 11.8; DB 14; Length 50;  
ilarity 86.7%; Pred. No. 9.8e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

HAGTGAAGATCCCC 15

|||||

HAGTGGAGACCCCC 35

79/c

Application US/10131827

. US20040009479A1

ATION:

hlgemuth, Jay

ry, Kirk

oodward, Robert

y, Ngoc

ATION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

INTION: CHRONIC INFLAMMATORY DISEASES

IE: 506612000120

ATION NUMBER: US/10/131,827

IG DATE: 2002-09-06

ATION NUMBER: US 10/006,290

DATE: 2001-10-22

ATION NUMBER: US 60/296,764

DATE: 2001-06-08

ID NOS: 9090

entIn version 3.1

mo sapiens

.79

69.4%; Score 11.8; DB 15; Length 50;  
ilarity 86.7%; Pred. No. 9.8e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

HTGAAGATCCCCCTT 17

|||||

HTGAAGAAGCCTT 33

265/c

Application US/08781986A

. US20030054436A1

INATION:

Charles Kunsch

VENTION: Staphylococcus aureus Polynucleotides and Sequences

SEQUENCES: 5255

ANCE ADDRESS:

Human Genome Sciences, Inc.

9410 Key West Avenue

ockville

aryland

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2265

Query Match 69.4%; Score 11.8; DB 8; Length 52;  
Best Local Similarity 86.7%; Pred. No. 9.8e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

OY 3 AGTGAAGATCCCCCTT 17

|||||

Db 39 AGTTAAGCTCCCCCTT 25

RESULT 43

US-09-908-975-8556

Sequence 8556, Application US/09908975

Publication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: SHOSHAN, Avi

APPLICANT: WASSERMAN, Alon

APPLICANT: MINTZ, Eli

APPLICANT: MINTZ, Liat

APPLICANT: FAIGLER, Simchon

TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRJ

FILE REFERENCE: 36688-0005

CURRENT APPLICATION NUMBER: US/09/908,975

CURRENT FILING DATE: 2001-07-20

PRIOR APPLICATION NUMBER: US 60/287,724

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/221,607

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 32337

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8556

LENGTH: 60

TYPE: DNA

ORGANISM: Homo sapiens

US-09-908-975-8556

Query Match 69.4%; Score 11.8; DB 10; Length 60;  
Best Local Similarity 86.7%; Pred. No. 9.8e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

OY 2 GAGTGAAGATCCCCCTT 16

|||||

Db 33 GAATGAGGATCCCCCTT 47

09:38:23 2004

us-10-090-326-17.max.rnpb

73/c  
Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
: 36688-0005  
ATION NUMBER: US/09/908,975  
DATE: 2001-07-20  
ION NUMBER: US 60/287,724  
ATE: 2001-05-02  
ION NUMBER: US 60/221,607  
ATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

o sapiens  
73  
69.4%; Score 11.8; DB 10; Length 60;  
larity 86.7%; Pred. No. 9.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GAAGATCCCGCTT 17  
|||||  
GCAGATCCCGCTT 46

74/c  
Application US/09780533A  
US20030060611A1  
TION:  
Ozyme Pharmaceuticals, Inc.  
att, Larry  
Swiggen, Jim  
owrira, Bharat  
eberli, Pete  
TION: Method and Reagent for the Inhibition of NOGO Gene  
: MBHE00,878-A (400/011)  
ATION NUMBER: US/09/780,533A  
DATE: 2001-02-09  
ION NUMBER: US 60/181,797  
ATE: 2000-02-11  
ID NOS: 6679  
ntIn version 3.0

o sapiens  
74  
67.1%; Score 11.4; DB 10; Length 17;  
larity 92.3%; Pred. No. 1.6e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGATCCCGCTT 17  
|||||  
ATATCCCGCTT 5

February 29, 2004, 13:43:02  
9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1276.1 Seconds  
(without alignments)  
397.818 Million cell updates/sec

US-10-090-326-17

1 csgtgaagatccctt 17

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

EST:\*

1: em\_estba: \*  
2: em\_esthm: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_estc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_hic: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: em\_gss\_hum: \*  
18: em\_gss\_inv: \*  
19: em\_gss\_pln: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_fun: \*  
22: em\_gss\_man: \*  
23: em\_gss\_mus: \*  
24: em\_gss\_pro: \*  
25: em\_gss\_rod: \*  
26: em\_gss\_phg: \*  
27: em\_gss\_vrl: \*  
28: gb\_gss1: \*  
29: gb\_gss2: \*

is the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

# SUMMARIES

Query	Match	Length	ID	Description
75.3	60	9	A1116273	A1116273 ucl1g10.r
71.8	52	10	BE321851	BE321851 NF009F11
70.6	37	14	R37577	R37577 yd02a09.sl
69.4	49	12	BM862480	BM862480 mgcm003XC

59	29	29	AL763440	AL763440
60	14	CB353581	CB353581	CB353581
61	47	AZ624452	AZ624452	AZ624452
62	28	AZ769807	AZ769807	AZ769807
63	31	TA122G04P	TA122G04P	TA122G04P
64	29	CG720952	CG720952	CG720952
65	35	AZ771147	AZ771147	AZ771147
66	43	BM395597	BM395597	BM395597
67	45	AA288062	AA288062	AA288062
68	9	BU605161	BU605161	BU605161
69	51	AL611423	AL611423	AL611423
70	13	BN771762	BN771762	BN771762
71	56	BR910991	BR910991	BR910991
72	58	AW511427	AW511427	AW511427
73	59	AA466912	AA466912	AA466912
74	53	BH800373	BH800373	BH800373
75	57	AL767128	AL767128	AL767128
76	28	BF639034	BF639034	BF639034
77	60	AZ423553	AZ423553	AZ423553
78	22	AZ994980	AZ994980	AZ994980
79	29	BJ064687	BJ064687	BJ064687
80	36	X88090 H	X88090 H	X88090 H
81	38	AL947310	AL947310	AL947310
82	40	AZ598104	AZ598104	AZ598104
83	41	BM022920	BM022920	BM022920
84	28	AZ854808	AZ854808	AZ854808
85	55	AL944839	AL944839	AL944839
86	55	AZ821330	AZ821330	AZ821330
87	28	AA500076	AA500076	AA500076
88	58	AZ597097	AZ597097	AZ597097
89	28	AL753395	AL753395	AL753395
90	58	AZ487436	AZ487436	AZ487436
91	59	AZ339854	AZ339854	AZ339854
92	27	AI187871	AI187871	AI187871
93	46	AL261842	AL261842	AL261842
94	51	AA737190	AA737190	AA737190
95	52	AZ435804	AZ435804	AZ435804
96	28	AV833997	AV833997	AV833997
97	55	AV956623	AV956623	AV956623
98	55	BJ032890	BJ032890	BJ032890
99	56	AA896471	AA896471	AA896471
100	57	AY125858	AY125858	AY125858
101	57	AZ777527	AZ777527	AZ777527
102	57	BH218589	BH218589	BH218589
103	58	CF340173	CF340173	CF340173
104	19	AU253942	AU253942	AU253942
105	37	AZ429862	AZ429862	AZ429862
106	37	BX532099	BX532099	BX532099
107	39	AU252932	AU252932	AU252932
108	41	AI205721	AI205721	AI205721
109	43	AA429927	AA429927	AA429927
110	43	AI200861	AI200861	AI200861
111	46	N44633	N44633	N44633
112	47	AA712026	AA712026	AA712026
113	49	BH629223	BH629223	BH629223
114	52	AZ810048	AZ810048	AZ810048
115	52			
116	53			



us-10-090-326-17.max.rst





54.1	41	29	BX288982	BX288982 Arabidops	c 589	9.2	54.1	48	29	BX533275	BX533275
54.1	41	29	BX291553	BX291553 Arabidops	590	9.2	54.1	49	9	AI118170	AI118170
54.1	41	29	TA77D03Q	TA77D03Q T. brucei	c 591	9.2	54.1	49	9	AI152487	AI152487
54.1	42	14	CA797521	CA797521 Cac BL 46	592	9.2	54.1	49	9	AI264752	AI264752
54.1	42	28	AZ351396	AZ351396 IM0089M21	c 593	9.2	54.1	49	13	C21077	C21077
54.1	42	28	BH256477	BH256477 KG03309-3	c 594	9.2	54.1	49	28	BZ764534	BZ764534
54.1	42	28	BZ762011	BZ762011 SALK_0842	c 595	9.2	54.1	49	29	AL759656	AL759656
54.1	42	29	AL770919	AL770919 Arabidops	c 596	9.2	54.1	49	29	AL761341	AL761341
54.1	42	29	AL940280	AL940280 Arabidops	c 597	9.2	54.1	49	29	AL947669	AL947669
54.1	42	29	AL946068	AL946068 Arabidops	c 598	9.2	54.1	49	29	BX289548	BX289548
54.1	42	29	AL952663	AL952663 Arabidops	c 599	9.2	54.1	49	29	BX891921	BX891921
54.1	42	29	BX291769	BX291769 Arabidops	c 600	9.2	54.1	49	29	BX893214	BX893214
54.1	42	29	BX897261	BX897261 Arabidops	601	9.2	54.1	50	9	AU011291	AU011291
54.1	42	29	TA34702Q	TA34702Q T. brucei	c 602	9.2	54.1	50	9	AU102376	AU102376
54.1	42	29	TA95B10Q	TA95B10Q T. brucei	603	9.2	54.1	50	9	AU106387	AU106387
54.1	43	9	AA967042	AA967042 ua39e07.r	c 604	9.2	54.1	50	9	AU106406	AU106406
54.1	43	9	AI917027	AI917027 ts51aj12.x	c 605	9.2	54.1	50	9	AU106468	AU106468
54.1	43	29	AL770788	AL770788 Arabidops	c 606	9.2	54.1	50	9	AU106529	AU106529
54.1	43	29	AL947531	AL947531 Arabidops	c 607	9.2	54.1	50	9	AU106541	AU106541
54.1	43	29	BX002308	BX002308 Arabidops	c 608	9.2	54.1	50	9	AU106544	AU106544
54.1	43	29	BX288411	BX288411 Arabidops	609	9.2	54.1	50	9	AU106881	AU106881
54.1	43	29	BX292237	BX292237 Arabidops	c 610	9.2	54.1	50	9	AU106891	AU106891
54.1	43	29	BX661875	BX661875 Arabidops	c 611	9.2	54.1	50	10	BF461263	BF461263
54.1	44	9	AV967136	AV967136 AV967136	612	9.2	54.1	50	28	AZ308799	AZ308799
54.1	44	28	AZ804533	AZ804533 2M0065L01	c 613	9.2	54.1	50	29	AL754688	AL754688
54.1	44	29	AL757660	AL757660 Arabidops	c 614	9.2	54.1	50	29	AL767249	AL767249
54.1	44	29	AL758953	AL758953 Arabidops	c 615	9.2	54.1	50	29	AL938385	AL938385
54.1	44	29	AL763755	AL763755 Arabidops	c 616	9.2	54.1	50	29	AL938433	AL938433
54.1	44	29	AL766239	AL766239 Arabidops	c 617	9.2	54.1	50	29	AL944393	AL944393
54.1	44	29	AL771654	AL771654 Arabidops	c 618	9.2	54.1	50	29	AL944953	AL944953
54.1	44	29	AL938680	AL938680 Arabidops	c 619	9.2	54.1	50	29	AL947641	AL947641
54.1	44	29	BX292587	BX292587 Arabidops	c 620	9.2	54.1	50	29	BX204795	BX204795
54.1	44	14	H64922	H64922 yu65h09.r1	c 621	9.2	54.1	50	29	BX650252	BX650252
54.1	45	28	AZ575902	AZ575902 AST-T22B0	c 622	9.2	54.1	51	14	H30101	H30101
54.1	45	28	BH809064	BH809064 1008083H0	623	9.2	54.1	51	28	AZ329549	AZ329549
54.1	45	29	AL760580	AL760580 Arabidops	c 624	9.2	54.1	51	28	AZ837490	AZ837490
54.1	45	29	AL764340	AL764340 Arabidops	625	9.2	54.1	51	28	B00387	B00387
54.1	45	29	BX002842	BX002842 Arabidops	626	9.2	54.1	51	29	AL758135	AL758135
54.1	45	29	BX286485	BX286485 Arabidops	c 627	9.2	54.1	51	29	AL762242	AL762242
54.1	45	29	BX287762	BX287762 Arabidops	c 628	9.2	54.1	51	29	AL952873	AL952873
54.1	45	29	BX897142	BX897142 Arabidops	c 629	9.2	54.1	51	29	AL953734	AL953734
54.1	46	9	AA953796	AA953796 oo38b09.s	c 630	9.2	54.1	51	29	BX291747	BX291747
54.1	46	9	AA616469	AA616469 vne6d10.r	c 631	9.2	54.1	51	29	BX292378	BX292378
54.1	46	28	AZ404113	AZ404113 IM0172A15	c 632	9.2	54.1	51	29	BX292425	BX292425
54.1	46	29	AL944055	AL944055 Arabidops	c 633	9.2	54.1	51	29	BX653622	BX653622
54.1	47	9	AV832665	AV832665 AV832665	c 634	9.2	54.1	51	29	BX662436	BX662436
54.1	47	12	BI685348	BI685348 603310374	635	9.2	54.1	51	29	TA162H07Q	TA162H07Q
54.1	47	28	AZ400633	AZ400633 IM0167F06	c 636	9.2	54.1	51	29	AL487732	AL487732
54.1	47	28	AZ624632	AZ624632 IM0463M21	c 637	9.2	54.1	52	9	AI554319	AI554319
54.1	47	28	BH791124	BH791124 SALK_0587	c 638	9.2	54.1	52	9	AI747503	AI747503
54.1	47	28	BH791157	BH791157 SALK_0588	639	9.2	54.1	52	9	AI799301	AI799301
54.1	47	28	BH891856	BH891856 3526_1.19	c 640	9.2	54.1	52	9	AU012497	AU012497
54.1	47	28	BZ662640	BZ662640 SALK_0261	c 641	9.2	54.1	52	9	AU012546	AU012546
54.1	47	29	AL758034	AL758034 Arabidops	c 642	9.2	54.1	52	9	AU012547	AU012547
54.1	47	29	AL759250	AL759250 Arabidops	643	9.2	54.1	52	28	BH614721	BH614721
54.1	47	29	AL946412	AL946412 Arabidops	644	9.2	54.1	52	28	BH622642	BH622642
54.1	47	29	BX201354	BX201354 Danlo rer	645	9.2	54.1	52	28	BH904986	BH904986
54.1	47	29	BX292218	BX292218 Arabidops	646	9.2	54.1	52	29	CG782579	CG782579
54.1	48	9	AV833378	AV833378 AV833378	c 647	9.2	54.1	52	29	AL751664	AL751664
54.1	48	9	AV834599	AV834599 AV834599	c 648	9.2	54.1	52	29	AL757821	AL757821
54.1	48	12	BI730786	BI730786 603350475	c 649	9.2	54.1	52	29	AL759350	AL759350
54.1	48	28	AZ576812	AZ576812 Old05 Shc	c 650	9.2	54.1	52	29	AL936314	AL936314
54.1	48	28	AZ833039	AZ833039 2M0113P15	c 651	9.2	54.1	52	29	BX289135	BX289135
54.1	48	28	AZ942244	AZ942244 2M0202M14	c 652	9.2	54.1	52	29	BX291412	BX291412
54.1	48	28	BH911554	BH911554 SALK_0694	c 653	9.2	54.1	52	29	BX655031	BX655031
54.1	48	29	CG722350	CG722350 1119071F0	c 654	9.2	54.1	52	29	BX661610	BX661610
54.1	48	29	AL765906	AL765906 Arabidops	c 655	9.2	54.1	52	29	BX891532	BX891532
54.1	48	29	AL767661	AL767661 Arabidops	656	9.2	54.1	53	12	BG521345	BG521345
54.1	48	29	AL938919	AL938919 Arabidops	657	9.2	54.1	53	12	BI439906	BI439906
54.1	48	29	AL941984	AL941984 Arabidops	658	9.2	54.1	53	13	BX704759	BX704759
54.1	48	29	AL947540	AL947540 Arabidops	659	9.2	54.1	53	14	W07998	W07998
54.1	48	29	BX288820	BX288820 Arabidops	c 660	9.2	54.1	53	28	B06774	B06774
54.1	48	29	BX288861	BX288861 Arabidops	c 661	9.2	54.1	53	28	BH790547	BH790547

54.1	53	29	AL765150	AL765150 Arabidops	C 735	9.2	54.1	56	29	EX292089	EX292089
54.1	53	29	AL766638	AL766638 Arabidops	C 736	9.2	54.1	56	29	EX292375	EX292375
54.1	53	29	AL770675	AL770675 Arabidops	C 737	9.2	54.1	56	29	EX655581	EX655581
54.1	53	29	AL938469	AL938469 Arabidops	C 738	9.2	54.1	56	29	EX659639	EX659639
54.1	53	29	EX291332	EX291332 Arabidops	C 739	9.2	54.1	57	12	BJ031394	BJ031394
54.1	53	29	EX533126	EX533126 Arabidops	740	9.2	54.1	57	14	H28537	H28537
54.1	53	29	EX533575	EX533575 Arabidops	741	9.2	54.1	57	28	AZ921731	AZ921731
54.1	53	29	EX657916	EX657916 Arabidops	C 742	9.2	54.1	57	28	B02087	B02087
54.1	54	9	AU257493	AU257493 Arabidops	C 743	9.2	54.1	57	28	BH11906	BH11906
54.1	54	28	A2346920	A2346920 Arabidops	744	9.2	54.1	57	28	BH89487	BH89487
54.1	54	28	BH233691	BH233691 Arabidops	745	9.2	54.1	57	28	BH89495	BH89495
54.1	54	28	BH909216	BH909216 Arabidops	C 746	9.2	54.1	57	29	AL758777	AL758777
54.1	54	28	BZ380337	BZ380337 Arabidops	C 747	9.2	54.1	57	29	AL944349	AL944349
54.1	54	28	CC457855	CC457855 Arabidops	C 748	9.2	54.1	57	29	EX002702	EX002702
54.1	54	29	AL751431	AL751431 Arabidops	C 749	9.2	54.1	57	29	EX004487	EX004487
54.1	54	29	AL751983	AL751983 Arabidops	C 750	9.2	54.1	57	29	EX291765	EX291765
54.1	54	29	AL756050	AL756050 Arabidops	C 751	9.2	54.1	57	29	EX291770	EX291770
54.1	54	29	AL765764	AL765764 Arabidops	C 752	9.2	54.1	57	29	EX651229	EX651229
54.1	54	29	AL770564	AL770564 Arabidops	C 753	9.2	54.1	57	29	EX652026	EX652026
54.1	54	29	AL945423	AL945423 Arabidops	C 754	9.2	54.1	57	29	EX654520	EX654520
54.1	54	29	AL945582	AL945582 Arabidops	C 755	9.2	54.1	57	29	EX661212	EX661212
54.1	54	29	AL953799	AL953799 Arabidops	C 756	9.2	54.1	57	29	EX662190	EX662190
54.1	54	29	EX001192	EX001192 Arabidops	C 757	9.2	54.1	57	29	EX893754	EX893754
54.1	54	29	EX001254	EX001254 Arabidops	C 758	9.2	54.1	58	9	AL193125	AL193125
54.1	54	29	EX288739	EX288739 Arabidops	759	9.2	54.1	58	9	AL266959	AL266959
54.1	54	29	EX291744	EX291744 Arabidops	C 760	9.2	54.1	58	9	AL315720	AL315720
54.1	54	29	EX291866	EX291866 Arabidops	C 761	9.2	54.1	58	12	BI416933	BI416933
54.1	54	29	EX533244	EX533244 Arabidops	C 762	9.2	54.1	58	14	CF312550	CF312550
54.1	54	29	EX659227	EX659227 Arabidops	C 763	9.2	54.1	58	14	R34882	R34882
54.1	54	29	EX892126	EX892126 Arabidops	C 764	9.2	54.1	58	28	AZ364641	AZ364641
54.1	54	29	EX893146	EX893146 Arabidops	C 765	9.2	54.1	58	28	AZ921711	AZ921711
54.1	54	29	EX893664	EX893664 Arabidops	C 766	9.2	54.1	58	28	B02422	B02422
54.1	54	29	EX895924	EX895924 Arabidops	C 767	9.2	54.1	58	28	B46574	B46574
54.1	55	9	AI354331	AI354331 Arabidops	C 768	9.2	54.1	58	28	BH410854	BH410854
54.1	55	9	AI354331	AI354331 Arabidops	C 769	9.2	54.1	58	28	BH901568	BH901568
54.1	55	9	AI354331	AI354331 Arabidops	C 770	9.2	54.1	58	28	BZ762173	BZ762173
54.1	55	10	BG073100	BG073100 Arabidops	C 771	9.2	54.1	58	28	BZ767910	BZ767910
54.1	55	12	BG314660	BG314660 Arabidops	C 772	9.2	54.1	58	29	CC887783	CC887783
54.1	55	14	UL7539	UL7539 Arabidops	C 773	9.2	54.1	58	29	CG781019	CG781019
54.1	55	28	B02262	B02262 Arabidops	C 774	9.2	54.1	58	29	AL767671	AL767671
54.1	55	29	CG671812	CG671812 Arabidops	C 775	9.2	54.1	58	29	AL767748	AL767748
54.1	55	29	AL758499	AL758499 Arabidops	C 776	9.2	54.1	58	29	AL768047	AL768047
54.1	55	29	AL761941	AL761941 Arabidops	C 777	9.2	54.1	58	29	AL938875	AL938875
54.1	55	29	AL765668	AL765668 Arabidops	C 778	9.2	54.1	58	29	AL947689	AL947689
54.1	55	29	AL942454	AL942454 Arabidops	C 779	9.2	54.1	58	29	AL948740	AL948740
54.1	55	29	AL944123	AL944123 Arabidops	C 780	9.2	54.1	58	29	AL949035	AL949035
54.1	55	29	AL944727	AL944727 Arabidops	C 781	9.2	54.1	58	29	AL949322	AL949322
54.1	55	29	AL950225	AL950225 Arabidops	C 782	9.2	54.1	58	29	AL951825	AL951825
54.1	55	29	AL950485	AL950485 Arabidops	C 783	9.2	54.1	58	29	EX536333	EX536333
54.1	55	29	EX289789	EX289789 Arabidops	C 784	9.2	54.1	58	29	EX547884	EX547884
54.1	55	29	EX291339	EX291339 Arabidops	C 785	9.2	54.1	58	29	EX892137	EX892137
54.1	55	29	EX531700	EX531700 Arabidops	C 786	9.2	54.1	58	29	EX893348	EX893348
54.1	55	29	EX661592	EX661592 Arabidops	C 787	9.2	54.1	59	9	AU256445	AU256445
54.1	56	9	AL800543	AL800543 Arabidops	C 788	9.2	54.1	59	9	AW053615	AW053615
54.1	56	9	AA389121	AA389121 Arabidops	C 789	9.2	54.1	59	12	BI218087	BI218087
54.1	56	9	AA464776	AA464776 Arabidops	C 790	9.2	54.1	59	13	EX700090	EX700090
54.1	56	28	A2657747	A2657747 Arabidops	C 791	9.2	54.1	59	14	CF312549	CF312549
54.1	56	28	A2687618	A2687618 Arabidops	C 792	9.2	54.1	59	14	CF851726	CF851726
54.1	56	28	AZ938203	AZ938203 Arabidops	C 793	9.2	54.1	59	28	AZ458586	AZ458586
54.1	56	28	BH231699	BH231699 Arabidops	794	9.2	54.1	59	28	AZ475901	AZ475901
54.1	56	28	BH862524	BH862524 Arabidops	C 795	9.2	54.1	59	28	AZ537411	AZ537411
54.1	56	29	CG707530	CG707530 Arabidops	C 796	9.2	54.1	59	28	BH908548	BH908548
54.1	56	29	AL754220	AL754220 Arabidops	C 797	9.2	54.1	59	29	AL753933	AL753933
54.1	56	29	AL760112	AL760112 Arabidops	C 798	9.2	54.1	59	29	AL757646	AL757646
54.1	56	29	AL762719	AL762719 Arabidops	C 799	9.2	54.1	59	29	AL766809	AL766809
54.1	56	29	AL943659	AL943659 Arabidops	C 800	9.2	54.1	59	29	AL766957	AL766957
54.1	56	29	AL951045	AL951045 Arabidops	C 801	9.2	54.1	59	29	AL767458	AL767458
54.1	56	29	AL952124	AL952124 Arabidops	C 802	9.2	54.1	59	29	AL938432	AL938432
54.1	56	29	EX001808	EX001808 Arabidops	C 803	9.2	54.1	59	29	AL938434	AL938434
54.1	56	29	EX002727	EX002727 Arabidops	C 804	9.2	54.1	59	29	AL938456	AL938456
54.1	56	29	EX002873	EX002873 Arabidops	C 805	9.2	54.1	59	29	AL939854	AL939854
54.1	56	29	EX003041	EX003041 Arabidops	C 806	9.2	54.1	59	29	AL950618	AL950618
54.1	56	29	EX291501	EX291501 Arabidops	C 807	9.2	54.1	59	29	AL952471	AL952471
54.1	56	29	EX291890	EX291890 Arabidops							

09:38:24 2004

us-10-090-326-17.max.rst

54.1	59	29	AL953723	AL953723 Arabidops	C 881	9	52.9	42	14	CF338219	CF338219
54.1	59	29	BX291316	BX291316 Arabidops	C 882	9	52.9	42	14	CF339767	CF339767
54.1	59	29	BX547090	BX547090 Arabidops	C 883	9	52.9	42	28	AZ514593	AZ514593
54.1	59	29	BX652724	BX652724 Arabidops	C 884	9	52.9	42	28	AZ789082	AZ789082
54.1	59	29	BX656793	BX656793 Arabidops	C 885	9	52.9	42	28	BZ383008	BZ383008
54.1	59	29	BX891291	BX891291 Arabidops	C 886	9	52.9	42	28	BZ662280	BZ662280
54.1	60	9	AA834171	AA834171 of14ell.s	C 887	9	52.9	42	29	TA14F10Q	TA14F10Q
54.1	60	9	AA174457	AA174457 mc09f10.x	C 888	9	52.9	43	9	AA523903	AA523903
54.1	60	12	BG910408	BG910408 602806048	C 889	9	52.9	43	12	BI328315	BI328315
54.1	60	28	AZ778764	AZ778764 2M0014C15	C 890	9	52.9	43	14	CF338563	CF338563
54.1	60	29	CC596088	CC596088 CH240.398	C 891	9	52.9	43	14	CF338824	CF338824
54.1	60	29	AL758869	AL758869 Arabidops	C 892	9	52.9	43	14	CF339433	CF339433
54.1	60	29	AL763865	AL763865 Arabidops	C 893	9	52.9	43	14	CF339728	CF339728
54.1	60	29	AL766515	AL766515 Arabidops	C 894	9	52.9	43	14	CF339743	CF339743
54.1	60	29	AL936419	AL936419 Arabidops	C 895	9	52.9	43	14	CF340327	CF340327
54.1	60	29	AL940643	AL940643 Arabidops	C 896	9	52.9	43	28	BZ382990	BZ382990
54.1	60	29	AL942427	AL942427 Arabidops	C 897	9	52.9	43	29	BX546561	BX546561
54.1	60	29	AL947740	AL947740 Arabidops	C 898	9	52.9	44	9	AV842450	AV842450
54.1	60	29	BX286093	BX286093 Arabidops	C 899	9	52.9	44	29	CC888677	CC888677
54.1	60	29	BX290391	BX290391 Arabidops	C 900	9	52.9	44	29	CG705740	CG705740
54.1	60	29	BX291566	BX291566 Arabidops	C 901	9	52.9	45	28	AZ769215	AZ769215
54.1	60	29	BX292263	BX292263 Arabidops	C 902	9	52.9	45	28	AZ815371	AZ815371
54.1	60	29	BX531561	BX531561 Arabidops	C 903	9	52.9	45	28	AZ853600	AZ853600
54.1	60	29	BX534355	BX534355 Arabidops	C 904	9	52.9	45	28	BH641805	BH641805
54.1	60	29	BX893293	BX893293 Arabidops	C 905	9	52.9	46	9	AAU52407	AAU52407
54.1	60	29	BX893699	BX893699 Arabidops	C 906	9	52.9	46	9	AI863959	AI863959
54.1	60	29	BX895086	BX895086 Arabidops	C 907	9	52.9	46	14	CF315365	CF315365
54.1	60	29	BX897088	BX897088 Arabidops	C 908	9	52.9	46	29	CG712534	CG712534
54.1	60	29	BX897414	BX897414 Arabidops	C 909	9	52.9	47	12	BI916743	BI916743
54.1	60	29	BM399000	BM399000 5009-0-51	C 910	9	52.9	47	28	CC199541	CC199541
52.9	21	28	AZ852233	AZ852233 2M0154D23	C 911	9	52.9	48	29	CG672207	CG672207
52.9	22	9	AL930371	AL930371 AL930371	C 912	9	52.9	49	9	AA690317	AA690317
52.9	24	12	BM399134	BM399134 5009-0-53	C 913	9	52.9	49	9	AA987399	AA987399
52.9	24	28	AZ848167	AZ848167 2M0149C11	C 914	9	52.9	49	9	AI521631	AI521631
52.9	26	12	BM398348	BM398348 5009-0-44	C 915	9	52.9	49	9	AI528223	AI528223
52.9	26	28	BZ290508	BZ290508 SALK_0898	C 916	9	52.9	49	9	AI889232	AI889232
52.9	26	28	BZ763068	BZ763068 SALK_1118	C 917	9	52.9	49	9	AI900473	AI900473
52.9	26	29	CG712062	CG712062 1119023H1	C 918	9	52.9	49	9	AA620370	AA620370
52.9	27	14	D19578	D19578 MUGS00985	C 919	9	52.9	49	14	W17887	W17887
52.9	27	29	TA249G06Q	TA249G06Q T. brucei	C 920	9	52.9	49	28	AZ808932	AZ808932
52.9	28	28	AZ475208	AZ475208 LM0293E18	C 921	9	52.9	49	29	CC886568	CC886568
52.9	28	10	AW246945	AW246945 2822529.5	C 922	9	52.9	49	29	CG723151	CG723151
52.9	29	28	BZ665244	BZ665244 SALK_1109	C 923	9	52.9	49	29	CG779221	CG779221
52.9	29	29	TA190B07P	TA190B07P T. brucei	C 924	9	52.9	49	29	TA108E04P	TA108E04P
52.9	30	12	BM395595	BM395595 5009-0-1-	C 925	9	52.9	50	9	AA847284	AA847284
52.9	30	28	AZ317049	AZ317049 LM0035B14	C 926	9	52.9	50	9	AI750109	AI750109
52.9	30	28	AZ433900	AZ433900 LM0220F03	C 927	9	52.9	50	9	AI103184	AI103184
52.9	30	28	BH909588	BH909588 SALK_0545	C 928	9	52.9	50	9	AI103635	AI103635
52.9	31	9	AA667984	AA667984 v93D11.x	C 929	9	52.9	50	9	AI103636	AI103636
52.9	31	12	BI830964	BI830964 603080801	C 930	9	52.9	50	9	AI105856	AI105856
52.9	31	28	BH791155	BH791155 SALK_0588	C 931	9	52.9	50	9	AI105857	AI105857
52.9	31	29	TA209E04P	TA209E04P T. brucei	C 932	9	52.9	50	9	AI106307	AI106307
52.9	32	9	AU252838	AU252838 AU252838	C 933	9	52.9	50	9	AI106367	AI106367
52.9	32	10	BF568357	BF568357 602184546	C 934	9	52.9	50	9	AI106372	AI106372
52.9	32	29	BX891555	BX891555 Arabidops	C 935	9	52.9	50	9	AI106375	AI106375
52.9	33	29	AL945047	AL945047 Arabidops	C 936	9	52.9	50	9	AI106379	AI106379
52.9	35	28	BZ356521	BZ356521 SALK_1292	C 937	9	52.9	50	9	AI106382	AI106382
52.9	37	9	AI539693	AI539693 tp71h05.x	C 938	9	52.9	50	9	AI106434	AI106434
52.9	37	9	AI794982	AI794982 sb74e12.Y	C 939	9	52.9	50	9	AI106828	AI106828
52.9	37	10	BE307655	BE307655 601096785	C 940	9	52.9	50	9	AI106834	AI106834
52.9	37	14	D38654	D38654 HUNC110242	C 941	9	52.9	50	9	AI106835	AI106835
52.9	37	29	BX288367	BX288367 Arabidops	C 942	9	52.9	50	9	AI106837	AI106837
52.9	38	14	CF338710	CF338710 RCL1--02-	C 943	9	52.9	50	9	AI107179	AI107179
52.9	38	28	AZ964176	AZ964176 2M0233F13	C 944	9	52.9	50	9	AI107180	AI107180
52.9	38	28	BH863233	BH863233 SALK_0934	C 945	9	52.9	50	9	AI107181	AI107181
52.9	39	10	BE275929	BE275929 601121563	C 946	9	52.9	50	9	AA594651	AA594651
52.9	40	9	AA912227	AA912227 o193a08.8	C 947	9	52.9	50	11	CNS08XE7	CNS08XE7
52.9	40	28	BH801511	BH801511 1008117C0	C 948	9	52.9	50	28	AZ480460	AZ480460
52.9	40	28	BH864142	BH864142 SALK_0954	C 949	9	52.9	50	28	BH862793	BH862793
52.9	41	28	BH908025	BH908025 SALK_0452	C 950	9	52.9	50	28	BZ663576	BZ663576
52.9	41	28	BZ357757	BZ357757 SALK_1312	C 951	9	52.9	50	28	AL756931	AL756931
52.9	41	28	CC028458	CC028458 3591_1.10	C 952	9	52.9	51	12	BI175753	BI175753
52.9	41	29	CG720602	CG720602 1119063A0	C 953	9	52.9	51	13	BQ626411	BQ626411

51 28 AQ025577 51 28 AQ025577 fs(3)0708  
52.9 51 28 BH218157 52.9 51 28 BH218157 1006077D0  
52.9 51 29 CC502382 52.9 51 29 CC502382 CH240\_341  
52.9 51 29 BX207707 52.9 51 29 BX207707 Danio rer  
52.9 52 9 AI022550 52.9 52 9 AI022550 ow58d11.s  
52.9 52 9 AI309536 52.9 52 9 AI309536 qo65f01.x  
52.9 52 9 AI524189 52.9 52 9 AI524189 th0c09.x  
52.9 52 9 AI571481 52.9 52 9 AI571481 tr56g03.x  
52.9 52 10 AW693191 52.9 52 10 AW693191 NF061C10S  
52.9 52 14 CF338464 52.9 52 14 CF338464 RCL1-01-  
52.9 52 28 AZ447457 52.9 52 28 AZ447457 IMC244E08  
52.9 52 28 BH637952 52.9 52 28 BH637952 1008019F0  
52.9 52 28 BZ764623 52.9 52 28 BZ764623 SALK\_1259  
52.9 52 29 AG217042 52.9 52 29 AG217042 Drosophi  
52.9 53 9 AU259367 52.9 53 9 AU259367 AU259367  
52.9 53 10 BG037362 52.9 53 10 BG037362 dg49b08.Y  
52.9 53 28 AZ814606 52.9 53 28 AZ814606 2M0082J20  
52.9 53 28 BH640167 52.9 53 28 BH640167 1008034C0  
52.9 53 29 CG724037 52.9 53 29 CG724037 1119079D0  
52.9 53 29 AG215854 52.9 53 29 AG215854 Drosophi  
52.9 53 29 TA300B07P 52.9 53 29 TA300B07P  
52.9 54 10 BE042301 52.9 54 10 BE042301 hk35c06.Y  
52.9 54 12 BG863207 52.9 54 12 BG863207 602796693  
52.9 54 12 BJ046711 52.9 54 12 BJ046711 BJ046711  
52.9 54 14 CA797539 52.9 54 14 CA797539 CacBL\_46  
52.9 54 14 CF859400 52.9 54 14 CF859400 ps2G006xF  
52.9 54 14 CF927815 52.9 54 14 CF927815 laf57h10.  
52.9 54 28 AF149434 52.9 54 28 AF149434 AF149434  
52.9 54 28 BH638103 52.9 54 28 BH638103 1008020D0  
52.9 54 29 AL767122 52.9 54 29 AL767122 Arabidops  
52.9 54 29 AL944217 52.9 54 29 AL944217 Arabidops  
52.9 54 29 AL949602 52.9 54 29 AL949602 Arabidops  
52.9 55 9 AA983584 52.9 55 9 AA983584 on41c07.s  
52.9 55 14 W31056 52.9 55 14 W31056 zb86c10.r1  
52.9 55 28 AZ804709 52.9 55 28 AZ804709 2M0065D20  
52.9 55 28 B03369 52.9 55 28 B03369 CSRL-177B9-  
52.9 55 28 BH222077 52.9 55 28 BH222077 1006105B0  
52.9 55 28 BH409434 52.9 55 28 BH409434 1007012C0  
52.9 55 28 BZ763166 52.9 55 28 BZ763166 SALK\_1140  
52.9 55 29 CG722070 52.9 55 29 CG722070 1119070C0  
52.9 56 9 AU257475 52.9 56 9 AU257475  
52.9 56 12 BJ063843 52.9 56 12 BJ063843 BJ063843  
52.9 56 28 BH628418 52.9 56 28 BH628418 1007079H0  
52.9 56 28 BH852370 52.9 56 28 BH852370 SALK\_0745  
52.9 57 13 BX740623 52.9 57 13 BX740623 BX740623  
52.9 57 28 BH864081 52.9 57 28 BH864081 SALK\_0952  
52.9 57 28 BH889151 52.9 57 28 BH889151 3526\_1\_32

6273 60 bp mRNA linear EST 02-SEP-1998  
g10.r1 Soares mammary\_gland\_NbMMG Mus musculus cDNA clone  
R1398306 5' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8  
AN1; mRNA sequence.  
6273  
6273.1 GI:3516597

musculus (house mouse)  
myota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 60)  
a.M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
el, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, B.,  
illenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, R.,  
sing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
rston, R.  
WashU-HMI Mouse EST Project  
blished (1996)

COMMENT  
Contact: Marria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouse@watson.wustl.edu  
This clone is available royalty-free through LLNL; cont  
IMAGE Consortium (info@image.llnl.gov) for further infor  
MGI:910022  
Trace considered overall poor quality  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
source  
1. 60  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1398306"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_mammary\_gland\_NbMMG"  
/notes="Organ: mammary gland; Vector: pRT73D-Pac  
(Pharmacia) with a modified polylinker; Site 1:  
Site 2: Eco RI; 1st strand cDNA was primed with  
oligo(dT) primer [5',  
TGTTACCAATCTGAGTGGGCGGCGCGAATGGTTT  
T 3']; double-stranded cDNA was ligated to Eco  
adaptors (Pharmacia), digested with Not I and  
the Not I and Eco RI sites of the modified pRT  
RNA provided by Dr. Minoru Ko, Wayne State Univ  
constructed and normalized by Bento Soares and  
Bonaldo."

ORIGIN  
Query Match 75.3%; Score 12.8; DB 9; Length 60;  
Best Local Similarity 87.5%; Pred. No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 1 CGAGTGAAGATCCCT 16  
|||||  
Db 29 CGAGTGAAGTCCCT 44  
|||||

RESULT 2  
BE321851  
LOCUS BE321851 52 bp mRNA linear EST  
DEFINITION NF009F111N1F092 Insect herbivory Medicago truncatula cD  
NF009F111N 5', mRNA sequence.  
ACCESSION BE321851  
VERSION BE321851.2 GI:11963009  
EST  
KEYWORDS Medicago truncatula (barrel medic)  
SOURCE Medicago truncatula  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; T  
Medicago.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C  
Flores, H.R., Imman, J.T., Weiler, J.W. and May, G.D.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Fo  
Medicago truncatula insect herbivory library  
JOURNAL Unpublished (2000)  
COMMENT On Jul 14, 2000 this sequence version replaced gi:919562  
Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191

09:38:24 2004

us-10-090-326-17.max.rst

```
501 575 7601
: korthcomp.uark.edu
ago Genome Initiative accession: MGI:S:23216
t Length: 501 Std Error: 0.00
: 009 row: F column: 11
rimer: TCACACGAGAAAGCTATGAC.
Location/Qualifiers
1..52
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF009F11N"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/clone_lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
71.8%; Score 12.2; DB 10; Length 52;
larity 82.4%; Pred. No. 4.2e+04; Indels 0; Gaps 0;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
GTGAGATCCCTT 17
|||||
CTGAGATCTCT 32
37 bp mRNA linear EST 04-MAY-1995
09.s1 Soares infant brain LNB Homo sapiens cDNA clone
:24408 3' similar to gb:X66114.mnal MITOCHONDRIAL
GLUTARATE/MALATE CARRIER PROTEIN (HUMAN); mRNA sequence.
7
7.1 GI:795033
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 37)
er.L., Clark.N., Dubuque.T., Elliston.K., Hawkins.M.,
n.M., Hultman.M., Kucaba.T., Le.M., Lennon.G., Marra.M.,
ns.J., Rifkin.L., Rohlfing.T., Soares.M., Tan.F.,
skis.E., Waterston.R., Williamson.A., Woldmann.P. and
n.R.
ashU-Merck EST Project
lished (1995)
ct: Wilson RK
ngton University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
: est@watson.wustl.edu
t Size: 1676
quality sequence starts: 1 High quality sequence stops: 1
e: IMAGE Consortium, LNL This clone is available royalty-free
gh LNL; contact the IMAGE Consortium (info@image.lnl.gov)
urther information. Trace considered overall poor quality
t Length: 1676 Std Error: 0.00
rimer: -21ml3
quality sequence stop: 1.
Location/Qualifiers
1..37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:396755"
/db_xref="taxon:9606"
/clone="IMAGE:24408"
```

```
/sex="female"
/dev stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain LNB"
/note="Organ: whole brain; Vector: Lfamid BA; Si
I; Site 2: Hind III; 1st strand cDNA was primed
I - oligo(dT) primer [5',
AACTGGAAGAATCGCGCGCAGGAATTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Hind III ada
(Pharmacia), digested with Not I and directional
into the Not I and Hind III sites of the Lfamid
Library went through one round of normalization.
constructed by Bento Soares and M.Fatima Bonaldc
Query Match 70.6%; Score 12; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.7e+04; Indels 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
QY 6 GAAGATCCCTT 17
|||||
Db 29 GAAGATCCCTT 18
RESULT 4
BM862480/c
LOCUS
DEFINITION
ACCESSION
BM862480
VERSION
BM862480.2 GI:30392312
EST.
KEYWORDS
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc
Sordariomycetes; incertae sedis; Magnaportheaceae; Magnapor
1 (bases 1 to 49)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatteai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magna
grisea
Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19230162
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, US
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see cont
person:
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm003 row: C column: 08
Seq primer: T3.
Location/Qualifiers
1..49
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm003xC08"
/sex="Mati-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Lib
XhoI; Vector: pBluescriptSK-; Site 1: EcoRI; Si
XhoI; Unidirectional cloning. EcoRI side has T3
predominantly 5' reads. T7 primer on XhoI side o
Strain inoculated into complete medium grown for
at room temperature, 150 rpm, harvested, blended
reinoculated into complete medium 24 h, room tem
```

150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

69.4%; Score 11.8; DB 12; Length 49;  
 ilarity 86.7%; Pred. No. 6.7e+04;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 AGTGAAGATCCCC 15  
 |||||  
 AGAAGATCGCC 9

3440 59 bp DNA linear GSS 18-JUN-2002  
 idopsis thaliana T-DNA flanking sequence GK-037A01-015009,  
 mic survey sequence.

3440  
 3440.1 GI:21512904

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

zhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.  
 Weissshaar, B.  
 peline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 sformed lines  
 blished

o.M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished  
 bases 1 to 59)  
 .; Rosso, M., Strizhov, N. and Weissshaar, B.  
 ct Submission  
 itted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer  
 htungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 . sequence is recovered from the left border of the T-DNA. It  
 . cares an insertion close to or within gene At2g36300. The  
 . ences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 t Genomics program designated 'GABI'. Information on line  
 lability can be found at:  
 .://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1.59  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-037A01-015009"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector PAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

Query Match 69.4%; Score 11.8; DB 29; Length 59;  
 Best Local Similarity 86.7%; Pred. No. 7.2e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCC 15  
 |||||  
 Db 27 CGCTGAAGATCCCC 13

# RESULT 6

CB353581/c

LOCUS  
 DEFINITION

CB353581 60 bp mRNA linear EST  
 ZF001-P00007-DPE-F-C E05 GISZF001 Danio rerio cDNA clone  
 IMAGE:6894154 5' similar to fx68c08.y1 Zebrafish SJD 5 d  
 Danio rerio cDNA clone IMAGE:5628303 5' similar to SW:AC  
 P53485 ACTIN, CYTOPLASMIC 2, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Ruan Y

Laboratory of Molecular Biotechnology

Genome Institute of Singapore

1 Science Park Road, The Capricorn #05-01, Singapore 117

Tel: +65 6827 5200

Fax: +65 6827 5201

Email: gisry@nus.edu.sg

GIS Clone ID: ZF001-P00007-PP\_J09

PCR Primers

FORWARD: M13

BACKWARD: M13

Plate: ZF001-P00007-DPE-F-C

Seq primer: CCGCATAACTGTATAGCA

High quality sequence stop: 60.

Location/Qualifiers

1.60

/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="IMAGE:6894154"

/tissue\_type="Embryo"

/dev\_stage="7 Different embryonic Stages ( From

fertilized Embryos to 72 hours just hatched bal

/lab\_host="DH10B"

/clone\_lib="GISZF001"

/note="Vector: pDNR-LIB; Site 1: Sfi A (GGCCATT

Site 2: Sfi B (GGCCGCTCGGC) Priming method:

Primed; Priming sequence: 5.ATTCTAGA GGCCGAGGC

GACAG(T)30VN; Directionally cloned, 5' cl

Sfi A site GGCCATTACGGCC; 5' linker/adaptc

5.AAGCAGTGTATCAACGAGAGTGCC; 3' cloning

site GGCCGCTCGGC; 3' linker/adaptor sequ

as the priming sequence; Average insert size:

PCR insert analysis: Use M13 Forward and revers

Library Amplified Recombinants (inserts): 98%

complexity: 5x106; Full-length construction (n

SMART, a Clontech method; Library constructed

Mathavan, Chia-Lin Wei, and Yijun Ruan Genome I

Singapore"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 14; Length 60;  
 Best Local Similarity 86.7%; Pred. No. 7.3e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

TGAAGATCCCT 16  
|||||  
TGAAGATCTCT 29

1452 47 bp DNA linear GSS 13-DEC-2000  
3108F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
UUGC1M0463108 F, genomic survey sequence.  
1452  
1452.1 GI:11746642

musculus (house mouse)  
musculus  
Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
Mus musculus (house mouse)  
1 (bases 1 to 47)  
D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,  
SLC, UT  
801 585 5606  
801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0463 row: I column: 08  
Seq primer: CGTGTAAACGACGGCAGT  
3: plasmid ends  
quality sequence stop: 47.

Location/Qualifiers  
1. .47  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0463108"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

67.1%; Score 11.4; DB 28; Length 47;  
ilarity 92.3%; Pred. No. 1.1e+05;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTGAAGATCCCC 15  
|||||  
DB 19 AGTGATGATCCCC 7

RESULT 8  
AZ769807/c  
LOCUS  
DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL  
COMMENT

AZ769807 57 bp DNA linear GSS  
1M0570A22R Mouse 10kb plasmid UUGC1M library Mus musculus  
clone UUGC1M0570A22 R, genomic survey sequence.

AZ769807  
AZ769807.1 GI:12890335  
GSS.  
Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
Mus musculus (house mouse)  
1 (bases 1 to 57)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,  
SLC, UT  
801 585 5606  
801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0570 row: A column: 22  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 57.

FEATURES  
source

Location/Qualifiers  
1. .57  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0570A22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from  
musculus C57BL/6J (male) was obtained from the  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage  
through a 0.005 inch orifice at constant velocity. The sheared  
DNA was blunt end-repaired with T4 DNA polymerase and  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a  
derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 67.1%; Score 11.4; DB 28; Length 57;  
Best Local Similarity 92.3%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

FTGAAGATCCC 14  
|||||  
FTGAAGATCCC 12

2G04P 31 bp DNA linear GSS 13-DEC-2000  
brucei sheared genomic DNA clone 122g04, forward sequence,  
mic survey sequence.

2661  
2661.1 GI:11833541

anosoma brucei  
anosoma brucei  
ryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
anosoma.  
bases 1 to 31)  
N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
lingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
ille, S.E., Rajandream, M.A. and Barrell, B.G.

ct Submission  
itted (10-DEC-2000) Trypanosoma brucei genome sequencing  
ect, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
ridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
sanger.ac.uk  
tracted at the Institute for Genomic Research (TIGR),  
ville, MD. Genomic DNA isolated from a cloned population of  
anosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
ive a tight size distribution (  
). The v + i method used for the library construction is  
ribed in detail in Smith, H. and Venter, J.C. (Making small  
it libraries for whole genome shotgun sequencing projects. In  
me Sequencing: A Practical Approach, eds. M. Vaudin and B.  
ell, Oxford University Press, 1999).

l: nelsay@tigr.org  
ils of T. brucei sequencing at the Sanger Centre are available  
http://www.sanger.ac.uk/Projects/T\_brucei/.

Location/Qualifiers  
1. 31  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="122g04"

65.9%; Score 11.2; DB 29; Length 31;  
ilarity 81.2%; Pred. No. 1.2e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCGT 17  
|||||  
AGCAAGATCCCGT 9

20952 35 bp DNA linear GSS 20-OCT-2003  
3064F11.2EL\_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic  
vey sequence.

20952  
20952.1 GI:37754344

mays  
mays  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
de; Panicoideae; Andropogoneae; Zea.  
(bases 1 to 35)  
bot, v  
ze genomic sequences found using engineered RescueMu transposon  
ublished (2001)

## COMMENT

Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonu  
Reverse complemented post-ligation sequence from source  
Plate: 1119064 row: F column: 11  
Class: transposon-tagged.

## FEATURES

Location/Qualifiers  
1. 35  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - RescueMu Grid AA"  
/note="Organ: leaf; Vector: RescueMu (engineere  
pBlueScript backbone); Site 1: BamHI; Site 2: P  
RescueMu is a 4.9 kb, modified maize Mu transpc  
designed to allow plasmid rescue from total gen  
Mu elements insert preferentially into transcri  
sites. For more information on RescueMu, go to  
site 'www.zmdb.iastate.edu' and follow the link  
'RescueMu.' Grid AA was grown at UC San Diego i  
was extracted from leaf strips, double digested  
BamHI and BglII, and ligated to form circular p  
DH10B cells were transformed and then screened  
plates with ampicillin."

## ORIGIN

Query Match 65.9%; Score 11.2; DB 29; Length 35;  
Best Local Similarity 81.2%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCGT 16

Db 14 CGAAAAAAGATCCCGT 29

RESULT 11  
AZ771147  
LOCUS  
DEFINITION  
1M0573B07F Mouse 10kb plasmid UUGC1M library Mus musculi  
clone UUGC1M0573B07 F, genomic survey sequence.

ACCESSION  
AZ771147  
VERSION  
AZ771147.1 GI:12893094

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu  
1 (bases 1 to 43)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Har  
Islam, H., Longacre, S., Mahmoud, M., Meener, E., Pedersen,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fr  
plasmid inserts  
Unpublished (2000)

## JOURNAL

COMMENT  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00



0573 row: B column: 07  
 primer: CGTTGTAAACGACGGCCAGT  
 : plasmid ends  
 quality sequence stop: 43.  
 Location/Qualifiers  
 1. 43

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCIM0573B07"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCIM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

65.9%; Score 11.2; DB 28; Length 43;  
 ilarity 81.2%; Pred. No. 1.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 16  
 |||||  
 AGTCAGTCCCTT 22

3597 45 bp mRNA linear EST 17-JAN-2002  
 -0-1-R12.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
 ahymena thermophila cDNA, mRNA sequence.

3597 GI:18195650

ahymena thermophila  
 ahymena thermophila  
 tyota; Alveolata; Ciliophora; Oligohymenophorea;  
 nostomatida; Tetrahymenina; Tetrahymena.  
 bases 1 to 45)  
 witz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
 kel,J. and Klobutcher,L.  
 from Tetrahymena thermophila, strain CU428.1, growing cells  
 blished (2002)

act: Turkewitz AP  
 cular Genetics and Cell Biology  
 ersity of Chicago  
 E. 58th Street, Chicago, IL 60637, USA  
 773 702 4374  
 773 702 3172

1: apturkew@midway.uchicago.edu  
 primer: T3.  
 Location/Qualifiers

1. 45  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"

/strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large frac  
 /notes="Vector: Bluescript SK+; Details on libr  
 preparation can be found in Chilcoat and Turkew  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

# ORIGIN

Query Match 65.9%; Score 11.2; DB 12; Length 45;  
 Best Local Similarity 81.2%; Pred. No. 1.4e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 2 GACTGAAGATCCCTT 17  
 |||||  
 Db 22 GCGTAAAGATCCCTT 7

## RESULT 13

AA288062/c  
 LOCUS

DEFINITION  
 va25f06.r1 GuayWoodford Beier mouse kidney day 7 Mus mus

RNA POLYMERASE II 14.4 KD POLYPEPTIDE ; mRNA sequence.

AA288062  
 VERSION  
 AA288062.1 GI:1934314

KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 COMMENT

Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; cont  
 IMAGE Consortium (info@image.llnl.gov) for further infor  
 MGI:449467

Possible reversed clone: similarity on wrong strand  
 High quality sequence stop: 1.  
 Location/Qualifiers

1. 49  
 source

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:732419"

/tissue\_type="kidney"  
 /dev\_stage="juvenile (7 days old)"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="GuayWoodford Beier mouse kidney day

/note="Organ: kidney; Vector: pBluescript SK-;  
 EcoRI; Site: 2; XhoI; Cloned unidirectionally.  
 Oligo dt. Average insert size: 1.0 Kb; Uni-ZAP  
 -5' adaptor sequence: 5' GAATTCGGCAG 3' ~3'  
 sequence: 5' CTCGAGTTTTTTTTTTT 3' Librar  
 by Lisa Guay-Woodford."

# ORIGIN

Query Match 65.9%; Score 11.2; DB 9; Length 49;  
 Best Local Similarity 81.2%; Pred. No. 1.4e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0;

GTGAGATCCCTT 17  
|||||  
GTTGATCGCTT 8

5161 51 bp mRNA linear EST 20-SEP-2002  
7902.y1 McCarrey Eddy 18 day leptotene and zygotene  
matocytes Mus musculus cDNA clone IMAGE:6367659 5', mRNA  
ence.  
5161

5161.1 GI:23261331

musculus (house mouse)

musculus  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 51;  
rey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,  
in, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,  
er, E., Tsagaris, R., Ronko, L., Maguire, L., Kennedy, S.,  
ett, J., Waterston, R. and Wilson, R.  
S Mouse

blished (2002)

act: McCarrey/Eddy NIEHS Mouse

S Mouse

ington University School of Medicine  
Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

314 286 1800

314 286 1810

l: est@watson.wustl.edu

ary constructed and donated by J. McCarrey, Ph.D. (Southwest  
ation for Biomedical Research, Dept. of Genetics) - excision  
by E.M. Eddy, Ph.D. (National Institutes of Health, National  
itute of Environmental Health Sciences).

2045091

primer: -40RP from Gibco.

Location/Qualifiers

1..51

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:6367659"

/sex="male"

/tissue\_type="18-day leptotene and zygotene spermatocytes"

/lab\_host="PH10B (phage-resistant)"

/clone\_lib="McCarrey Eddy 18 day leptotene and zygotene  
spermatocytes"

/note="Organ: testis; Vector: pBluescript SK+

(Stratagene); Site 1: EcoRI; Site 2: XhoII; cDNA oligo

dt-primed [5'-(GA)10-ACTAGTCGAGTTTCTTTT-3'] and

directionally cloned using 5' linkers 5'-AATTCGACAGAG-3'

and 5'-CTCGGCGC-3'. Size selection of >400bp material

gives average insert size ranging from 1-2 kb. Library was

mass excised (from lambda-UnizAP-XR) and resulting

single-stranded phagemids were prepped and transformed into

PH10B. Library constructed and donated by J. McCarrey,

Ph.D. (Southwest Foundation for Biomedical Research, Dept.

of Genetics); excision done by E.M. Eddy, Ph.D. (National

Institutes of Health, National Institute of Environmental

Health Sciences)."

65.9%; Score 11.2; DB 13; Length 51;

ilarity 81.2%; Pred. No. 1.4e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTGAGATCCCTT 17

|||||

AGTACGATCGCTT 23

RESULT 15

CNS07HRH

LOCUS

DEFINITION

CNS07HRH 51 bp DNA linear GSS  
Anopheles gambiae GSS T7 end of clone 30D22 of library N  
from strain PEST of Anopheles gambiae (African malaria m  
genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL611423.1 GI:15962846  
GSS.  
Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
Anopheles.

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 51)  
Genoscope.  
Direct Submission  
Submitted (01-OCT-2001) Genoscope - Centre National de S  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genosc  
- Web : www.genoscope.cns.fr)

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 51)  
Roth, C.W., Brey, P.T., Ke, Z. and Collins, F.H.  
Direct Submission  
Submitted (01-OCT-2001) BIMI, Institut Pasteur, 25, rue  
Roux, Paris 75015, France  
This clone is from an A. gambiae BAC library provided by  
Collins and sequenced by Genoscope in collaboration with  
Laboratory of Biochem. and Biol. Molec. of Insects, Inst  
Pasteur.

FEATURES

source

1..51

/organism="Anopheles gambiae"

/mol\_type="genomic DNA"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="30D22"

/clone\_lib="NotreDamel"

/note="end : T7"

ORIGIN

Query Match 65.9%; Score 11.2; DB 29; Length 51;

Best Local Similarity 81.2%; Pred. No. 1.4e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 16

|||||

Db 36 CGATGAGATCGCTT 51

RESULT 16

LOCUS

DEFINITION

BX771762 56 bp mRNA linear EST  
BX771762 XGC-egg Silurana tropicalis cDNA clone TEGG042-  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BX771762.1 GI:39678967  
EST.  
Silurana tropicalis (western clawed frog)  
Silurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pi;  
Xenopodinae; Silurana.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 56)  
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and I  
Sanger Xenopus tropicalis EST project 2001 (11\_2003)  
Unpublished (2003)  
Contact: Croning MDR  
Sanger Institute  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TEGG042j14.q1k77  
Sequencing primer: T7

09:38:24 2004

us-10-090-326-17.max.rst

sequence is from a Xenopus Gene Collection (XGC) library  
ructed by Aaron M. Zorn.  
was oligo dt primed from Sug of poly A+ RNA from egg.  
-NotI cut cDNA was then ligated into pCS107 with EcoRI at the  
d and NotI at the 3' end.  
r: pCS107; Site 1: EcoRI; Site 2: NotI  
Escherichia coli XLI-blue.

Location/Qualifiers  
1. .56  
/organism="Silurana tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="TEGG042j14"  
/dev stage="egg"  
/lab\_host="Escherichia coli XLI-blue"  
/clone\_lib="XGC-egg"  
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dt primed from Sug of poly A+ RNA from egg.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end"

65.9%; Score 11.2; DB 13; Length 56;  
Clarity 81.2%; Pred. No. 1.5e+05; Indels 0; Gaps 0;  
Conservative 0; Mismatches 3; Indels 0;  
AGTGAAGATCCCT 16  
|||||  
JGGGAGATCCGCT 56

9991 58 bp DNA linear GSS 04-SEP-2002  
064381.30.15.x Arabidopsis thaliana TDNA insertion lines  
Idopsis thaliana genomic clone SALK\_064381.30.15.x, genomic  
ay sequence.

9991 58 bp DNA linear GSS 04-SEP-2002  
0991.1 GI:22723924  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
as; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
bases 1 to 58)  
so, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
rab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
n, P., Zimmerman, J., and Ecker, J.R.  
quence-indexed library of insertion mutations in the  
idopsis Genome  
blished (2001)  
act: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
0 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 558 6379

1: eckersalk.edu  
is single pass sequence recovered from the left border of  
.. This sequence lies within 300 bases of the 3' end of  
02400.

is: TDNA tagged.  
Location/Qualifiers  
1. .58  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_064381.30.15.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion

ORIGIN

Query Match 65.9%; Score 11.2; DB 28; Length 58;  
Best Local Similarity 81.2%; Pred. No. 1.5e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 2 GAGTGAAGATCCCTT 17  
|||||

Db 34 GAATGAGATGCCCT 19  
|||||

RESULT 18  
AW511427 59 bp mRNA linear EST  
LOCUS  
XU58h01.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:28  
DEFINITION  
mRNA sequence.

ACCESSION  
AW511427  
VERSION  
AW511427.1 GI:7149592  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
1 (bases 1 to 59)  
REFERENCE  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS  
National Cancer Institute, Cancer Genome Anatomy Project  
TITLE  
Tumor Gene Index

JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., M  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequenc  
Clone distribution: NCI-CGAP clone distribution informa  
found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
Seq primer: -40UP from Gibco.

FEATURES  
source

1. .59  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2805937"  
/tissue type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Ut1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site  
Site 2: NotI; Cloned unidirectionally. Primer:  
Average insert size 1.75 kb. Life Technologies  
11538-014"

ORIGIN

Query Match 65.9%; Score 11.2; DB 10; Length 59;  
Best Local Similarity 81.2%; Pred. No. 1.5e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 2 GAGTGAAGATCCCTT 17  
|||||

Db 11 GAGTGACAATCCACTT 26  
|||||

RESULT 19  
AA466912 53 bp mRNA linear EST  
LOCUS  
vfi0f03.x1 Knowles Solter mouse blastocyst B3 Mus muscul  
DEFINITION  
clone IMAGE:835325 5' similar to gb:M36829 Mouse heat-st

4 mRNA (MOUSE); mRNA sequence.  
6912  
6912.1 GI:2193052

musculus (house mouse)

musculus  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 53)  
a.M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
ei, S., Kucaba, I., Lacy, M., Le, M., Martin, J., Morris, M.,  
llenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
sing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
rston, R.

WashU-HHMI Mouse EST Project

blished (1996)

act: Marra M/Mouse EST Project

U-HHMI Mouse EST Project

ington University School of MedicineP

Forest Park Parkway, Box 8501, St. Louis, MO 63108

314 286 1800

314 286 1810

l: mouse@watson.wustl.edu

clone is available royalty-free through LLNL; contact the  
E Consortium (info@image.llnl.gov) for further information.

495541

e considered overall poor quality

ive full length read

or to vector length is 120

quality sequence stop: 1.

Location/Qualifiers

1..53

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6J x DBA/2J F1"

/db\_xref="taxon:10090"

/clone="IMAGE:835325"

/tissue\_type="blastocyst"

/dev\_stage="embryo (pre-implantation)"

/lab\_host="DH10B"

/clone\_lib="Knowles Solter mouse blastocyst B3"

/note="Organ: embryo; Vector: pSPORT; Site:1: NotI;

Site 2: SalI; Cloned unidirectionally from mRNA prepared

from 800 blastocysts. Primer: SalI(dn):

5'-CGGTCGACCGTCGACCGTGTGTTT-3'. cDNAs were

cloned into the NotI/SalI sites of a pSPORT vector (Life

Technologies). Two different size selections: B1 (larger

inserts) and B3."

64.7%; Score 11; DB 9; Length 53;

similarity 100.0%; Pred. No. 1.9e+05;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCT 16

|||||

AGATCCCT 16

30373 8124D09.2EL x1 1008 - RescueMu Grid I Zea mays genomic, Genomic  
vey sequence.

00373

00373.1 GI:20312363

mays

mays

aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

de; Panicoideae; Andropogoneae; Zea.

(bases 1 to 57)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Walbot, V.  
Maize genomic sequences found using engineered RescueMu  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonu  
Reverse complemented post-ligation sequence from source  
Plate: 1008124 row: 32  
Class: transposon-tagged.

FEATURES  
source

1..57  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1008 - RescueMu Grid I"  
/note="Organ: leaf; Vector: RescueMu (engineere  
pBlueScript backbone); Site 1: BamHI; Site 2: B  
RescueMu is a 4.9 Kb, modified maize Mu transpc  
designed to allow plasmid rescue from total gen  
Mu elements insert preferentially into transcri  
units. For more information on RescueMu, go to  
site www.zmdb.iastate.edu and follow the links  
'RescueMu.' Grid I was grown at Berkeley in 200  
extracted from leaf punches, double digested u  
and BglII, and ligated to form circular plasmid  
cells were transformed and then screened on LB  
ampicillin."

ORIGIN

Query Match 64.7%; Score 11; DB 28; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 2 GAGTGAAGATC 12

DB 47 GAGTGAAGATC 57

RESULT 21

AL767128/c

LOCUS

AL767128 59 bp DNA linear GSS  
Arabidopsis thaliana T-DNA flanking sequence GK-216G01-(  
genomic survey sequence.

AL767128

AL767128.1 GI:21520247

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

3 (bases 1 to 59)

2  
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and W  
A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics  
Unpublished  
3 (bases 1 to 59)

1  
Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S  
and Weissman, B.  
A pipeline for automated high-throughput generation of I  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines  
Unpublished

hov,N., Li,Y., Rosso,M. and Weishaar,B.  
 at Submission  
 tted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer  
 tungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 ates an insertion within the locus defined by clone R6F9. The  
 nces are generated at the MPI for Plant Breeding Research in  
 ontext of the GABI-Kat project. GABI-Kat is part of the German  
 Genomics program designated 'GABI'. Information on line  
 ability can be found at:  
 //www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

1. .59  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-216G01-014145"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

64.7%; Score 11; DB 29; Length 59;  
 ilarity 100.0%; Pred. No. 2e+05;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FTGAAGATC 12  
 |||||  
 FTGAAGATC 24

2034 60 bp mRNA linear EST 19-DEC-2000  
 IG04PL1F1034 Phosphate starved leaf Medicago truncatula cDNA  
 3 NF064G04PL 5', mRNA sequence.  
 3034  
 3034.1 GI:11903192

ago truncatula (barrel medic)  
 ago truncatula  
 cyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 is; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 ago.  
 bases 1 to 60)  
 J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 ss,H.R., Iman,J.T., Wellner,J.W., May,G.D. and Harrison,M.J.  
 ssed Sequence Tags from the Samuel Roberts Noble Foundation  
 ago truncatula phosphate-starved leaf library  
 ublished (2000)  
 act: Harrison MJ  
 t Biology Division  
 Samuel Roberts Noble Foundation  
 Sam Noble Parkway, Ardmore, OK 73402, USA  
 580 221 7325  
 580 221 7380  
 l: mjharrison@noble.org  
 rt Length: 60 Std Error: 0.00  
 e: 064 row: G column: 04  
 primer: TCACACAGGAACAGCTATGAC.  
 Location/Qualifiers

1. .60  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"

/db\_xref="taxon:3880"  
 /clone="NF064G04PL"  
 /tissue\_type="leaf"  
 /dev\_stage="trifoliolate"  
 /clone\_lib="Phosphate starved leaf"  
 /note="Vector: Lambda Zap; At the trifoliolate st  
 truncatula plants were transplanted to phosphat  
 and grown for a further 30 days. During this 3  
 period, the plants were fertilized twice weekly  
 Hoaglands solution containing only 20uM potassi  
 phosphate. RNA was prepared from above ground

## ORIGIN

Query Match 64.7%; Score 11; DB 10; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGAT 11  
 |||||  
 Db 5 CGAGTGAAGAT 15

## RESULT 23

AZ423553 22 bp DNA linear GSS  
 LOCUS  
 1M0202N09R Mouse 10kb plasmid UGCLM library Mus musculus  
 DEFINITION  
 clone UGCLM0202N09 R, genomic survey sequence.

ACCESSION  
 AZ423553  
 VERSION  
 AZ423553.1 GI:10547566  
 GSS.

KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euc  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur

## REFERENCE

AUTHORS  
 1 (bases 1 to 22)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ham  
 Islam,H., Longacre,S., Mahmod,M., Meenen,E., Pedersen,T  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from  
 plasmid inserts

## JOURNAL

COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177

Email: adunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0202 row: N column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

## FEATURES

source  
 1. .22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLM0202N09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resista  
 /clone\_lib="Mouse 10kb plasmid UGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA fr  
 musculus C57BL/6J (male) was obtained from the  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/  
 was hydrodynamically sheared by repeated passag  
 0.005 inch orifice at constant velocity. The sh  
 was blunt end-repaired with T4 DNA polymerase a  
 polynucleotide kinase. Adaptor oligonucleotides

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 63.5%; Score 10.8; DB 28; Length 22;  
Best Local Similarity 85.7%; Pred. No. 1.8e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGATCCCTT 17  
||| ||| |||  
Db 18 GAACATCCACTT 16

4980 29 bp DNA linear GSS 27-APR-2001  
80G07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
e UUGC2M0280G07 R, genomic survey sequence.  
4980  
4980.1 GI:13866207

musculus (house mouse)  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
The information of this clone is available through the f

1: ddun@genetics.utah.edu  
rt Length: 10000 Std Error: 0.00  
e: 0280 row: G column: 07  
primer: CACACAGGAACAGCTATGACC  
s: plasmid ends  
quality sequence stop: 29.  
Location/Qualifiers  
1. .29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0280G07"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess adapted DNA was purified and size-selected for 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 63.5%; Score 10.8; DB 28; Length 29;  
Best Local Similarity 85.7%; Pred. No. 1.9e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 2 GAGTGAAGATCCCC 15  
||| ||| ||| |||  
Db 18 GAGTGAAGATTCAC 5

RESULT 25  
BJ064687  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
The information of this clone is available through the f

BJ064687 36 bp mRNA linear EST  
BJ064687 NIBB Mochii normalized Xenopus tailbud library  
laevis cDNA clone XL080g16 5', mRNA sequence.  
BJ064687  
BJ064687.1 GI:17471662  
EST.  
Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pip Xenopodinae; Xenopus.  
1 (bases 1 to 36)  
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T., Kohara, Y.  
Expressed genes in X. laevis embryo  
Contact: Tadasu Shin-i  
Unpublished (2001)  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
The information of this clone is available through the f

URL: <http://xenopus.nibb.ac.jp>.  
Location/Qualifiers  
1. .36  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL080g16"  
/tissue\_type="whole embryo"  
/dev\_stage="stage 25"  
/clone\_lib="NIBB Mochii normalized Xenopus tail  
library"

Query Match 63.5%; Score 10.8; DB 12; Length 36;  
Best Local Similarity 85.7%; Pred. No. 2.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 4 GTGAAGATCCCTT 17  
||| ||| ||| |||  
Db 2 GTGAACACCCCTT 15

## ORIGIN

Query Match 63.5%; Score 10.8; DB 12; Length 36;  
Best Local Similarity 85.7%; Pred. No. 2.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 4 GTGAAGATCCCTT 17  
||| ||| ||| |||  
Db 2 GTGAACACCCCTT 15

RESULT 26  
HSMC39C10

09:38:24 2004

us-10-090-326-17.max.rst

9C10  
iens DNA for trapped exon (ID HMC39C10), genomic survey  
nce.  
0  
0.1 GI:1437968  
sapiens (human)  
sapiens  
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
lia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
ases 1 to 38)  
H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and  
arakis, S.E.  
ng of 559 potential exons of genes of human chromosome 21 by  
trapping  
e Res. 6 (8), 747-760 (1996)  
340  
50  
ases 1 to 38)  
H.M., Rossier, C., Chrast, R. and Antonarakis, S.E.  
ng of trapped exons from human chromosome 21  
lished  
ases 1 to 38)  
arakis, S.E.  
t Submission  
ted (17-MAR-1995) Stylianos E. Antonarakis, Division of  
al Genetics, University and Cantonal Hospital of Geneva, CMU,  
Michel-Servet, 1211 Geneva, SWITZERLAND  
Location/Qualifiers  
1  
38  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="21"  
1  
38  
/note="trapped exon"  
63.5%; Score 10.8; DB 29; Length 38;  
larity 85.7%; Pred. No. 2.1e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TGAGAGTCCCC 15'  
|||||  
AGAAAGTCCCC 26'  
310  
dopsis thaliana T-DNA flanking sequence GK-303C11-015560,  
ic survey sequence.  
310  
310.1 GI:24403932  
dopsis thaliana (thale cress)  
dopsis thaliana  
yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ls; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
hov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.  
eisshaar, B.  
eline for automated high-throughput generation of FSTs  
iking sequence tags) from Arabidopsis thaliana T-DNA  
formed lines  
lished  
M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.  
Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
lanking sequence tag based reverse genetics  
lished  
ases 1 to 40)

AUTHORS  
Li, Y., Rosso, M., Strizhov, N. and Weisshaar, B.  
Direct Submission  
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut  
Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829,  
This sequence is recovered from the left border of the T.  
indicates an insertion within the locus defined by clone  
The sequences are generated at the MPI for Plant Breeding  
in the context of the GABI-Kat project. GABI-Kat is part  
German Plant Genomics program designated 'GABI'. Informa  
line availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/  
Location/Qualifiers  
1  
40  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strains="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-303C11-015560"  
/clone\_lib="Arabidopsis thaliana T-DNA insertio  
/note="PCR was performed on DNA from Arabidopsis  
plants (T1) which were transformed with the T-DN  
vector pAC161. The lines contain one or more T-I  
insertions. The DNA fragment(s) resulting from t  
were directly sequenced to determine the genomic  
flanking the insertion. Sequences displaying si  
similarity to the A. thaliana nuclear genome se  
processed for submission. T-DNA derived sequen  
removed"

Query Match 63.5%; Score 10.8; DB 29; Length 40;  
Best Local Similarity 85.7%; Pred. No. 2.2e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;  
QY 1 CGAGTCAAGATCCC 14  
|||||  
DB 28 CGAGTCAAGATCCC 15  
|||||  
RESULT 28  
AZ598104  
LOCUS  
IM0412M.2R Mouse 10kb plasmid UUGC1M library Mus musculus  
clone UUGC1M0412M12 R, genomic survey sequence.  
AZ598104  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ598104 41 bp DNA linear GSS J  
IM0412M.2R Mouse 10kb plasmid UUGC1M library Mus musculus  
clone UUGC1M0412M12 R, genomic survey sequence.  
AZ598104  
AZ598104.1 GI:11720294  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mur  
1 (bases 1 to 41)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hami  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0412 row: M column: 12  
Seq primer: CACACAGGAACACAGTATGACC  
Class: plasmid ends  
High quality sequence stop: 41.  
Location/Qualifiers

1. .41  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0412M12"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ilarity 63.5%; Score 10.8; DB 28; Length 41;  
 Conservativity 85.7%; Pred.No. 2.2e+05; Mismatches 2; Indels 0; Gaps 0;

ACTGAAGATCCC 14  
 |||||  
 TTGTGATATCCC 34

1610 43 bp DNA linear GSS 04-DEC-2002  
 idopsis thaliana T-DNA flanking sequence GK-357D05-016834,  
 mic survey sequence.

1610.1 GI:26186570

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

zhov.N., Li.Y., Rosso.M., Viehoveer.P., Dekker,K., Saedler,H.  
 Weishaar,B.  
 peline for automated high-throughput generation of ESTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 sformed lines  
 blished

o.M., Strizhov.N., Li.Y., Reiss.B., Dekker,K. and Weishaar,B.  
 x Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished

bases 1 to 43)  
 zhov.N., Rosso.M., Li.Y. and Weishaar,B.  
 ct Submission  
 itted (04-DEC-2002) Weishaar B., Max-Planck-Institut fuer  
 htungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 cates an insertion within the locus defined by clone K22F20.  
 sequences are generated at the MPI for Plant Breeding Research  
 he context of the GABI-Kat project. GABI-Kat is part of the

German Plant Genomics program designated 'GABI'. Informa  
 line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

#### FEATURES source

1. .43  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-357D05-016834"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertio  
 /note="PCR was performed on DNA from Arabidopsi  
 plants (T1) which were transformed with the T-D  
 vector pAC161. The lines contain one or more T-  
 insertions. The DNA fragment(s) resulting from  
 were directly sequenced to determine the genom  
 flanking the insertion. Sequences displaying si  
 similarity to the A. thaliana nuclear genome se  
 processed for submission. T-DNA derived sequenc  
 removed"

#### ORIGIN

Query Match 63.5%; Score 10.8; DB 29; Length 43;  
 Best Local Similarity 85.7%; Pred.No. 2.2e+05;  
 Matches 12; Conservativity 0; Mismatches 2; Indels 0;

Qy 3 AGTGAAGATCCCC 16  
 |||||  
 Db 36 AGGGAAGATCCCAT 23

#### RESULT 30

EX625656  
 LOCUS BX625656 NAPI Anopheles gambiae cDNA clone ANGNP1153F02T  
 DEFINITION sequence.

ACCESSION BX625656

VERSION BX625656.1 GI:33551353

KEYWORDS EST.

SOURCE

ORGANISM Anopheles gambiae (African malaria mosquito)

Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Insecta; Ptery  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
 Anopheles.

REFERENCE 1 (bases 1 to 44)

AUTHORS Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.  
 TITLE Anopheles gambiae EST, Center for Tropical Disease Resea  
 JOURNAL Training  
 COMMENT Unpublished (2003)

Contact: Frank H. Collins  
 Center for Tropical Disease Research and Training  
 University of Notre Dame  
 Notre Dame, IN 46556, USA  
 Tel: 574-631-9245  
 Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

#### FEATURES source

1. .44  
 Location/Qualifiers  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7165"  
 /clone="ANGNP1153F02T7"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"  
 /note="Vector: pT73D-Pac (Pharmacia); Site 1:  
 Site 2: EcoRI; ESTs sequenced from the T7 primi  
 that reads from the 5' end of cDNA. The NAPI is  
 directionally cloned and normalized. Oligo-T pr  
 library constructed from a mixture of Anopheles  
 developmental stages according to: Bonaldo, Len  
 Soares (1996): Normalization and Subtraction: T  
 Approaches To Facilitate Gene Discovery, Genome  
 6, 791-806."



63.5%; Score 10.8; DB 13; Length 44;  
 larity 85.7%; Pred. No. 2.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 TGAAGATCCCC 15  
 ||||| |||||  
 TGAATTTCGCC 18

311  
 dopsis thaliana T-DNA flanking sequence GK-303C11-015563,  
 dic survey sequence.

311.1 GI:24403933  
 dopsis thaliana (thale cress)  
 dopsis thaliana  
 yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 us; eurosid II; Brassicales; Brassicaceae; Arabidopsis;

hov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 Feisshaar,B.  
 eline for automated high-throughput generation of FSTs  
 king sequence tags) from Arabidopsis thaliana T-DNA  
 formed lines  
 ublished

,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 lanking sequence tag based reverse genetics  
 ublished

ases 1 to 44)  
 hov,N., Li,Y., Rosso,M. and Weisshaar,B.  
 t Submission

tungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 ates an insertion within the locus defined by clone T25K17.  
 sequences are generated at the MPI for Plant Breeding Research  
 e context of the GABI-Kat project. GABI-Kat is part of the  
 n Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 //www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

1..44  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-303C11-015563"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

63.5%; Score 10.8; DB 29; Length 44;  
 larity 85.7%; Pred. No. 2.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 GTGAAGATCCCC 14  
 ||||| |||||

Db 31 CGAGTGATGATGCC 18

RESULT 32  
 AA410197  
 LOCUS  
 DEFINITION  
 zV32d06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA cl  
 IMAGE:755339 5', similar to TR:G307153 G307153 MAC-2 BIND:  
 PRECURSOR. ; mRNA sequence.

ACCESSION  
 AA410197  
 VERSION  
 AA410197.1 GI:2069220  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute]  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
 1 (bases 1 to 46)  
 AUTHORS  
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,  
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.  
 Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,I  
 White,Y., Wyllie,T., Waterston,R. and Wilson,R.  
 WashU-Merck EST Project 1997  
 JOURNAL  
 Unpublished (1997)  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; conta  
 IMAGE Consortium (info@image.llnl.gov) for further infor  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28m3 rev2 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

FEATURES  
 source  
 1..46  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:755339"  
 /sex="Female"  
 /tissue\_type="ovarian tumor"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares ovary tumor NbHOT"  
 /note="Organ: ovary; Vector: pT73D (Pharmacia)  
 modified polylinker; Site 1: Not 1; Site 2: Eco  
 strand cDNA was primed with a Not I - oligo (dT)  
 TGTACCAATCGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT  
 double-stranded cDNA was size selected, ligated  
 adapters (Pharmacia), digested with Not I and c  
 the Not I and Eco RI sites of a modified pT73  
 (Pharmacia). Library constructed by Bento Soares  
 M.Fatima Bonaldo."

ORIGIN  
 Query Match 63.5%; Score 10.8; DB 9; Length 46;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;  
 QY 4 GTGAGATCCCTT 17  
 ||||| |||||  
 Db 23 GAGAAGATCCGCTT 36

RESULT 33  
 BH759458/c  
 LOCUS  
 DEFINITION  
 KG04418-3prime Drosophila melanogaster P(SUPor-P) p elem  
 insertion lines Drosophila melanogaster genomic Sequence  
 from 3', end of P element, genomic survey sequence.

ACCESSION  
 BH759458  
 VERSION  
 BH759458.1 GI:19352697

ophila melanogaster (fruit fly)  
 ophila melanogaster  
 yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 tera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 droidea; Drosophilidae; Drosophila.  
 bases 1 to 46)  
 s.R., Hoskins,R., Liao,G., Morden,N., Tsang,G., He,Y.,  
 en,G., Bellen,H., Rubin,G. and Spradling,A.  
 Berkeley Drosophila Genome Project Gene Disruption Project  
 blished (2001)  
 act: Gerald Rubin  
 eley Drosophila Genome Project  
 ersity of California, Berkeley  
 Building, Berkeley, CA 94720-3200, USA  
 5106439947  
 l: gerry@fruitfly.berkeley.edu  
 ence recovery method was inverse PCR.  
 uence orientation is forward strand relative to 5' end of P  
 ent  
 P element insertion position is base 1 in the 46 bases. This  
 rion position refers to the first base of the 8 base target  
 gnition sequence.  
 s: transposon-tagged.  
 Location/Qualifiers  
 1. 46  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Drosophila melanogaster P{SUPor-P} P element  
 insertion lines"  
 /note="Inverse PCR was performed on Drosophila  
 melanogaster strains each of which contains one or more  
 P{SUPor-P} P-element transposon insertion. The resultant  
 fragment for each strain was directly sequenced to  
 determine the genomic sequence at the site of insertion.  
 Details of the protocols used can be found at  
 http://www.fruitfly.org/about/methods/inverse.pcr.html."  
 63.5%; Score 10.8; DB 28; Length 46;  
 ilarity 85.7%; Pred. No. 2.3e+05; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 2; Indels 0;  
 AGTGAAGATCCC 14  
 ||||| |||||  
 AGTGATATTC 7  
 5225  
 idopsis thaliana T-DNA flanking sequence GK-154H01-018348,  
 mic survey sequence.  
 5225.1 GI:28884221  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 macophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 zhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 Weissshaar,B.  
 peline for automated high-throughput generation of ESTs  
 unking sequence tags) from Arabidopsis thaliana T-DNA  
 isformed lines  
 blished  
 io.M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weissshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics

JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 46)  
 AUTHORS Li,Y., Rosso,M., Strizhov,N. and Weissshaar,B.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAR-2003) Weissshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion close to or within gene At2g37080  
 sequences are generated at the MPI for Plant Breeding Re  
 the context of the GABI-Kat project. GABI-Kat is part of  
 Plant Genomics program designated 'GABI'. Information or  
 availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.  
 FEATURES  
 source  
 Location/Qualifiers  
 1. 46  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-154H01-018348"  
 /note="T-DNA insertion  
 plants (T1) which were transformed with the T-D  
 vector pAC161. The lines contain one or more T-  
 insertions. The DNA fragment(s) resulting from  
 were directly sequenced to determine the genomic  
 flanking the insertion. Sequences displaying si  
 similarity to the A. thaliana nuclear genome se  
 processed for submission. T-DNA derived sequenc  
 removed"  
 ORIGIN  
 Query Match 63.5%; Score 10.8; DB 29; Length 46;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;  
 QY 3 AGTGAAGATCCCCT 16  
 ||||| |||||  
 Db 43 AGGGAAGATCCCAT 30  
 RESULT 35  
 EX290413/c  
 LOCUS  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-436B11-C  
 genomic survey sequence.  
 ACCESSION BX290413  
 VERSION BX290413.1 GI:28889409  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidof  
 1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., S  
 and Weissshaar,B.  
 A pipeline for automated high-throughput generation of F  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished  
 2  
 REFERENCE  
 AUTHORS Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We  
 TITLE A new Arabidopsis thaliana T-DNA mutagenised population  
 for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 46)  
 Strizhov,N., Li,Y., Rosso,M. and Weissshaar,B.  
 Direct Submission  
 TITLE Submitted (07-MAR-2003) Weissshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion close to or within gene At4g38760

ences are generated at the MPI for Plant Breeding Research in context of the GABI-Kat project. GABI-Kat is part of the German Genomics program designated 'GABI'. Information on line labiliy can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

1. .46  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"

/db\_xref="taxon:3702"  
 /clone="GK-436B11-018181"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

63.5%; Score 10.8; DB 29; Length 46;  
 ilarity 85.7%; Pred. No. 2.3e+05;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAAGATCCCT 16

|||||  
 GGAAGATCCAT 24

2068  
 idopsis thaliana T-DNA flanking sequence GK-340G01-016161,  
 mac survey sequence.

2068.1 GI:24408690

idopsis thaliana (thale cress)

idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov.N., Li.Y., Rosso.M., Viehoveer,P., Dekker,K., Saedler,H.  
 Weisshaar,B.  
 peline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 stformed lines  
 blished

O.M., Strizhov.N., Li.Y., Reiss.B., Dekker,K. and Weisshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished

bases 1 to 47)  
 .. Rosso.M., Strizhov.N. and Weisshaar,B.  
 ct Submission

ited (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer  
 hungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 cates an insertion within the locus defined by clone F16N3. The  
 ences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 t Genomics program designated 'GABI'. Information on line  
 labiliy can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1. .47

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-340G01-016161"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion  
 /note="PCR was performed on DNA from Arabidopsis  
 plants (T1) which were transformed with the T-DNA  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence  
 processed for submission. T-DNA derived sequences  
 removed"

ORIGIN  
 Query Match 63.5%; Score 10.8; DB 29; Length 47;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0;

Oy 3 AGTGAAGATCCCT 16

|||||  
 Db 46 AGTGAAGATGCCAT 33

RESULT 37

BX291286/c

LOCUS

DEFINITION  
 Arabidopsis thaliana T-DNA flanking sequence GK-461D01-0

Genomic survey sequence.

ACCESSION  
 BX291286

VERSION  
 BX291286.1

KEYWORDS  
 GSS.

SOURCE

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidof

REFERENCE

AUTHORS

TITLE

A pipeline for automated high-throughput generation of F  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

JOURNAL

REFERENCE

AUTHORS

TITLE

Rosso.M., Strizhov.N., Li.Y., Reiss.B., Dekker,K. and We  
 A new Arabidopsis thaliana T-DNA mutagenised population  
 for flanking sequence tag based reverse genetics  
 Unpublished

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institu  
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion close to or within gene At1g07530  
 sequences are generated at the MPI for Plant Breeding Re  
 the context of the GABI-Kat project. GABI-Kat is part of  
 Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1. .49

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-461D01-018951"

/clone\_lib="Arabidopsis thaliana T-DNA insertion  
 /note="PCR was performed on DNA from Arabidopsi  
 plants (T1) which were transformed with the T-D  
 vector pAC161. The lines contain one or more T-



quality sequence stop: 1.

Location/Qualifiers  
1..52  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1137811"  
/dev\_stage="8 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Barstead mouse irradiated colon MPLB7"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'TGTTAGGATCTGAGTGGAGCGCGCCCTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors [AATTCGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73  
vector. Library constructed by Bob Barstead."

63.5%; Score 10.8; DB 9; Length 52;  
ilarity 85.7%; Pred. No. 2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAGATCCCC 15  
|||||  
GTCAAGAGCCCC 33

2627 53 bp mRNA linear EST 08-NOV-2001  
2627 Nori Satoh unpublished cDNA library, larva Ciona  
sinensis cDNA clone rcilv18e20 3', mRNA sequence.

2627  
2627.1 GI:16837961

a intestinalis  
a intestinalis  
ryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
bobranchia; Cionidae; Ciona.  
bases 1 to 53)  
h.N., Satou,Y., Kohara,Y. and Shin-I,T.  
essed genes in Ciona intestinalis  
blished (2000)  
act: Nori Satoh  
rtment of Zoology  
o University  
o-ku, Kyoto, Kyoto 606-8502, Japan  
81-75-753-4081  
81-75-705-1113  
1: satohascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1..53  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="rcilv18e20"  
/tissue\_type="whole animal"  
/dev\_stages="larva"  
/clone\_lib="Nori Satoh unpublished cDNA library, larva"

63.5%; Score 10.8; DB 9; Length 53;  
ilarity 85.7%; Pred. No. 2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GAAGATCCCCCTT 17  
|||||  
GAAGATCACTTT 40

RESULT 42  
AL944840/c  
LOCUS  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-285C03-(  
genomic survey sequence.  
ACCESSION  
AL944840  
VERSION  
AL944840.1 GI:24401462  
KEYWORDS  
GSS.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabido  
1  
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., S  
and Weissshaar,B.  
A pipeline for automated high-throughput generation of T  
(flanking sequence tags) from Arabidopsis thaliana T-DN  
transformed lines  
Unpublished  
2  
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We  
A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics  
Unpublished  
3 (bases 1 to 53)  
Li,Y., Rosso,M., Strizhov,N. and Weissshaar,B.  
Direct Submission  
Submitted (21-OCT-2002) Weissshaar B., Max-Planck-Institu  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
This sequence is recovered from the left border of the T  
indicates an insertion within the locus defined by clone  
The sequences are generated at the MPI for Plant Breedi  
in the context of the GABI-Kat project. GABI-Kat is part  
German Plant Genomics program designated 'GABI'. Informa  
line availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
source

1..53  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-285C03-015290"  
/clone\_lib="Arabidopsis thaliana T-DNA insertic  
/note="PCR was performed on DNA from Arabidopsi  
plants (T1) which were transformed with the T-D  
vector pAC161. The lines contain one or more T-  
insertions. The DNA fragment(s) resulting from  
were directly sequenced to determine the genom  
flanking the insertion. Sequences displaying si  
similarity to the A. thaliana nuclear genome se  
processed for submission. T-DNA derived sequenc  
removed"

ORIGIN

Query Match 63.5%; Score 10.8; DB 29; Length 53;  
Best Local Similarity 85.7%; Pred. No. 2.4e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 3 AGTGAGATCCCCCT 16  
|||||  
Db 48 AGGAGATCCCCCT 35

RESULT 43  
BH853866  
LOCUS  
DEFINITION Arabidopsis thaliana T-DNA insertion  
survey sequence.  
54 bp DNA linear GSS  
BH853866  
SALK\_078396.38.70.x Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_078396.38.70.x,

53866 53866.1 GI:21424737

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
(bases 1 to 54)  
nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
rtnab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
n,P., Zimmerman,J. and Ecker,J.R.  
equence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
ublished (2001)  
ct: Joseph R. Ecker  
t: Institute Genomic Analysis Laboratory (SIGAL)  
alk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
: 858 453 4100 x1752  
: 858 558 6379  
il: ecker@salg.edu  
s is single pass sequence recovered from the left border of  
A.  
ss: TDNA tagged.  
Location/Qualifiers.  
1. 54  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GALK 078396.38.70.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

63.5%;	Score 10.8;	DB 28;	Length 54;
similarity 85.7%;	Pred. No. 2.4e+05;		
Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

AGTGAAGATCCCC 15  
|||||  
AGTGAAGATCACC 19

10566  
Arabidopsis thaliana T-DNA flanking sequence GK-249D07-01444,  
omic survey sequence.

10566.1 GI:24397015

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
zhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
Weisshaar,B.  
ipeline for automated high-throughput generation of FGTs  
anking sequence tags) from Arabidopsis thaliana T-DNA  
sformed lines  
ublished

so,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
aw Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

for flanking sequence tag based reverse genetics

Unpublished  
3 (bases 1 to 54)  
Rosso,M., Strizhov,N., Li,Y. and Weishaar,B.  
Direct Submission  
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut für Zuchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50823  
This sequence is recovered from the left border of the R plasmid.  
Indicates an insertion close to or within gene At2g3440 sequences are generated at the MPI for Plant Breeding R and the context of the GABI-Kat project. GABI-Kat is part of the Plant Genomics program designated 'GABI'. Information on availability can be found at:  
[http://www.mpiz-koein.mpg.de/GABI-Kat/.](http://www.mpiz-koeln.mpg.de/GABI-Kat/)

Location/Qualifiers  
1..54  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-249D07-014444"  
/clone\_lib="Arabidopsis thaliana T-DNA insertions"  
/note="PCR was performed on DNA from Arabidopsis plants (T1) which were transformed with the T-vector pAC161. The lines contain one or more T-insertions. The DNA fragment(s) resulting from were directly sequenced to determine the genomic flanking the insertion. Sequences displaying similarity to the A. thaliana nuclear genome s processed for submission. T-DNA derived sequences removed"

ORIGIN  
Query Match 63.5%; Score 10.8; DB 29; Length 54;  
Best Local Similarity 85.7%; Pred.No. 2.4e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

QY  
47 AGTGAGGATCCCAT 34  
|||||  
|||||

Db  
3 AGTGAGGATCCCAT 16  
|||||  
|||||

RESULT 45  
BM022920  
LOCUS  
DEFINITION  
musculus cdna clone IMAGE:5667979 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus 1 (bases 1 to 55)

REFERENCE  
AUTHORS  
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaest Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Cliff Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blis Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons M., McCann,R., Cole,R., Teagareish Williams,T., Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Ir Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing Washington University Genome Sequencing Center For information

TITLE  
JOURNAL  
COMMENT

ining a clone please contact: Juliana Brown  
 wh@fas.harvard.edu  
 1954305 This sequence now available from the IMAGE consortium,  
 clone orders contact: info@image.llnl.gov.

Location/Qualifiers  
 1. 55  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="ICR"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5667979"  
 /sex="Both for embryonic & newborn, male for adult and  
 adult islet"  
 /dev\_stage="Embryonic day 10.5, E12.5, E16.5, newborn,  
 adult, mixed"  
 /lab\_host="DH10B"  
 /clone\_lib="Melton Normalized Mixed Mouse Pancreas 1  
 N1-MMS1"  
 /note="vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five  
 libraries representing E10.5/12.5 pancreatic bud, E16.5  
 pancreas, newborn pancreas, adult pancreas, and adult  
 islets of Langerhans were separately constructed using  
 SuperScript Plasmid Library kit (Life Technologies). cDNA  
 was made by oligo-dT priming and size-selected by column  
 fractionation. Libraries were amplified once on solid  
 support and plasmid DNA from each library was prepared  
 and mixed in equal amounts. The mixed library DNA was  
 normalized by method #4 from Bonaldo, Lennon, and Soares  
 1996 Genome Research 6:791-806; 0.5 microgram  
 single-stranded mixed library plasmid DNA was mixed with  
 5 micrograms PCR product representing mixed library  
 inserts and hybridized to an EcoT of 6. Single-stranded  
 (unhybridized) plasmids were isolated by hydroxyapatite  
 chromatography and used to make this library."

63.5%; Score 10.8; DB 12; Length 55;  
 ilarity 85.7%; Pred.No. 2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAAGATCCCT 16  
 |||||  
 TGAATATCCCT 55

: February 29, 2004, 11:21:57  
 1 secs